

519
224

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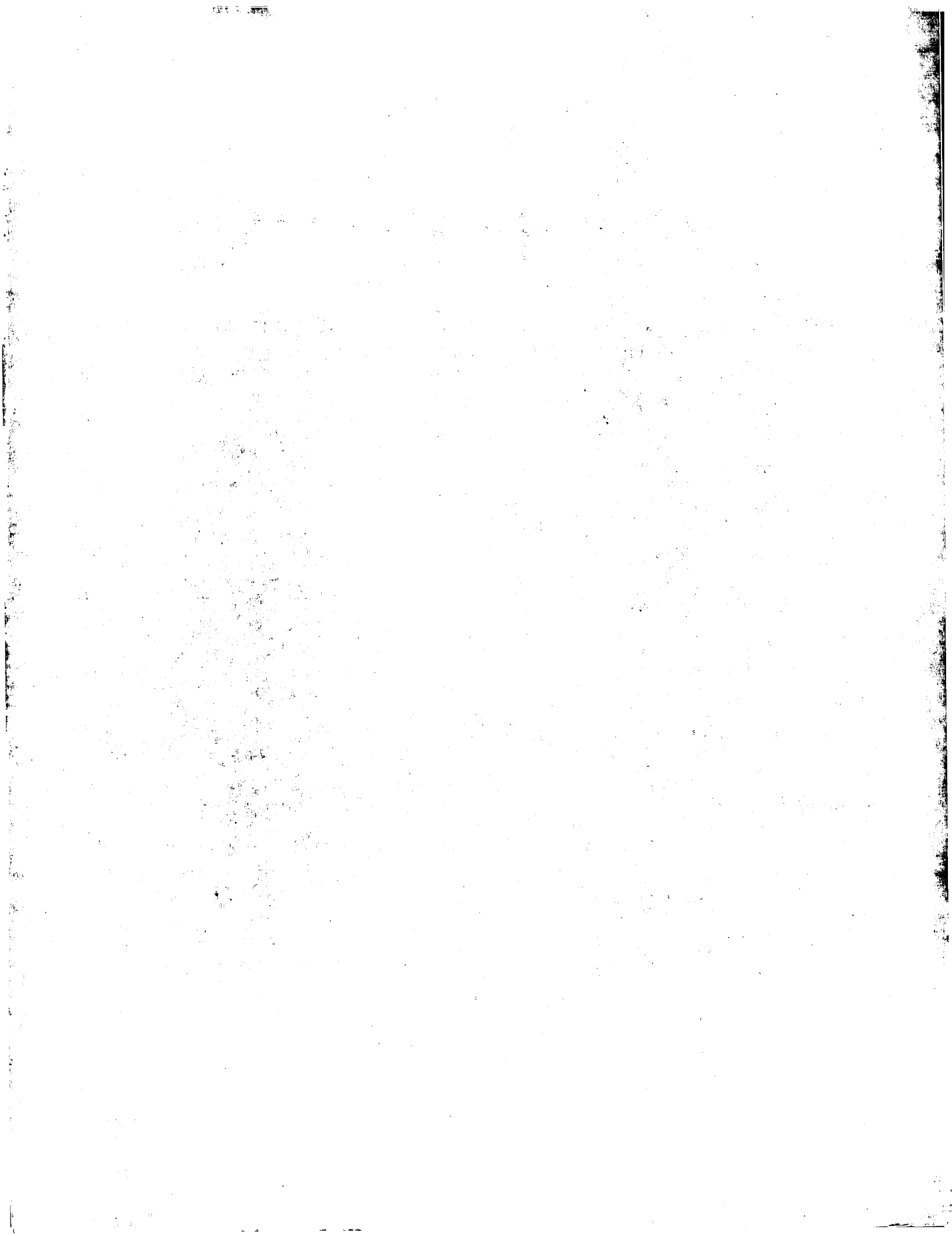
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(54) Title: **NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO HELICOBACTER PYLORI FOR DIAGNOSTICS AND THERAPEUTICS**

(57) Abstract

Recombinant or substantially pure preparations of *H. pylori* polypeptides are described. The nucleic acids encoding the polypeptides also are described. The *H. pylori* polypeptides are useful for diagnostics and vaccine compositions.

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**NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
HELICOBACTER PYLORI FOR DIAGNOSTICS AND THERAPEUTICS**

Background of the Invention

5 *Helicobacter pylori* is a gram-negative, S-shaped, microaerophilic bacterium that was discovered and cultured from a human gastric biopsy specimen. (Warren, J.R. and B. Marshall, (1983) *Lancet* 1: 1273-1275; and Marshall et al., (1984) *Microbios Lett.* 25: 83-88). *H. pylori* has been strongly linked to chronic gastritis and duodenal ulcer disease. (Rathbone et. al., (1986) *Gut* 27: 635-641). Moreover, evidence is accumulating for an
10 etiologic role of *H. pylori* in nonulcer dyspepsia, gastric ulcer disease, and gastric adenocarcinoma. (Blaser M. J., (1993) *Trends Microbiol.* 1: 255-260). Transmission of the bacteria occurs via the oral route, and the risk of infection increases with age. (Taylor, D.N. and M. J. Blaser, (1991) *Epidemiol. Rev* 13: 42-50). *H. pylori* colonizes the human gastric mucosa, establishing an infection that usually persists for decades. Infection by *H.*
15 *pylori* is prevalent worldwide. Developed countries have infection rates over 50% of the adult population, while developing countries have infection rates reaching 90% of the adults over the age of 20. (Hopkins R. J. and J. G. Morris (1994) *Am. J. Med.* 97: 265-277).

 The bacterial factors necessary for colonization of the gastric environment, and for virulence of this pathogen, are poorly understood. Examples of the putative virulence
20 factors include the following: urease, an enzyme that may play a role in neutralizing gastric acid pH (Eaton et al., (1991) *Infect. Immunol.* 59: 2470-2475; Ferrero, R.L. and A. Lee (1991) *Microb. Ecol. Hlth. Dis.* 4: 121-134; Labigne et al., (1991) *J. Bacteriol.* 173: 1920-1931); the bacterial flagellar proteins responsible for motility across the mucous layer. (Hazell et al., (1986) *J. Inf. Dis.* 153: 658-663; Leying et al., (1992) *Mol. Microbiol.* 6:
25 2863-2874; and Haas et al., (1993) *Mol. Microbiol.* 8: 753-760); Vac A, a bacterial toxin that induces the formation of intracellular vacuoles in epithelial cells (Schmitt, W. and R. Haas, (1994) *Molecular Microbiol.* 12(2): 307-319); and several gastric tissue-specific adhesins. (Boren et al., (1993) *Science* 262: 1892-1895; Evans et al., (1993) *J. Bacteriol.* 175: 674-683; and Falk et al., (1993) *Proc. Natl. Acad. Sci. USA* 90: 2035-203).

30 Numerous therapeutic agents are currently available that eradicate *H. pylori* infections *in vitro*. (Huesca et. al., (1993) *Zbl. Bakt.* 280: 244-252; Hopkins, R. J. and J. G. Morris, supra). However, many of these treatments are suboptimally effective *in vivo* because of bacterial resistance, altered drug distribution, patient non-compliance or poor drug availability. (Hopkins, R. J. and J. G. Morris, supra). Treatment with antibiotics
35 combined with bismuth are part of the standard regime used to treat *H. pylori* infection. (Malfertheiner, P. and J. E. Dominguez-Munoz (1993) *Clinical Therapeutics* 15 Supp. B: 37-48). Recently, combinations of a proton pump inhibitors and a single antibiotic have been shown to ameliorate duodenal ulcer disease. (Malfertheiner, P. and J. E. Dominguez-Munoz supra). However, methods employing antibiotic agents can have the problem of the

-2-

emergence of bacterial strains which are resistant to these agents. (Hopkins, R. J. and J. G. Morris, supra). These limitations demonstrate that new more effective methods are needed to combat *H. pylori* infections *in vivo*. In particular, the design of new vaccines that may prevent infection by this bacterium is highly desirable.

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Summary of the Invention

This invention relates to novel genes, e.g., genes encoding polypeptides such as bacterial surface proteins, from the organism *Helicobacter pylori* (*H. pylori*), and other related genes, their products, and uses thereof. The nucleic acids and peptides of the present invention have utility for diagnostic and therapeutics for *H. pylori* and other *Helicobacter* species. They can also be used to detect the presence of *H. pylori* and other *Helicobacter* species in a sample; and for use in screening compounds for the ability to interfere with the *H. pylori* life cycle or to inhibit *H. pylori* infection. More specifically, this invention features compositions of nucleic acids corresponding to entire coding sequences of *H. pylori* proteins, including surface or secreted proteins or parts thereof, nucleic acids capable of binding mRNA from *H. pylori* proteins to block protein translation, and methods for producing *H. pylori* proteins or parts thereof using peptide synthesis and recombinant DNA techniques. This invention also features antibodies and nucleic acids useful as probes to detect *H. pylori* infection. In addition, vaccine compositions and methods for the protection or treatment of infection by *H. pylori* are within the scope of this invention.

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Detailed Description of the Drawings

Figure 1 is a bar graph that depicts the antibody titer in serum of mice following immunization with specific *H. pylori* antigens.

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Figure 2 is a bar graph that depicts the antibody titer in mucous of mice following immunization with specific *H. pylori* antigens.

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Figure 3 is a bar graph that depicts therapeutic immunization of *H. pylori* infected mice with specific antigens dissolved in HEPES buffer.

Figure 4 is a bar graph that depicts therapeutic immunization of *H. pylori* infected mice with specific antigens dissolved in buffer containing DOC.

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Detailed Description of the Invention

In one aspect, the invention features a recombinant or substantially pure preparation of *H. pylori* polypeptide of SEQ ID NO: 384. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide of SEQ ID NO: 384, such nucleic acid

is contained in SEQ ID NO: 1. The *H. pylori* polypeptide sequences of the invention described herein are contained in the Sequence Listing, and the nucleic acids encoding *H. pylori* polypeptides of the invention are contained in the Sequence Listing.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 384 through SEQ ID NO: 389, SEQ ID NO: 391 through SEQ ID NO: 400, SEQ ID NO: 402 through SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 411 through SEQ ID NO: 412, SEQ ID NO: 414 through SEQ ID NO: 430, SEQ ID NO: 432 through SEQ ID NO: 434, SEQ ID NO: 436 through SEQ ID NO: 441, and SEQ ID NO: 443. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 384 through SEQ ID NO: 389, SEQ ID NO: 391 through SEQ ID NO: 400, SEQ ID NO: 402 through SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 411 through SEQ ID NO: 412, SEQ ID NO: 414 through SEQ ID NO: 430, SEQ ID NO: 432 through SEQ ID NO: 434, SEQ ID NO: 436 through SEQ ID NO: 441, and SEQ ID NO: 443, such nucleic acids are contained in SEQ ID NO: 1 through SEQ ID NO: 50.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 444, SEQ ID NO: 446 through SEQ ID NO: 448, SEQ ID NO: 450 through SEQ ID NO: 462, SEQ ID NO: 465 through SEQ ID NO: 466, SEQ ID NO: 468 through SEQ ID NO: 469, SEQ ID NO: 471 through SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 478 through SEQ ID NO: 479, SEQ ID NO: 481 through SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488 through SEQ ID NO: 501, and SEQ ID NO: 503 through SEQ ID NO: 506. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 444, SEQ ID NO: 446 through SEQ ID NO: 448, SEQ ID NO: 450 through SEQ ID NO: 462, SEQ ID NO: 465 through SEQ ID NO: 466, SEQ ID NO: 468 through SEQ ID NO: 469, SEQ ID NO: 471 through SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 478 through SEQ ID NO: 479, SEQ ID NO: 481 through SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488 through SEQ ID NO: 501, and SEQ ID NO: 503 through SEQ ID NO: 506, such nucleic acids are contained in SEQ ID NO: 51 through SEQ ID NO: 100.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 509 through SEQ ID NO: 510, SEQ ID NO: 512 through SEQ ID NO: 514, SEQ ID NO: 516, SEQ ID NO: 518 through SEQ ID NO: 520, SEQ ID NO: 522 through SEQ ID NO: 525, SEQ ID NO: 527 through SEQ ID NO: 533, SEQ ID NO: 535 through SEQ ID NO: 537, SEQ ID NO: 539 through SEQ ID NO: 540, SEQ ID NO: 542 through SEQ ID NO: 544, SEQ ID NO: 546 through SEQ ID NO: 548, SEQ ID NO:

550, SEQ ID NO: 553 through SEQ ID NO: 556, SEQ ID NO: 558, SEQ ID NO: 560, SEQ ID NO: 562 through SEQ ID NO: 568, SEQ ID NO: 570, and SEQ ID NO: 572 through SEQ ID NO: 575. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 509 through SEQ ID NO: 510, SEQ ID NO: 512 through SEQ ID NO: 514, SEQ ID NO: 516, SEQ ID NO: 518 through SEQ ID NO: 520, SEQ ID NO: 522 through SEQ ID NO: 525, SEQ ID NO: 527 through SEQ ID NO: 533, SEQ ID NO: 535 through SEQ ID NO: 537, SEQ ID NO: 539 through SEQ ID NO: 540, SEQ ID NO: 542 through SEQ ID NO: 544, SEQ ID NO: 546 through SEQ ID NO: 548, SEQ ID NO: 550, SEQ ID NO: 553 through SEQ ID NO: 556, SEQ ID NO: 558, SEQ ID NO: 560, SEQ ID NO: 562 through SEQ ID NO: 568, SEQ ID NO: 570, and SEQ ID NO: 572 through SEQ ID NO: 575, such nucleic acids are contained in SEQ ID NO: 101 through SEQ ID NO: 150.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 576 through SEQ ID NO: 579, SEQ ID NO: 581 through SEQ ID NO: 583, SEQ ID NO: 585 through SEQ ID NO: 593, SEQ ID NO: 596 through SEQ ID NO: 614, SEQ ID NO: 617 through SEQ ID NO: 623, SEQ ID NO: 625, SEQ ID NO: 627, SEQ ID NO: 629 through SEQ ID NO: 631, SEQ ID NO: 633, and SEQ ID NO: 635 through SEQ ID NO: 636. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 576 through SEQ ID NO: 579, SEQ ID NO: 581 through SEQ ID NO: 583, SEQ ID NO: 585 through SEQ ID NO: 593, SEQ ID NO: 596 through SEQ ID NO: 614, SEQ ID NO: 617 through SEQ ID NO: 623, SEQ ID NO: 625, SEQ ID NO: 627, SEQ ID NO: 629 through SEQ ID NO: 631, SEQ ID NO: 633, and SEQ ID NO: 635 through SEQ ID NO: 636, such nucleic acids are contained in SEQ ID NO: 151 through SEQ ID NO: 200.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 638 through SEQ ID NO: 640, SEQ ID NO: 642 through SEQ ID NO: 643, SEQ ID NO: 647, SEQ ID NO: 649 through SEQ ID NO: 651, SEQ ID NO: 653 through SEQ ID NO: 661, SEQ ID NO: 663 through SEQ ID NO: 670, SEQ ID NO: 673 through SEQ ID NO: 674, SEQ ID NO: 676, SEQ ID NO: 678 through SEQ ID NO: 683, SEQ ID NO: 687 through SEQ ID NO: 692, and SEQ ID NO: 694 through SEQ ID NO: 702. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 638 through SEQ ID NO: 640, SEQ ID NO: 642 through SEQ ID NO: 643, SEQ ID NO: 647, SEQ ID NO: 649 through SEQ ID NO: 651, SEQ ID NO: 653 through SEQ ID NO: 661, SEQ ID NO: 663 through SEQ ID NO: 670, SEQ ID NO: 673 through SEQ ID NO: 674, SEQ ID NO: 676, SEQ ID NO: 678 through SEQ ID NO: 683, SEQ ID NO: 687

through SEQ ID NO: 692, and SEQ ID NO: 694 through SEQ ID NO: 702, such nucleic acids are contained in SEQ ID NO: 201 through SEQ ID NO: 250.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 705 through SEQ ID NO: 708, SEQ ID NO: 712 through SEQ ID NO: 714, SEQ ID NO: 716 through SEQ ID NO: 722, SEQ ID NO: 725 through SEQ ID NO: 730, SEQ ID NO: 732 through SEQ ID NO: 733, SEQ ID NO: 735 through SEQ ID NO: 744, SEQ ID NO: 746 through SEQ ID NO: 752, SEQ ID NO: 755 through SEQ ID NO: 757, SEQ ID NO: 759, SEQ ID NO: 761 through SEQ ID NO: 763, and SEQ ID NO: 767 through SEQ ID NO: 770. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 705 through SEQ ID NO: 708, SEQ ID NO: 712 through SEQ ID NO: 714, SEQ ID NO: 716 through SEQ ID NO: 722, SEQ ID NO: 725 through SEQ ID NO: 730, SEQ ID NO: 732 through SEQ ID NO: 733, SEQ ID NO: 735 through SEQ ID NO: 744, SEQ ID NO: 746 through SEQ ID NO: 752, SEQ ID NO: 755 through SEQ ID NO: 757, SEQ ID NO: 759, SEQ ID NO: 761 through SEQ ID NO: 763, and SEQ ID NO: 767 through SEQ ID NO: 770, such nucleic acids are contained in SEQ ID NO: 251 through SEQ ID NO: 300.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 771 through SEQ ID NO: 773, SEQ ID NO: 775, SEQ ID NO: 777, SEQ ID NO: 779 through SEQ ID NO: 784, SEQ ID NO: 786 through SEQ ID NO: 787, SEQ ID NO: 789 through SEQ ID NO: 792, SEQ ID NO: 794, SEQ ID NO: 796, SEQ ID NO: 798 through SEQ ID NO: 805, SEQ ID NO: 807 through SEQ ID NO: 811, SEQ ID NO: 813 through SEQ ID NO: 819, SEQ ID NO: 821 through SEQ ID NO: 822, SEQ ID NO: 824 through SEQ ID NO: 826, SEQ ID NO: 828 through SEQ ID NO: 832, and SEQ ID NO: 835. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 771 through SEQ ID NO: 773, SEQ ID NO: 775, SEQ ID NO: 777, SEQ ID NO: 779 through SEQ ID NO: 784, SEQ ID NO: 786 through SEQ ID NO: 787, SEQ ID NO: 789 through SEQ ID NO: 792, SEQ ID NO: 794, SEQ ID NO: 796, SEQ ID NO: 798 through SEQ ID NO: 805, SEQ ID NO: 807 through SEQ ID NO: 811, SEQ ID NO: 813 through SEQ ID NO: 819, SEQ ID NO: 821 through SEQ ID NO: 822, SEQ ID NO: 824 through SEQ ID NO: 826, SEQ ID NO: 828 through SEQ ID NO: 832, and SEQ ID NO: 835, such nucleic acids are contained in SEQ ID NO: 301 through SEQ ID NO: 350.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 836 through SEQ ID NO: 841, SEQ ID NO: 843 through SEQ ID NO: 851, SEQ ID NO: 853, SEQ ID NO: 855 through SEQ ID NO: 857, SEQ ID NO:

-6-

859 through SEQ ID NO: 862, SEQ ID NO: 866, SEQ ID NO: 868 through SEQ ID NO: 871, SEQ ID NO: 873 through SEQ ID NO: 876, and SEQ ID NO: 879. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 836 through SEQ ID NO: 841, SEQ ID NO: 843 through SEQ ID NO: 851, SEQ ID NO: 853, SEQ ID NO: 855 through SEQ ID NO: 857, SEQ ID NO: 859 through SEQ ID NO: 862, SEQ ID NO: 866, SEQ ID NO: 868 through SEQ ID NO: 871, SEQ ID NO: 873 through SEQ ID NO: 876, and SEQ ID NO: 879, such nucleic acids are contained in SEQ ID NO: 351 through SEQ ID NO: 383.

10 In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 385, SEQ ID NO: 390, SEQ ID NO: 401, SEQ ID NO: 407, SEQ ID NO: 409 through SEQ ID NO: 410, SEQ ID NO: 413, SEQ ID NO: 431, SEQ ID NO: 435, SEQ ID NO: 442, SEQ ID NO: 445, SEQ ID NO: 449, SEQ ID NO: 463 through SEQ ID NO: 464, SEQ ID NO: 467, SEQ ID NO: 470, SEQ ID NO: 474, SEQ ID NO: 476 through SEQ ID NO: 477, SEQ ID NO: 480, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 502, SEQ ID NO: 507 through SEQ ID NO: 508, SEQ ID NO: 511, SEQ ID NO: 515, SEQ ID NO: 517, SEQ ID NO: 521, SEQ ID NO: 526, SEQ ID NO: 534, SEQ ID NO: 538, SEQ ID NO: 541, SEQ ID NO: 545, SEQ ID NO: 549, SEQ ID NO: 551 through SEQ ID NO: 552, SEQ ID NO: 557, SEQ ID NO: 559, SEQ ID NO: 561, SEQ ID NO: 569, SEQ ID NO: 571, SEQ ID NO: 580, SEQ ID NO: 584, SEQ ID NO: 594 through SEQ ID NO: 595, SEQ ID NO: 615 through SEQ ID NO: 616, SEQ ID NO: 624, and SEQ ID NO: 626. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 385, SEQ ID NO: 390, SEQ ID NO: 401, SEQ ID NO: 407, SEQ ID NO: 409 through SEQ ID NO: 410, SEQ ID NO: 413, SEQ ID NO: 431, SEQ ID NO: 435, SEQ ID NO: 442, SEQ ID NO: 445, SEQ ID NO: 449, SEQ ID NO: 463 through SEQ ID NO: 464, SEQ ID NO: 467, SEQ ID NO: 470, SEQ ID NO: 474, SEQ ID NO: 476 through SEQ ID NO: 477, SEQ ID NO: 480, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 502, SEQ ID NO: 507 through SEQ ID NO: 508, SEQ ID NO: 511, SEQ ID NO: 515, SEQ ID NO: 517, SEQ ID NO: 521, SEQ ID NO: 526, SEQ ID NO: 534, SEQ ID NO: 538, SEQ ID NO: 541, SEQ ID NO: 545, SEQ ID NO: 549, SEQ ID NO: 551 through SEQ ID NO: 552, SEQ ID NO: 557, SEQ ID NO: 559, SEQ ID NO: 561, SEQ ID NO: 569, SEQ ID NO: 571, SEQ ID NO: 580, SEQ ID NO: 584, SEQ ID NO: 594 through SEQ ID NO: 595, SEQ ID NO: 615 through SEQ ID NO: 616, SEQ ID NO: 624, and SEQ ID NO: 626, such nucleic acids are contained in SEQ ID NO: 881 through SEQ ID NO: 930.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 628, SEQ ID NO: 632, SEQ ID NO: 634, SEQ ID NO: 637,

-7-

SEQ ID NO: 641, SEQ ID NO: 644 through SEQ ID NO: 646, SEQ ID NO: 648, SEQ ID NO: 652, SEQ ID NO: 662, SEQ ID NO: 671 through SEQ ID NO: 672, SEQ ID NO: 675, SEQ ID NO: 677, SEQ ID NO: 684 through SEQ ID NO: 686, SEQ ID NO: 693, SEQ ID NO: 703 through SEQ ID NO: 704, SEQ ID NO: 709 through SEQ ID NO: 711, SEQ ID NO: 715, SEQ ID NO: 723 through SEQ ID NO: 724, SEQ ID NO: 731, SEQ ID NO: 734, SEQ ID NO: 745, SEQ ID NO: 753 through SEQ ID NO: 754, SEQ ID NO: 758, SEQ ID NO: 760, SEQ ID NO: 764 through SEQ ID NO: 766, SEQ ID NO: 774, SEQ ID NO: 776, SEQ ID NO: 778, SEQ ID NO: 785, SEQ ID NO: 788, SEQ ID NO: 793, SEQ ID NO: 795, SEQ ID NO: 797, SEQ ID NO: 806, SEQ ID NO: 812, SEQ ID NO: 820, SEQ ID NO: 823, and SEQ ID NO: 827. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 628, SEQ ID NO: 632, SEQ ID NO: 634, SEQ ID NO: 637, SEQ ID NO: 641, SEQ ID NO: 644 through SEQ ID NO: 646, SEQ ID NO: 648, SEQ ID NO: 652, SEQ ID NO: 662, SEQ ID NO: 671 through SEQ ID NO: 672, SEQ ID NO: 675, SEQ ID NO: 677, SEQ ID NO: 684 through SEQ ID NO: 686, SEQ ID NO: 693, SEQ ID NO: 703 through SEQ ID NO: 704, SEQ ID NO: 709 through SEQ ID NO: 711, SEQ ID NO: 715, SEQ ID NO: 723 through SEQ ID NO: 724, SEQ ID NO: 731, SEQ ID NO: 734, SEQ ID NO: 745, SEQ ID NO: 753 through SEQ ID NO: 754, SEQ ID NO: 758, SEQ ID NO: 760, SEQ ID NO: 764 through SEQ ID NO: 766, SEQ ID NO: 774, SEQ ID NO: 776, SEQ ID NO: 778, SEQ ID NO: 785, SEQ ID NO: 788, SEQ ID NO: 793, SEQ ID NO: 795, SEQ ID NO: 797, SEQ ID NO: 806, SEQ ID NO: 812, SEQ ID NO: 820, SEQ ID NO: 823, and SEQ ID NO: 827, such nucleic acids are contained in SEQ ID NO: 931 through SEQ ID NO: 980.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 833 through SEQ ID NO: 834, SEQ ID NO: 842, SEQ ID NO: 852, SEQ ID NO: 854, SEQ ID NO: 858, SEQ ID NO: 863, SEQ ID NO: 864 through SEQ ID NO: 865, SEQ ID NO: 867, SEQ ID NO: 872, SEQ ID NO: 877 through SEQ ID NO: 878, and SEQ ID NO: 880. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 833 through SEQ ID NO: 834, SEQ ID NO: 842, SEQ ID NO: 852, SEQ ID NO: 854, SEQ ID NO: 858, SEQ ID NO: 863, SEQ ID NO: 864 through SEQ ID NO: 865, SEQ ID NO: 867, SEQ ID NO: 872, SEQ ID NO: 877 through SEQ ID NO: 878, and SEQ ID NO: 880, such nucleic acids are contained in SEQ ID NO: 981 through SEQ ID NO: 994.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 1446 through SEQ ID NO: 1461, SEQ ID NO: 1463, and SEQ ID NO: 1465 through SEQ ID NO: 1495. The invention also includes substantially

pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 1446 through SEQ ID NO: 1461, SEQ ID NO: 1463, and SEQ ID NO: 1465 through SEQ ID NO: 1495, such nucleic acids are contained in SEQ ID NO: 995 through SEQ ID NO: 1010, SEQ ID NO: 1012, and SEQ ID NO: 1014 through SEQ ID NO: 1044.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 1497 through SEQ ID NO: 1515, and SEQ ID NO: 1517 through SEQ ID NO: 1545. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 1497 through SEQ ID NO: 1515, and SEQ ID NO: 1517 through SEQ ID NO: 1545, such nucleic acids are contained in SEQ ID NO: 1046 through SEQ ID NO: 1064, and SEQ ID NO: 1066 through SEQ ID NO: 1094.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 1546 through SEQ ID NO: 1595. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 1546 through SEQ ID NO: 1595, such nucleic acids are contained in SEQ ID NO: 1095 through SEQ ID NO: 1144.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 1596 through SEQ ID NO: 1617, SEQ ID NO: 1620 through SEQ ID NO: 1645. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 1596 through SEQ ID NO: 1617, SEQ ID NO: 1620 through SEQ ID NO: 1645, such nucleic acids are contained in SEQ ID NO: 1145 through SEQ ID NO: 1166, and SEQ ID NO: 1169 through SEQ ID NO: 1194.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 1646 through SEQ ID NO: 1681, and SEQ ID NO: 1683 through SEQ ID NO: 1695. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 1646 through SEQ ID NO: 1681, and SEQ ID NO: 1683 through SEQ ID NO: 1695, such nucleic acids are contained in SEQ ID NO: 1195 through SEQ ID NO: 1230, and SEQ ID NO: 1232 through SEQ ID NO: 1244.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 1696 through SEQ ID NO: 1745. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group

consisting of *H. pylori* polypeptides SEQ ID NO: 1696 through SEQ ID NO: 1745, such nucleic acids are contained in SEQ ID NO: 1245 through SEQ ID NO: 1294.

5 In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 1746 through SEQ ID NO: 1783, and SEQ ID NO: 1786 through SEQ ID NO: 1795. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 1746 through SEQ ID NO: 1783, and SEQ ID NO: 1786 through SEQ ID NO: 1795, such nucleic acids are contained in SEQ ID NO: 1295 through SEQ ID
10 NO: 1332, and SEQ ID NO: 1335 through SEQ ID NO: 1344.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 1796 through SEQ ID NO: 1817, SEQ ID NO: 1819, SEQ ID NO: 1821, SEQ ID NO: 1823 through SEQ ID NO: 1836, and SEQ ID NO: 1838 through
15 SEQ ID NO: 1845. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 1796 through SEQ ID NO: 1817, SEQ ID NO: 1819, SEQ ID NO: 1821, SEQ ID NO: 1823 through SEQ ID NO: 1836, and SEQ ID NO: 1838 through SEQ ID NO: 1845, such nucleic acids are contained in SEQ ID NO: 1345 through SEQ ID NO: 1366, SEQ ID NO: 1368, SEQ ID NO: 1370, SEQ ID NO: 1372 through SEQ ID NO: 1385, and SEQ ID NO: 1387 through SEQ ID NO: 1394.
20

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 1846 through SEQ ID NO: 1896. The invention also includes
25 substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 1846 through SEQ ID NO: 1896, such nucleic acids are contained in SEQ ID NO: 1395 through SEQ ID NO: 1445.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of the invention as set forth in the Sequence Listing. The invention also
30 includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of the invention as set forth in the Sequence Listing. It should be understood that this invention encompasses each of the *H. pylori* polypeptides and nucleic acids encoding such polypeptides as identified in the Sequence
35 Listing by a given sequence identification number. For example, a representative *H. pylori* polypeptide is contained in SEQ ID NO: 1450. Therefore, this invention encompasses a recombinant or substantially pure preparation of an *H. pylori* polypeptide of SEQ ID NO: 1450. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide of SEQ ID NO: 1450.

In another aspect, the invention pertains to any individual *H. pylori* polypeptide member or nucleic acid encoding such member from the above-identified groups of *H. pylori* polypeptides (e.g., SEQ ID NO: 1546 through SEQ ID NO: 1595) or nucleic acids (e.g., SEQ ID NO: 1095-SEQ ID NO: 1144), as well as any subgroups from within the
 5 above-identified groups. Furthermore, the subgroups can preferably consists of 1, 3, 5, 10, 15, 20, 30 or 40 members of any of the groups identified above, as well as any combinations thereof. For example, the group consisting of *H. pylori* polypeptides SEQ ID NO: 1846 through SEQ ID NO: 1896 can be divided into one or more subgroups as follows: SEQ ID NO: 1846-SEQ ID NO: 1860; SEQ ID NO: 1861-SEQ ID NO: 1875;
 10 SEQ ID NO: 1876-SEQ ID NO: 1885; SEQ ID NO: 1886-SEQ ID NO: 1896; or any combinations thereof.

Particularly preferred is an isolated nucleic acid comprising a nucleotide sequence encoding an *H. pylori* cell envelope polypeptide or a fragment thereof. Such nucleic acid is selected from the group consisting of SEQ ID NO: 1020, SEQ ID NO: 1021, SEQ ID NO:
 15 1036, SEQ ID NO: 1050, SEQ ID NO: 1071, SEQ ID NO: 1101, SEQ ID NO: 1135, SEQ ID NO: 1276, SEQ ID NO: 1150, SEQ ID NO: 1187, SEQ ID NO: 1192, SEQ ID NO: 1361, SEQ ID NO: 1379, SEQ ID NO: 1399, SEQ ID NO: 1403, SEQ ID NO: 1400, SEQ ID NO: 1189, SEQ ID NO: 1002, SEQ ID NO: 1213, SEQ ID NO: 1214, SEQ ID NO: 1215, SEQ ID NO: 1234, SEQ ID NO: 1236, SEQ ID NO: 1237, SEQ ID NO: 1224, SEQ
 20 ID NO: 1251, SEQ ID NO: 1262, SEQ ID NO: 1149, SEQ ID NO: 1220, SEQ ID NO: 1240, SEQ ID NO: 1164, SEQ ID NO: 1165, SEQ ID NO: 1404, SEQ ID NO: 1144, SEQ ID NO: 1182, SEQ ID NO: 1157, SEQ ID NO: 1160, SEQ ID NO: 1300, SEQ ID NO: 1321, SEQ ID NO: 1323, SEQ ID NO: 1329, SEQ ID NO: 1332, SEQ ID NO: 1345, SEQ ID NO: 1358, SEQ ID NO: 1375, SEQ ID NO: 1417, SEQ ID NO: 1283, SEQ ID NO:
 25 1335, SEQ ID NO: 1368, SEQ ID NO: 1179, SEQ ID NO: 1255, SEQ ID NO: 1258, SEQ ID NO: 1044, SEQ ID NO: 1273, SEQ ID NO: 1219, SEQ ID NO: 1274, SEQ ID NO: 1210, SEQ ID NO: 1422, SEQ ID NO: 1302, SEQ ID NO: 1308, SEQ ID NO: 1310, SEQ ID NO: 1331, SEQ ID NO: 1432. SEQ ID NO: 1052, SEQ ID NO: 1091, SEQ ID NO: 1421, SEQ ID NO: 1069, SEQ ID NO: 1005, SEQ ID NO: 1007, SEQ ID NO: 1166, SEQ
 30 ID NO: 1177, SEQ ID NO: 1193, SEQ ID NO: 1206, SEQ ID NO: 1207, SEQ ID NO: 1304, SEQ ID NO: 1305, SEQ ID NO: 1346, SEQ ID NO: 1348, SEQ ID NO: 1350, SEQ ID NO: 1032, SEQ ID NO: 1053, SEQ ID NO: 1081, SEQ ID NO: 1124, SEQ ID NO: 1382, SEQ ID NO: 1437, SEQ ID NO: 1263, SEQ ID NO: 1173, SEQ ID NO: 1405, SEQ ID NO: 1406, SEQ ID NO: 1410, SEQ ID NO: 1086, SEQ ID NO: 1322, SEQ ID NO:
 35 1266, SEQ ID NO: 1282, SEQ ID NO: 1271, SEQ ID NO: 1208, SEQ ID NO: 1126, SEQ ID NO: 1270, SEQ ID NO: 1278, SEQ ID NO: 1419, SEQ ID NO: 1125, SEQ ID NO: 1181, SEQ ID NO: 1416, SEQ ID NO: 1096, SEQ ID NO: 1082, SEQ ID NO: 1146, SEQ ID NO: 1145, SEQ ID NO: 1108, SEQ ID NO: 1148, SEQ ID NO: 1337, SEQ ID NO: 1338, SEQ ID NO: 1424, SEQ ID NO: 1000, SEQ ID NO: 1027, SEQ ID NO: 1175, SEQ

ID NO: 1330, SEQ ID NO: 217, SEQ ID NO: 217, SEQ ID NO: 367, SEQ ID NO:
 911, SEQ ID NO: 944, SEQ ID NO: 18, SEQ ID NO: 107, SEQ ID NO: 894, SEQ ID NO:
 943, SEQ ID NO: 203, SEQ ID NO: 85, SEQ ID NO: 290, SEQ ID NO: 5, SEQ ID NO:
 199, SEQ ID NO: 992, SEQ ID NO: 934, SEQ ID NO: 899, SEQ ID NO: 302, SEQ ID
 5 NO: 215, SEQ ID NO: 893, SEQ ID NO: 984, SEQ ID NO: 97, SEQ ID NO: 22, SEQ ID
 NO: 49, SEQ ID NO: 309, SEQ ID NO: 150, SEQ ID NO: 240, SEQ ID NO: 957, SEQ ID
 NO: 57, SEQ ID NO: 2, SEQ ID NO: 92, SEQ ID NO: 255, SEQ ID NO: 164, SEQ ID NO:
 201, SEQ ID NO: 278, SEQ ID NO: 245, SEQ ID NO: 921, SEQ ID NO: 896, SEQ ID
 NO: 248, SEQ ID NO: 159, SEQ ID NO: 979, SEQ ID NO: 194, SEQ ID NO: 194, SEQ
 10 ID NO: 946, SEQ ID NO: 916, SEQ ID NO: 76, SEQ ID NO: 905, SEQ ID NO: 914, SEQ
 ID NO: 931, SEQ ID NO: 50, SEQ ID NO: 250, SEQ ID NO: 969, SEQ ID NO: 66, SEQ
 ID NO: 275, SEQ ID NO: 330, SEQ ID NO: 204, SEQ ID NO: 383, SEQ ID NO: 303,
 SEQ ID NO: 70, SEQ ID NO: 983, SEQ ID NO: 972, SEQ ID NO: 929, SEQ ID NO: 972,
 SEQ ID NO: 936, SEQ ID NO: 267, SEQ ID NO: 197, SEQ ID NO: 55, SEQ ID NO: 54,
 15 SEQ ID NO: 210, SEQ ID NO: 90, SEQ ID NO: 15, SEQ ID NO: 913, SEQ ID NO: 227,
 SEQ ID NO: 79, SEQ ID NO: 191, SEQ ID NO: 238, SEQ ID NO: 274, SEQ ID NO: 27,
 SEQ ID NO: 258, SEQ ID NO: 295, SEQ ID NO: 10, SEQ ID NO: 160, SEQ ID NO: 225,
 SEQ ID NO: 964, SEQ ID NO: 166, SEQ ID NO: 56, SEQ ID NO: 980, SEQ ID NO: 903,
 SEQ ID NO: 261, SEQ ID NO: 71, SEQ ID NO: 955, SEQ ID NO: 361, SEQ ID NO: 58,
 20 SEQ ID NO: 114, SEQ ID NO: 940, SEQ ID NO: 960, SEQ ID NO: 144, SEQ ID NO:
 362, SEQ ID NO: 40, SEQ ID NO: 285, SEQ ID NO: 11, SEQ ID NO: 161, SEQ ID NO:
 974, SEQ ID NO: 111, SEQ ID NO: 316, SEQ ID NO: 257, SEQ ID NO: 78, SEQ ID NO:
 966, SEQ ID NO: 352, SEQ ID NO: 981, SEQ ID NO: 158, SEQ ID NO: 989, SEQ ID
 NO: 963, SEQ ID NO: 48, SEQ ID NO: 68, SEQ ID NO: 135, SEQ ID NO: 910, SEQ ID
 25 NO: 236, SEQ ID NO: 241, SEQ ID NO: 949, SEQ ID NO: 945, SEQ ID NO: 207, SEQ
 ID NO: 977, SEQ ID NO: 978, SEQ ID NO: 994, SEQ ID NO: 163, SEQ ID NO: 256,
 SEQ ID NO: 287, SEQ ID NO: 184, SEQ ID NO: 45, SEQ ID NO: 136, SEQ ID NO: 214,
 SEQ ID NO: 16, SEQ ID NO: 192, SEQ ID NO: 373, SEQ ID NO: 892, SEQ ID NO: 239,
 SEQ ID NO: 34, SEQ ID NO: 340, SEQ ID NO: 41, SEQ ID NO: 332, SEQ ID NO: 134,
 30 and SEQ ID NO: 330.

In one embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is
 an *H. pylori* flagella-associated polypeptide or a fragment thereof encoded by the nucleic
 acid selected from the group consisting of SEQ ID NO: 1020, SEQ ID NO: 1021, SEQ ID
 NO: 1036, SEQ ID NO: 1050, SEQ ID NO: 1071, SEQ ID NO: 1101, SEQ ID NO: 1135,
 35 SEQ ID NO: 1276, SEQ ID NO: 1150, SEQ ID NO: 1187, SEQ ID NO: 1192, SEQ ID
 NO: 1361, SEQ ID NO: 1379, SEQ ID NO: 1399, SEQ ID NO: 1403, SEQ ID NO: 1400,
 SEQ ID NO: 1189, SEQ ID NO: 217, SEQ ID NO: 367, SEQ ID NO: 911, SEQ ID NO:
 944, SEQ ID NO: 18, SEQ ID NO: 107, SEQ ID NO: 894, SEQ ID NO: 943, SEQ ID NO:

-12-

203, SEQ ID NO: 85, SEQ ID NO: 290, SEQ ID NO: 5, SEQ ID NO: 199, SEQ ID NO: 992, SEQ ID NO: 934, SEQ ID NO: 899, SEQ ID NO: 302, and SEQ ID NO: 215.

In another embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* inner membrane polypeptide or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1002, SEQ ID NO: 1213, SEQ ID NO: 1214, SEQ ID NO: 1215, SEQ ID NO: 1234, SEQ ID NO: 1236, SEQ ID NO: 1237, SEQ ID NO: 1224, SEQ ID NO: 1251, SEQ ID NO: 1262, SEQ ID NO: 1149, SEQ ID NO: 1220, SEQ ID NO: 1240, SEQ ID NO: 1164, SEQ ID NO: 1165, SEQ ID NO: 1404, SEQ ID NO: 1144, SEQ ID NO: 1182, SEQ ID NO: 1157, SEQ ID NO: 1160, SEQ ID NO: 1300, SEQ ID NO: 1321, SEQ ID NO: 1323, SEQ ID NO: 1329, SEQ ID NO: 1332, SEQ ID NO: 1345, SEQ ID NO: 1358, SEQ ID NO: 1375, SEQ ID NO: 1417, SEQ ID NO: 1283, SEQ ID NO: 1335, SEQ ID NO: 1368, SEQ ID NO: 1179, SEQ ID NO: 1255, SEQ ID NO: 1258, SEQ ID NO: 1044, SEQ ID NO: 1273, SEQ ID NO: 893, SEQ ID NO: 984, SEQ ID NO: 97, SEQ ID NO: 22, SEQ ID NO: 49, SEQ ID NO: 309, SEQ ID NO: 150, SEQ ID NO: 240, SEQ ID NO: 957, SEQ ID NO: 57, SEQ ID NO: 2, SEQ ID NO: 92, SEQ ID NO: 255, SEQ ID NO: 164, SEQ ID NO: 201, SEQ ID NO: 278, SEQ ID NO: 245, SEQ ID NO: 921, SEQ ID NO: 896, SEQ ID NO: 248, SEQ ID NO: 159, SEQ ID NO: 979, SEQ ID NO: 194, SEQ ID NO: 194, SEQ ID NO: 946, SEQ ID NO: 916, SEQ ID NO: 76, SEQ ID NO: 905, SEQ ID NO: 914, SEQ ID NO: 931, SEQ ID NO: 50, SEQ ID NO: 250, SEQ ID NO: 969, SEQ ID NO: 66, SEQ ID NO: 275, SEQ ID NO: 330, SEQ ID NO: 204, SEQ ID NO: 383, SEQ ID NO: 303, SEQ ID NO: 70, SEQ ID NO: 983, SEQ ID NO: 972, SEQ ID NO: 929, SEQ ID NO: 972, SEQ ID NO: 936, SEQ ID NO: 267, SEQ ID NO: 197, SEQ ID NO: 55, SEQ ID NO: 54, and SEQ ID NO: 210.

In yet another embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* transporter polypeptide or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1219, SEQ ID NO: 1274, SEQ ID NO: 1210, SEQ ID NO: 1422, SEQ ID NO: 1302, SEQ ID NO: 1308, SEQ ID NO: 1310, SEQ ID NO: 1331, SEQ ID NO: 1432, SEQ ID NO: 1052, SEQ ID NO: 1091, SEQ ID NO: 1421, SEQ ID NO: 1069, SEQ ID NO: 1005, SEQ ID NO: 1007, SEQ ID NO: 1166, SEQ ID NO: 1177, SEQ ID NO: 1193, SEQ ID NO: 1206, SEQ ID NO: 1207, SEQ ID NO: 1304, SEQ ID NO: 1305, SEQ ID NO: 1346, SEQ ID NO: 1348, SEQ ID NO: 1350, SEQ ID NO: 1032, SEQ ID NO: 1053, SEQ ID NO: 1081, SEQ ID NO: 1124, SEQ ID NO: 1382, SEQ ID NO: 1437, SEQ ID NO: 1263, SEQ ID NO: 90, SEQ ID NO: 15, SEQ ID NO: 913, SEQ ID NO: 227, SEQ ID NO: 79, SEQ ID NO: 191, SEQ ID NO: 238, SEQ ID NO: 274, SEQ ID NO: 27, SEQ ID NO: 258, SEQ ID NO: 295, SEQ ID NO: 10, SEQ ID NO: 160, SEQ ID NO: 225, SEQ ID NO: 964, SEQ ID NO: 166, SEQ ID NO: 56, SEQ ID NO: 980, SEQ ID NO: 903, SEQ ID NO: 261, SEQ ID NO: 71, SEQ ID NO: 955, SEQ ID NO: 361, SEQ ID NO: 58, SEQ ID NO: 114, SEQ ID NO: 940, SEQ ID NO: 960, SEQ ID NO: 144, SEQ ID NO: 362, SEQ ID NO: 40, SEQ ID NO: 285, SEQ ID NO: 11, SEQ

ID NO: 161, SEQ ID NO: 974, SEQ ID NO: 111, SEQ ID NO: 316, SEQ ID NO: 257, SEQ ID NO: 78, and SEQ ID NO: 966.

In yet a further embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* outer membrane polypeptide or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1173, SEQ ID NO: 1405, SEQ ID NO: 1406, SEQ ID NO: 1410, SEQ ID NO: 1086, SEQ ID NO: 1322, SEQ ID NO: 1266, SEQ ID NO: 1282, SEQ ID NO: 1271, SEQ ID NO: 1208, SEQ ID NO: 1126, SEQ ID NO: 1270, SEQ ID NO: 1278, SEQ ID NO: 1419, SEQ ID NO: 1125, SEQ ID NO: 1181, SEQ ID NO: 1416, SEQ ID NO: 1096, SEQ ID NO: 1082, SEQ ID NO: 1146, SEQ ID NO: 1145, SEQ ID NO: 1108, SEQ ID NO: 1148, SEQ ID NO: 1337, SEQ ID NO: 1338, SEQ ID NO: 1424, SEQ ID NO: 1000, SEQ ID NO: 1027, SEQ ID NO: 1175, SEQ ID NO: 1330, SEQ ID NO: 352, SEQ ID NO: 981, SEQ ID NO: 158, SEQ ID NO: 989, SEQ ID NO: 963, SEQ ID NO: 48, SEQ ID NO: 68, SEQ ID NO: 135, SEQ ID NO: 910, SEQ ID NO: 236, SEQ ID NO: 241, SEQ ID NO: 949, SEQ ID NO: 945, SEQ ID NO: 207, and SEQ ID NO: 977.

Particularly preferred is an isolated nucleic acid comprising a nucleotide sequence encoding an *H. pylori* cytoplasmic polypeptide or a fragment thereof. Such nucleic acid is selected from the group consisting of SEQ ID NO: 1147, SEQ ID NO: 1288, SEQ ID NO: 1324, SEQ ID NO: 1363, SEQ ID NO: 997, SEQ ID NO: 1015, SEQ ID NO: 1084, SEQ ID NO: 1094, SEQ ID NO: 1099, SEQ ID NO: 1229, SEQ ID NO: 1250, SEQ ID NO: 1268, SEQ ID NO: 1293, SEQ ID NO: 1339, SEQ ID NO: 1408, SEQ ID NO: 1429, SEQ ID NO: 1434, SEQ ID NO: 1228, SEQ ID NO: 1031, SEQ ID NO: 1034, SEQ ID NO: 1008, SEQ ID NO: 1061, SEQ ID NO: 1064, SEQ ID NO: 1191, SEQ ID NO: 1217, SEQ ID NO: 1365, SEQ ID NO: 1394, SEQ ID NO: 1414, SEQ ID NO: 1415, SEQ ID NO: 1435, SEQ ID NO: 1058, SEQ ID NO: 1059, SEQ ID NO: 1080, SEQ ID NO: 1128, SEQ ID NO: 1133, SEQ ID NO: 1211, SEQ ID NO: 1252, SEQ ID NO: 1253, SEQ ID NO: 1286, SEQ ID NO: 1289, SEQ ID NO: 1291, SEQ ID NO: 1303, SEQ ID NO: 1396, SEQ ID NO: 996, SEQ ID NO: 1095, SEQ ID NO: 1156, SEQ ID NO: 1158, SEQ ID NO: 1159, SEQ ID NO: 1277, SEQ ID NO: 1038, SEQ ID NO: 1257, SEQ ID NO: 1357, SEQ ID NO: 1436, SEQ ID NO: 1047, SEQ ID NO: 1055, SEQ ID NO: 1141, SEQ ID NO: 1227, SEQ ID NO: 1327, SEQ ID NO: 1412, SEQ ID NO: 1003, SEQ ID NO: 1087, SEQ ID NO: 1116, SEQ ID NO: 1130, SEQ ID NO: 1132, SEQ ID NO: 1185, SEQ ID NO: 1188, SEQ ID NO: 1198, SEQ ID NO: 1218, SEQ ID NO: 1244, SEQ ID NO: 1306, SEQ ID NO: 1325, SEQ ID NO: 1397, SEQ ID NO: 1398, SEQ ID NO: 1407, SEQ ID NO: 1433, SEQ ID NO: 1216, SEQ ID NO: 1239, SEQ ID NO: 1362, SEQ ID NO: 1017, SEQ ID NO: 1019, SEQ ID NO: 1360, SEQ ID NO: 1423, SEQ ID NO: 1425, SEQ ID NO: 1374, SEQ ID NO: 1028, SEQ ID NO: 1037, SEQ ID NO: 1077, SEQ ID NO: 1115, SEQ ID NO: 1232, SEQ ID NO: 1241, SEQ ID NO: 1267, SEQ ID NO: 1163, SEQ ID NO: 1068, SEQ ID NO: 1025, SEQ ID NO: 1042, SEQ ID NO: 1046, SEQ ID NO:

1056, SEQ ID NO: 1039, SEQ ID NO: 1072, SEQ ID NO: 1073, SEQ ID NO: 1092, SEQ ID NO: 1100, SEQ ID NO: 1102, SEQ ID NO: 1103, SEQ ID NO: 1104, SEQ ID NO: 1111, SEQ ID NO: 1119, SEQ ID NO: 1136, SEQ ID NO: 1137, SEQ ID NO: 1140, SEQ ID NO: 1142, SEQ ID NO: 1233, SEQ ID NO: 1238, SEQ ID NO: 1243, SEQ ID NO: 1245, SEQ ID NO: 1247, SEQ ID NO: 1249, SEQ ID NO: 1261, SEQ ID NO: 1269, SEQ ID NO: 1279, SEQ ID NO: 1284, SEQ ID NO: 1290, SEQ ID NO: 1297, SEQ ID NO: 1328, SEQ ID NO: 1370, SEQ ID NO: 1372, SEQ ID NO: 1377, SEQ ID NO: 1383, SEQ ID NO: 1384, SEQ ID NO: 1385, SEQ ID NO: 1388, SEQ ID NO: 1401, SEQ ID NO: 1402, SEQ ID NO: 1418, SEQ ID NO: 1420, SEQ ID NO: 1427, SEQ ID NO: 1070, SEQ ID NO: 1151, SEQ ID NO: 1176, SEQ ID NO: 999, SEQ ID NO: 1006, SEQ ID NO: 1012, SEQ ID NO: 1018, SEQ ID NO: 1030, SEQ ID NO: 1033, SEQ ID NO: 1041, SEQ ID NO: 1049, SEQ ID NO: 1054, SEQ ID NO: 1057, SEQ ID NO: 1090, SEQ ID NO: 1097, SEQ ID NO: 1129, SEQ ID NO: 1139, SEQ ID NO: 1143, SEQ ID NO: 1152, SEQ ID NO: 1153, SEQ ID NO: 1155, SEQ ID NO: 1161, SEQ ID NO: 1162, SEQ ID NO: 1169, SEQ ID NO: 1170, SEQ ID NO: 1171, SEQ ID NO: 1180, SEQ ID NO: 1194, SEQ ID NO: 1195, SEQ ID NO: 1199, SEQ ID NO: 1200, SEQ ID NO: 1201, SEQ ID NO: 1202, SEQ ID NO: 1205, SEQ ID NO: 1312, SEQ ID NO: 1336, SEQ ID NO: 1349, SEQ ID NO: 1355, SEQ ID NO: 1359, SEQ ID NO: 1413, SEQ ID NO: 1426, SEQ ID NO: 1430, SEQ ID NO: 882, SEQ ID NO: 382, SEQ ID NO: 130, SEQ ID NO: 230, SEQ ID NO: 269, SEQ ID NO: 312, SEQ ID NO: 211, SEQ ID NO: 959, SEQ ID NO: 938, SEQ ID NO: 110, SEQ ID NO: 244, SEQ ID NO: 328, SEQ ID NO: 235, SEQ ID NO: 315, SEQ ID NO: 296, SEQ ID NO: 976, SEQ ID NO: 321, SEQ ID NO: 43, SEQ ID NO: 281, SEQ ID NO: 326, SEQ ID NO: 272, SEQ ID NO: 344, SEQ ID NO: 139, SEQ ID NO: 30, SEQ ID NO: 220, SEQ ID NO: 364, SEQ ID NO: 369, SEQ ID NO: 372, SEQ ID NO: 991, SEQ ID NO: 128, SEQ ID NO: 347, SEQ ID NO: 52, SEQ ID NO: 12, SEQ ID NO: 247, SEQ ID NO: 64, SEQ ID NO: 101, SEQ ID NO: 338, SEQ ID NO: 83, SEQ ID NO: 46, SEQ ID NO: 348, SEQ ID NO: 223, SEQ ID NO: 39, SEQ ID NO: 232, SEQ ID NO: 168, SEQ ID NO: 65, SEQ ID NO: 952, SEQ ID NO: 341, SEQ ID NO: 69, SEQ ID NO: 924, SEQ ID NO: 4, SEQ ID NO: 197, SEQ ID NO: 313, SEQ ID NO: 119, SEQ ID NO: 188, SEQ ID NO: 956, SEQ ID NO: 935, SEQ ID NO: 246, SEQ ID NO: 196, SEQ ID NO: 376, SEQ ID NO: 172, SEQ ID NO: 25, SEQ ID NO: 126, SEQ ID NO: 951, SEQ ID NO: 147, SEQ ID NO: 895, SEQ ID NO: 14, SEQ ID NO: 154, SEQ ID NO: 277, SEQ ID NO: 363, SEQ ID NO: 342, SEQ ID NO: 378, SEQ ID NO: 130, SEQ ID NO: 198, SEQ ID NO: 243, SEQ ID NO: 19, SEQ ID NO: 9, SEQ ID NO: 149, SEQ ID NO: 167, SEQ ID NO: 349, SEQ ID NO: 209, SEQ ID NO: 990, SEQ ID NO: 185, SEQ ID NO: 883, SEQ ID NO: 8, SEQ ID NO: 887, SEQ ID NO: 350, SEQ ID NO: 987, SEQ ID NO: 63, SEQ ID NO: 249, SEQ ID NO: 118, SEQ ID NO: 132, SEQ ID NO: 47, SEQ ID NO: 106, SEQ ID NO: 324, SEQ ID NO: 155, SEQ ID NO: 121, SEQ ID NO: 153, SEQ ID NO: 87, SEQ ID NO: 986, SEQ ID NO: 262, SEQ ID NO: 333, SEQ ID NO: 36, SEQ ID NO: 982, SEQ ID

NO: 180, SEQ ID NO: 84, SEQ ID NO: 900, SEQ ID NO: 20, SEQ ID NO: 7, SEQ ID NO: 61, SEQ ID NO: 253, SEQ ID NO: 120, SEQ ID NO: 268, SEQ ID NO: 299, SEQ ID NO: 942, SEQ ID NO: 173, SEQ ID NO: 187, SEQ ID NO: 187, SEQ ID NO: 234, SEQ ID NO: 112, SEQ ID NO: 324, SEQ ID NO: 971, SEQ ID NO: 62, SEQ ID NO: 308, SEQ ID NO: 74, SEQ ID NO: 1, SEQ ID NO: 266, SEQ ID NO: 337, SEQ ID NO: 93, SEQ ID NO: 44, SEQ ID NO: 335, SEQ ID NO: 368, SEQ ID NO: 208, SEQ ID NO: 358, SEQ ID NO: 923, SEQ ID NO: 310, SEQ ID NO: 26, SEQ ID NO: 279, SEQ ID NO: 890, SEQ ID NO: 325, SEQ ID NO: 109, SEQ ID NO: 143, SEQ ID NO: 918, SEQ ID NO: 252, SEQ ID NO: 953, SEQ ID NO: 902, SEQ ID NO: 174, SEQ ID NO: 73, SEQ ID NO: 898, SEQ ID NO: 300, SEQ ID NO: 356, SEQ ID NO: 298, SEQ ID NO: 354, SEQ ID NO: 138, SEQ ID NO: 319, SEQ ID NO: 80, SEQ ID NO: 933, SEQ ID NO: 891, SEQ ID NO: 366, SEQ ID NO: 113, SEQ ID NO: 320, SEQ ID NO: 915, SEQ ID NO: 351, SEQ ID NO: 162, SEQ ID NO: 965, SEQ ID NO: 67, SEQ ID NO: 314, SEQ ID NO: 904, SEQ ID NO: 345, SEQ ID NO: 374, SEQ ID NO: 962, SEQ ID NO: 270, SEQ ID NO: 186, SEQ ID NO: 60, SEQ ID NO: 379, SEQ ID NO: 889, SEQ ID NO: 967, SEQ ID NO: 973, SEQ ID NO: 280, SEQ ID NO: 170, SEQ ID NO: 985, and SEQ ID NO: 932.

In one embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in energy conversion encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1147, SEQ ID NO: 1288, SEQ ID NO: 1324, SEQ ID NO: 1363, SEQ ID NO: 882, SEQ ID NO: 382, SEQ ID NO: 130, and SEQ ID NO: 230.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in amino acid metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 997, SEQ ID NO: 1015, SEQ ID NO: 1084, SEQ ID NO: 1094, SEQ ID NO: 1099, SEQ ID NO: 1229, SEQ ID NO: 1250, SEQ ID NO: 1268, SEQ ID NO: 1293, SEQ ID NO: 1339, SEQ ID NO: 1408, SEQ ID NO: 1429, SEQ ID NO: 1434, SEQ ID NO: 1228, SEQ ID NO: 1031, SEQ ID NO: 1034, SEQ ID NO: 1008, SEQ ID NO: 269, SEQ ID NO: 312, SEQ ID NO: 211, SEQ ID NO: 959, SEQ ID NO: 938, SEQ ID NO: 110, SEQ ID NO: 244, SEQ ID NO: 328, SEQ ID NO: 235, SEQ ID NO: 315, SEQ ID NO: 296, SEQ ID NO: 976, SEQ ID NO: 321, SEQ ID NO: 43, SEQ ID NO: 281, SEQ ID NO: 326, and SEQ ID NO: 272.

In yet another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in nucleotide metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1061, SEQ ID NO: 1064, SEQ ID NO: 1191, SEQ ID NO: 1217, SEQ ID NO: 1365, SEQ ID NO: 1394, SEQ ID NO: 1414, SEQ ID NO: 1415, SEQ ID NO: 1435, SEQ ID NO: 1058, SEQ ID NO: 1059, SEQ ID NO: 344, SEQ ID NO: 139, SEQ ID NO: 30, SEQ ID NO: 220,

SEQ ID NO: 364, SEQ ID NO: 369, SEQ ID NO: 372, SEQ ID NO: 991, SEQ ID NO: 128, SEQ ID NO: 347, and SEQ ID NO: 52.

In yet a further embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in carbohydrate metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1080, SEQ ID NO: 1128, SEQ ID NO: 1133, SEQ ID NO: 1211, SEQ ID NO: 1252, SEQ ID NO: 1253, SEQ ID NO: 1286, SEQ ID NO: 1289, SEQ ID NO: 1291, SEQ ID NO: 1303, SEQ ID NO: 1396, SEQ ID NO: 996, SEQ ID NO: 12, SEQ ID NO: 247, SEQ ID NO: 64, SEQ ID NO: 101, SEQ ID NO: 338, SEQ ID NO: 83, SEQ ID NO: 46, SEQ ID NO: 348, SEQ ID NO: 223, SEQ ID NO: 39, SEQ ID NO: 232, and SEQ ID NO: 168.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in cofactor metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1095, SEQ ID NO: 1156, SEQ ID NO: 1158, SEQ ID NO: 1159, SEQ ID NO: 1277, SEQ ID NO: 1038, SEQ ID NO: 65, SEQ ID NO: 952, SEQ ID NO: 341, SEQ ID NO: 69, SEQ ID NO: 924, and SEQ ID NO: 4.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in lipid metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1257, SEQ ID NO: 1357, SEQ ID NO: 1436, SEQ ID NO: 197, SEQ ID NO: 313, and SEQ ID NO: 119.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in mRNA translation and ribosome biogenesis encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1047, SEQ ID NO: 1055, SEQ ID NO: 1141, SEQ ID NO: 1227, SEQ ID NO: 1327, SEQ ID NO: 1412, SEQ ID NO: 188, SEQ ID NO: 956, SEQ ID NO: 935, SEQ ID NO: 246, SEQ ID NO: 196, and SEQ ID NO: 376.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in genome replication, transcription, recombination and repair encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1003, SEQ ID NO: 1087, SEQ ID NO: 1116, SEQ ID NO: 1130, SEQ ID NO: 1132, SEQ ID NO: 1185, SEQ ID NO: 1188, SEQ ID NO: 1198, SEQ ID NO: 1218, SEQ ID NO: 1244, SEQ ID NO: 1306, SEQ ID NO: 1325, SEQ ID NO: 1397, SEQ ID NO: 1398, SEQ ID NO: 1407, SEQ ID NO: 1433, SEQ ID NO: 172, SEQ ID NO: 25, SEQ ID NO: 126, SEQ ID NO: 951, SEQ ID NO: 147, SEQ ID NO: 895, SEQ ID NO: 14, SEQ ID NO: 154, SEQ ID NO: 277, SEQ ID NO: 363, SEQ ID NO: 342, SEQ ID NO: 378, SEQ ID NO: 130, SEQ ID NO: 198, SEQ ID NO: 243, SEQ ID NO: 19, and SEQ ID NO: 9.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in outer membrane or cell wall

biosynthesis encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1216, SEQ ID NO: 1239, SEQ ID NO: 1362, SEQ ID NO: 1017, SEQ ID NO: 1019, SEQ ID NO: 1360, SEQ ID NO: 149, SEQ ID NO: 167, SEQ ID NO: 349, SEQ ID NO: 209, SEQ ID NO: 990, SEQ ID NO: 185, SEQ ID NO: 883, and SEQ ID NO: 8.

5 In yet another embodiment, the *H. pylori* cytoplasmic polypeptide is an *H. pylori* chaperone polypeptide or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1423, SEQ ID NO: 1425, SEQ ID NO: 1374, SEQ ID NO: 887, SEQ ID NO: 350, and SEQ ID NO: 987.

10 Particularly preferred is an isolated nucleic acid comprising a nucleotide sequence encoding an *H. pylori* secreted or periplasmic polypeptide or a fragment thereof. Such nucleic acid is selected from the group consisting of SEQ ID NO: 1004, SEQ ID NO: 1138, SEQ ID NO: 1067, SEQ ID NO: 1078, SEQ ID NO: 1314, SEQ ID NO: 1319, SEQ ID NO: 1378, SEQ ID NO: 1105, SEQ ID NO: 1114, SEQ ID NO: 1118, SEQ ID NO: 1120, SEQ ID NO: 1123, SEQ ID NO: 1127, SEQ ID NO: 1212, SEQ ID NO: 1223, SEQ ID NO: 1225, SEQ ID NO: 1246, SEQ ID NO: 1248, SEQ ID NO: 1259, SEQ ID NO: 1264, SEQ ID NO: 1265, SEQ ID NO: 1281, SEQ ID NO: 1285, SEQ ID NO: 1294, SEQ ID NO: 1298, SEQ ID NO: 1299, SEQ ID NO: 1315, SEQ ID NO: 1316, SEQ ID NO: 1317, SEQ ID NO: 1318, SEQ ID NO: 1344, SEQ ID NO: 1351, SEQ ID NO: 1353, SEQ ID NO: 1373, SEQ ID NO: 1380, SEQ ID NO: 1387, SEQ ID NO: 1389, SEQ ID NO: 1393, SEQ ID NO: 1411, SEQ ID NO: 1428, SEQ ID NO: 1431, SEQ ID NO: 1439, SEQ ID NO: 1043, SEQ ID NO: 1183, SEQ ID NO: 1184, SEQ ID NO: 1196, SEQ ID NO: 1197, SEQ ID NO: 1203, SEQ ID NO: 995, SEQ ID NO: 998, SEQ ID NO: 1001, SEQ ID NO: 1022, SEQ ID NO: 1023, SEQ ID NO: 1029, SEQ ID NO: 1040, SEQ ID NO: 1051, SEQ ID NO: 1062, SEQ ID NO: 1154, SEQ ID NO: 1320, SEQ ID NO: 1075, SEQ ID NO: 1106, SEQ ID NO: 1109, SEQ ID NO: 1134, SEQ ID NO: 1221, SEQ ID NO: 1226, SEQ ID NO: 1235, SEQ ID NO: 1301, SEQ ID NO: 1311, SEQ ID NO: 1326, SEQ ID NO: 1341, SEQ ID NO: 1354, SEQ ID NO: 1364, SEQ ID NO: 1366, SEQ ID NO: 1376, SEQ ID NO: 1391, SEQ ID NO: 1395, SEQ ID NO: 1445, SEQ ID NO: 1079, SEQ ID NO: 1186, SEQ ID NO: 1010, SEQ ID NO: 1016, SEQ ID NO: 1172, SEQ ID NO: 1174, SEQ ID NO: 117, SEQ ID NO: 254, SEQ ID NO: 24, SEQ ID NO: 242, SEQ ID NO: 950, SEQ ID NO: 263, SEQ ID NO: 286, SEQ ID NO: 947, SEQ ID NO: 51, SEQ ID NO: 177, SEQ ID NO: 156, SEQ ID NO: 190, SEQ ID NO: 375, SEQ ID NO: 222, SEQ ID NO: 21, SEQ ID NO: 912, SEQ ID NO: 148, SEQ ID NO: 202, SEQ ID NO: 224, SEQ ID NO: 112, SEQ ID NO: 32, SEQ ID NO: 339, SEQ ID NO: 182, SEQ ID NO: 228, SEQ ID NO: 152, SEQ ID NO: 219, SEQ ID NO: 137, SEQ ID NO: 318, SEQ ID NO: 141, SEQ ID NO: 165, SEQ ID NO: 334, SEQ ID NO: 13, SEQ ID NO: 297, SEQ ID NO: 35, SEQ ID NO: 216, SEQ ID NO: 908, SEQ ID NO: 124, SEQ ID NO: 75, SEQ ID NO: 927, SEQ ID NO: 221, SEQ ID NO: 178, SEQ ID NO: 169, SEQ ID NO: 293, SEQ ID NO: 289, SEQ ID NO: 926, SEQ ID NO: 948, SEQ ID NO: 115, SEQ ID NO: 251, SEQ ID NO: 345, SEQ

-18-

- ID NO: 17, SEQ ID NO: 920, SEQ ID NO: 95, SEQ ID NO: 86, SEQ ID NO: 360, SEQ ID NO: 271, SEQ ID NO: 970, SEQ ID NO: 288, SEQ ID NO: 282, SEQ ID NO: 98, SEQ ID NO: 29, SEQ ID NO: 317, SEQ ID NO: 343, SEQ ID NO: 291, SEQ ID NO: 108, SEQ ID NO: 377, SEQ ID NO: 305, SEQ ID NO: 305, SEQ ID NO: 100, SEQ ID NO: 988, SEQ ID NO: 212, SEQ ID NO: 884, SEQ ID NO: 37, SEQ ID NO: 968, SEQ ID NO: 975, SEQ ID NO: 237, SEQ ID NO: 335, SEQ ID NO: 260, SEQ ID NO: 370, SEQ ID NO: 91, SEQ ID NO: 276, SEQ ID NO: 311, SEQ ID NO: 173, SEQ ID NO: 102, SEQ ID NO: 304, SEQ ID NO: 380, SEQ ID NO: 127, SEQ ID NO: 993, SEQ ID NO: 925, SEQ ID NO: 181, and SEQ ID NO: 171.
- 10 Particularly preferred is an isolated nucleic acid comprising a nucleotide sequence encoding an *H. pylori* surface or membrane polypeptide or a fragment thereof. Such nucleic acid is selected from the group consisting of SEQ ID NO: 1060, SEQ ID NO: 1110, SEQ ID NO: 1112, SEQ ID NO: 1230, SEQ ID NO: 1260, SEQ ID NO: 1280, SEQ ID NO: 1292, SEQ ID NO: 1296, SEQ ID NO: 1307, SEQ ID NO: 1442, SEQ ID NO: 1444, SEQ ID NO: 1122, SEQ ID NO: 1254, SEQ ID NO: 1256, SEQ ID NO: 1272, SEQ ID NO: 1275, SEQ ID NO: 1309, SEQ ID NO: 1313, SEQ ID NO: 1347, SEQ ID NO: 1352, SEQ ID NO: 1356, SEQ ID NO: 1438, SEQ ID NO: 1441, SEQ ID NO: 1009, SEQ ID NO: 1026, SEQ ID NO: 1048, SEQ ID NO: 1063, SEQ ID NO: 1190, SEQ ID NO: 1083, SEQ ID NO: 1113, SEQ ID NO: 1222, SEQ ID NO: 1295, SEQ ID NO: 1343, SEQ ID NO: 1392, SEQ ID NO: 1443, SEQ ID NO: 1085, SEQ ID NO: 1093, SEQ ID NO: 1117, SEQ ID NO: 1121, SEQ ID NO: 1131, SEQ ID NO: 1287, SEQ ID NO: 1440, SEQ ID NO: 1209, SEQ ID NO: 1342, SEQ ID NO: 1381, SEQ ID NO: 1390, SEQ ID NO: 1409, SEQ ID NO: 1035, SEQ ID NO: 1014, SEQ ID NO: 1088, SEQ ID NO: 1242, SEQ ID NO: 1178, SEQ ID NO: 1089, SEQ ID NO: 1340, SEQ ID NO: 1074, SEQ ID NO: 1107, SEQ ID NO: 1204, SEQ ID NO: 1066, SEQ ID NO: 381, SEQ ID NO: 229, SEQ ID NO: 323, SEQ ID NO: 371, SEQ ID NO: 284, SEQ ID NO: 116, SEQ ID NO: 3, SEQ ID NO: 6, SEQ ID NO: 907, SEQ ID NO: 193, SEQ ID NO: 145, SEQ ID NO: 59, SEQ ID NO: 322, SEQ ID NO: 94, SEQ ID NO: 306, SEQ ID NO: 939, SEQ ID NO: 205, SEQ ID NO: 123, SEQ ID NO: 906, SEQ ID NO: 928, SEQ ID NO: 346, SEQ ID NO: 129, SEQ ID NO: 307, SEQ ID NO: 133, SEQ ID NO: 131, SEQ ID NO: 886, SEQ ID NO: 179, SEQ ID NO: 104, SEQ ID NO: 213, SEQ ID NO: 359, SEQ ID NO: 140, SEQ ID NO: 146, SEQ ID NO: 327, SEQ ID NO: 365, SEQ ID NO: 33, SEQ ID NO: 331, SEQ ID NO: 175, SEQ ID NO: 200, SEQ ID NO: 292, SEQ ID NO: 23, SEQ ID NO: 336, SEQ ID NO: 301, SEQ ID NO: 28, SEQ ID NO: 941, SEQ ID NO: 103, SEQ ID NO: 231, SEQ ID NO: 176, SEQ ID NO: 31, SEQ ID NO: 917, SEQ ID NO: 151, SEQ ID NO: 922, SEQ ID NO: 265, SEQ ID NO: 142, SEQ ID NO: 259, SEQ ID NO: 122, SEQ ID NO: 206, SEQ ID NO: 96, SEQ ID NO: 353, SEQ ID NO: 38, SEQ ID NO: 89, SEQ ID NO: 77, SEQ ID NO: 954, SEQ ID NO: 264, SEQ ID NO: 937, SEQ ID NO: 226, SEQ ID NO: 283, SEQ ID NO: 88,

SEQ ID NO: 125, SEQ ID NO: 183, SEQ ID NO: 195, SEQ ID NO: 81, SEQ ID NO: 901, SEQ ID NO: 82, SEQ ID NO: 42, SEQ ID NO: 881, and SEQ ID NO: 885.

In one embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least one membrane spanning region encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1060, SEQ ID NO: 1110, SEQ ID NO: 1112, SEQ ID NO: 1230, SEQ ID NO: 1260, SEQ ID NO: 1280, SEQ ID NO: 1292, SEQ ID NO: 1296, SEQ ID NO: 1307, SEQ ID NO: 1442, SEQ ID NO: 1444, SEQ ID NO: 381, SEQ ID NO: 229, SEQ ID NO: 323, SEQ ID NO: 371, SEQ ID NO: 284, SEQ ID NO: 116, SEQ ID NO: 3, SEQ ID NO: 6, SEQ ID NO: 907, SEQ ID NO: 193, SEQ ID NO: 145, SEQ ID NO: 59, SEQ ID NO: 322, SEQ ID NO: 94, SEQ ID NO: 306, and SEQ ID NO: 881.

In another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least two membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1122, SEQ ID NO: 1254, SEQ ID NO: 1256, SEQ ID NO: 1272, SEQ ID NO: 1275, SEQ ID NO: 1309, SEQ ID NO: 1313, SEQ ID NO: 1347, SEQ ID NO: 1352, SEQ ID NO: 1356, SEQ ID NO: 1438, SEQ ID NO: 1441, SEQ ID NO: 1009, SEQ ID NO: 1026, SEQ ID NO: 1048, SEQ ID NO: 1063, SEQ ID NO: 1190, SEQ ID NO: 939, SEQ ID NO: 205, SEQ ID NO: 123, SEQ ID NO: 906, SEQ ID NO: 928, SEQ ID NO: 346, SEQ ID NO: 129, SEQ ID NO: 307, SEQ ID NO: 133, SEQ ID NO: 131, SEQ ID NO: 886, SEQ ID NO: 179, SEQ ID NO: 104, SEQ ID NO: 213, SEQ ID NO: 359, SEQ ID NO: 140, SEQ ID NO: 146, SEQ ID NO: 327, and SEQ ID NO: 365.

In yet another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least three membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1083, SEQ ID NO: 1113, SEQ ID NO: 1222, SEQ ID NO: 1295, SEQ ID NO: 1343, SEQ ID NO: 1392, SEQ ID NO: 1443, SEQ ID NO: 33, SEQ ID NO: 331, SEQ ID NO: 175, SEQ ID NO: 200, SEQ ID NO: 292, SEQ ID NO: 23, and SEQ ID NO: 336.

In yet a further embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least four membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1085, SEQ ID NO: 1093, SEQ ID NO: 1117, SEQ ID NO: 1121, SEQ ID NO: 1131, SEQ ID NO: 1287, SEQ ID NO: 1440, SEQ ID NO: 1209, SEQ ID NO: 301, SEQ ID NO: 28, SEQ ID NO: 941, SEQ ID NO: 103, SEQ ID NO: 231, SEQ ID NO: 176, SEQ ID NO: 31, SEQ ID NO: 917, SEQ ID NO: 151, and SEQ ID NO: 922.

In another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least five membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1342, SEQ ID NO: 1381, SEQ ID NO: 1390, SEQ ID NO: 1409, SEQ ID

NO: 1035, SEQ ID NO: 265, SEQ ID NO: 142, SEQ ID NO: 259, SEQ ID NO: 122, SEQ ID NO: 206, and SEQ ID NO: 885.

In another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least six
5 membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1014, SEQ ID NO: 1088, SEQ ID NO: 1242, SEQ ID NO: 1178, SEQ ID NO: 96, SEQ ID NO: 353, SEQ ID NO: 38, SEQ ID NO: 89, SEQ ID NO: 77, SEQ ID NO: 954, SEQ ID NO: 264.

In another embodiment, the *H. pylori* surface or membrane polypeptide or a
10 fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least seven membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1089, SEQ ID NO: 1340, SEQ ID NO: 1074, SEQ ID NO: 1107, SEQ ID NO: 1204, SEQ ID NO: 1066, SEQ ID NO: 937, SEQ ID NO: 226, SEQ ID NO: 283, SEQ ID NO: 88, SEQ ID NO: 125, SEQ ID NO: 183, SEQ ID NO: 195, SEQ ID NO: 81, SEQ
15 ID NO: 901, SEQ ID NO: 82, and SEQ ID NO: 42.

Particularly preferred is a purified or isolated *H. pylori* cell envelope polypeptide or a fragment thereof, wherein the polypeptide is selected from the group consisting of SEQ ID NO: 1471, SEQ ID NO: 1472, SEQ ID NO: 1487, SEQ ID NO: 1501, SEQ ID NO: 1522, SEQ ID NO: 1552, SEQ ID NO: 1586, SEQ ID NO: 1727, SEQ ID NO: 1601, SEQ
20 ID NO: 1638, SEQ ID NO: 1643, SEQ ID NO: 1812, SEQ ID NO: 1830, SEQ ID NO: 1850, SEQ ID NO: 1854, SEQ ID NO: 1851, SEQ ID NO: 1640, SEQ ID NO: 1453, SEQ ID NO: 1664, SEQ ID NO: 1665, SEQ ID NO: 1666, SEQ ID NO: 1685, SEQ ID NO: 1687, SEQ ID NO: 1688, SEQ ID NO: 1675, SEQ ID NO: 1702, SEQ ID NO: 1713, SEQ ID NO: 1600, SEQ ID NO: 1671, SEQ ID NO: 1691, SEQ ID NO: 1615, SEQ ID NO:
25 1616, SEQ ID NO: 1855, SEQ ID NO: 1595, SEQ ID NO: 1633, SEQ ID NO: 1608, SEQ ID NO: 1611, SEQ ID NO: 1751, SEQ ID NO: 1772, SEQ ID NO: 1774, SEQ ID NO: 1780, SEQ ID NO: 1783, SEQ ID NO: 1796, SEQ ID NO: 1809, SEQ ID NO: 1826, SEQ ID NO: 1868, SEQ ID NO: 1734, SEQ ID NO: 1786, SEQ ID NO: 1819, SEQ ID NO: 1630, SEQ ID NO: 1706, SEQ ID NO: 1709, SEQ ID NO: 1495, SEQ ID NO: 1724, SEQ
30 ID NO: 1670, SEQ ID NO: 1725, SEQ ID NO: 1661, SEQ ID NO: 1873, SEQ ID NO: 1753, SEQ ID NO: 1759, SEQ ID NO: 1761, SEQ ID NO: 1782, SEQ ID NO: 1883, SEQ ID NO: 1503, SEQ ID NO: 1542, SEQ ID NO: 1872, SEQ ID NO: 1520, SEQ ID NO: 1456, SEQ ID NO: 1458, SEQ ID NO: 1617, SEQ ID NO: 1628, SEQ ID NO: 1644, SEQ ID NO: 1657, SEQ ID NO: 1658, SEQ ID NO: 1755, SEQ ID NO: 1756, SEQ ID NO:
35 1797, SEQ ID NO: 1799, SEQ ID NO: 1801, SEQ ID NO: 1483, SEQ ID NO: 1504, SEQ ID NO: 1532, SEQ ID NO: 1575, SEQ ID NO: 1833, SEQ ID NO: 1888, SEQ ID NO: 1714, SEQ ID NO: 1624, SEQ ID NO: 1856, SEQ ID NO: 1857, SEQ ID NO: 1861, SEQ ID NO: 1537, SEQ ID NO: 1773, SEQ ID NO: 1717, SEQ ID NO: 1733, SEQ ID NO: 1722, SEQ ID NO: 1659, SEQ ID NO: 1577, SEQ ID NO: 1721, SEQ ID NO: 1729, SEQ

ID NO: 1870, SEQ ID NO: 1576, SEQ ID NO: 1632, SEQ ID NO: 1867, SEQ ID NO: 1547, SEQ ID NO: 1533, SEQ ID NO: 1597, SEQ ID NO: 1596, SEQ ID NO: 1559, SEQ ID NO: 1599, SEQ ID NO: 1788, SEQ ID NO: 1789, SEQ ID NO: 1875, SEQ ID NO: 1451, SEQ ID NO: 1478, SEQ ID NO: 1626, SEQ ID NO: 1781, SEQ ID NO: 660, SEQ ID NO: 660, SEQ ID NO: 855, SEQ ID NO: 534, SEQ ID NO: 675, SEQ ID NO: 404, SEQ ID NO: 518, SEQ ID NO: 464, SEQ ID NO: 672, SEQ ID NO: 640, SEQ ID NO: 490, SEQ ID NO: 755, SEQ ID NO: 389, SEQ ID NO: 635, SEQ ID NO: 877, SEQ ID NO: 637, SEQ ID NO: 477, SEQ ID NO: 772, SEQ ID NO: 658, SEQ ID NO: 463, SEQ ID NO: 852, SEQ ID NO: 503, SEQ ID NO: 411, SEQ ID NO: 441, SEQ ID NO: 782, SEQ ID NO: 575, SEQ ID NO: 691, SEQ ID NO: 724, SEQ ID NO: 452, SEQ ID NO: 386, SEQ ID NO: 497, SEQ ID NO: 712, SEQ ID NO: 591, SEQ ID NO: 638, SEQ ID NO: 740, SEQ ID NO: 697, SEQ ID NO: 569, SEQ ID NO: 470, SEQ ID NO: 700, SEQ ID NO: 586, SEQ ID NO: 823, SEQ ID NO: 627, SEQ ID NO: 627, SEQ ID NO: 684, SEQ ID NO: 551, SEQ ID NO: 478, SEQ ID NO: 508, SEQ ID NO: 545, SEQ ID NO: 628, SEQ ID NO: 443, SEQ ID NO: 702, SEQ ID NO: 776, SEQ ID NO: 461, SEQ ID NO: 737, SEQ ID NO: 809, SEQ ID NO: 642, SEQ ID NO: 879, SEQ ID NO: 773, SEQ ID NO: 468, SEQ ID NO: 842, SEQ ID NO: 788, SEQ ID NO: 624, SEQ ID NO: 788, SEQ ID NO: 644, SEQ ID NO: 727, SEQ ID NO: 631, SEQ ID NO: 450, SEQ ID NO: 448, SEQ ID NO: 653, SEQ ID NO: 495, SEQ ID NO: 400, SEQ ID NO: 541, SEQ ID NO: 673, SEQ ID NO: 482, SEQ ID NO: 622, SEQ ID NO: 689, SEQ ID NO: 736, SEQ ID NO: 417, SEQ ID NO: 716, SEQ ID NO: 762, SEQ ID NO: 395, SEQ ID NO: 587, SEQ ID NO: 669, SEQ ID NO: 758, SEQ ID NO: 593, SEQ ID NO: 451, SEQ ID NO: 827, SEQ ID NO: 502, SEQ ID NO: 719, SEQ ID NO: 469, SEQ ID NO: 715, SEQ ID NO: 847, SEQ ID NO: 453, SEQ ID NO: 527, SEQ ID NO: 652, SEQ ID NO: 745, SEQ ID NO: 567, SEQ ID NO: 848, SEQ ID NO: 430, SEQ ID NO: 748, SEQ ID NO: 396, SEQ ID NO: 588, SEQ ID NO: 795, SEQ ID NO: 523, SEQ ID NO: 791, SEQ ID NO: 714, SEQ ID NO: 481, SEQ ID NO: 765, SEQ ID NO: 837, SEQ ID NO: 833, SEQ ID NO: 585, SEQ ID NO: 865, SEQ ID NO: 764, SEQ ID NO: 440, SEQ ID NO: 465, SEQ ID NO: 555, SEQ ID NO: 526, SEQ ID NO: 687, SEQ ID NO: 692, SEQ ID NO: 693, SEQ ID NO: 677, SEQ ID NO: 649, SEQ ID NO: 812, SEQ ID NO: 820, SEQ ID NO: 880, SEQ ID NO: 590, SEQ ID NO: 713, SEQ ID NO: 750, SEQ ID NO: 613, SEQ ID NO: 437, SEQ ID NO: 556, SEQ ID NO: 657, SEQ ID NO: 402, SEQ ID NO: 623, SEQ ID NO: 862, SEQ ID NO: 449, SEQ ID NO: 690, SEQ ID NO: 424, SEQ ID NO: 821, SEQ ID NO: 432, SEQ ID NO: 811, SEQ ID NO: 554, and SEQ ID NO: 809.

In one embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* flagella-associated polypeptide or a fragment thereof selected from the group consisting of SEQ ID NO: 1471, SEQ ID NO: 1472, SEQ ID NO: 1487, SEQ ID NO: 1501, SEQ ID NO: 1522, SEQ ID NO: 1552, SEQ ID NO: 1586, SEQ ID NO: 1727, SEQ ID NO: 1601, SEQ ID NO: 1638, SEQ ID NO: 1643, SEQ ID NO: 1812, SEQ ID NO: 1830,

-22-

SEQ ID NO: 1850, SEQ ID NO: 1854, SEQ ID NO: 1851, SEQ ID NO: 1640, SEQ ID NO: 660, SEQ ID NO: 660, SEQ ID NO: 855, SEQ ID NO: 534, SEQ ID NO: 675, SEQ ID NO: 404, SEQ ID NO: 518, SEQ ID NO: 464, SEQ ID NO: 672, SEQ ID NO: 640, SEQ ID NO: 490, SEQ ID NO: 755, SEQ ID NO: 389, SEQ ID NO: 635, SEQ ID NO: 877, SEQ ID NO: 637, SEQ ID NO: 477, SEQ ID NO: 772, and SEQ ID NO: 658.

In another embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* inner membrane polypeptide or a fragment thereof selected from the group consisting of SEQ ID NO: 1453, SEQ ID NO: 1664, SEQ ID NO: 1665, SEQ ID NO: 1666, SEQ ID NO: 1685, SEQ ID NO: 1687, SEQ ID NO: 1688, SEQ ID NO: 1675, SEQ ID NO: 1702, SEQ ID NO: 1713, SEQ ID NO: 1600, SEQ ID NO: 1671, SEQ ID NO: 1691, SEQ ID NO: 1615, SEQ ID NO: 1616, SEQ ID NO: 1855, SEQ ID NO: 1595, SEQ ID NO: 1633, SEQ ID NO: 1608, SEQ ID NO: 1611, SEQ ID NO: 1751, SEQ ID NO: 1772, SEQ ID NO: 1774, SEQ ID NO: 1780, SEQ ID NO: 1783, SEQ ID NO: 1796, SEQ ID NO: 1809, SEQ ID NO: 1826, SEQ ID NO: 1868, SEQ ID NO: 1734, SEQ ID NO: 1786, SEQ ID NO: 1819, SEQ ID NO: 1630, SEQ ID NO: 1706, SEQ ID NO: 1709, SEQ ID NO: 1495, SEQ ID NO: 1724, SEQ ID NO: 463, SEQ ID NO: 852, SEQ ID NO: 503, SEQ ID NO: 411, SEQ ID NO: 441, SEQ ID NO: 782, SEQ ID NO: 575, SEQ ID NO: 691, SEQ ID NO: 724, SEQ ID NO: 452, SEQ ID NO: 386, SEQ ID NO: 497, SEQ ID NO: 712, SEQ ID NO: 591, SEQ ID NO: 638, SEQ ID NO: 740, SEQ ID NO: 697, SEQ ID NO: 569, SEQ ID NO: 470, SEQ ID NO: 700, SEQ ID NO: 586, SEQ ID NO: 823, SEQ ID NO: 627, SEQ ID NO: 627, SEQ ID NO: 684, SEQ ID NO: 551, SEQ ID NO: 478, SEQ ID NO: 508, SEQ ID NO: 545, SEQ ID NO: 628, SEQ ID NO: 443, SEQ ID NO: 702, SEQ ID NO: 776, SEQ ID NO: 461, SEQ ID NO: 737, SEQ ID NO: 809, SEQ ID NO: 642, SEQ ID NO: 879, SEQ ID NO: 773, SEQ ID NO: 468, SEQ ID NO: 842, SEQ ID NO: 788, SEQ ID NO: 624, SEQ ID NO: 788, SEQ ID NO: 644, SEQ ID NO: 727, SEQ ID NO: 631, SEQ ID NO: 450, SEQ ID NO: 448, and SEQ ID NO: 653.

In yet another embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* transporter polypeptide or a fragment thereof selected from the group consisting of SEQ ID NO: 1670, SEQ ID NO: 1725, SEQ ID NO: 1661, SEQ ID NO: 1873, SEQ ID NO: 1753, SEQ ID NO: 1759, SEQ ID NO: 1761, SEQ ID NO: 1782, SEQ ID NO: 1883, SEQ ID NO: 1503, SEQ ID NO: 1542, SEQ ID NO: 1872, SEQ ID NO: 1520, SEQ ID NO: 1456, SEQ ID NO: 1458, SEQ ID NO: 1617, SEQ ID NO: 1628, SEQ ID NO: 1644, SEQ ID NO: 1657, SEQ ID NO: 1658, SEQ ID NO: 1755, SEQ ID NO: 1756, SEQ ID NO: 1797, SEQ ID NO: 1799, SEQ ID NO: 1801, SEQ ID NO: 1483, SEQ ID NO: 1504, SEQ ID NO: 1532, SEQ ID NO: 1575, SEQ ID NO: 1833, SEQ ID NO: 1888, SEQ ID NO: 1714, SEQ ID NO: 495, SEQ ID NO: 400, SEQ ID NO: 541, SEQ ID NO: 673, SEQ ID NO: 482, SEQ ID NO: 622, SEQ ID NO: 689, SEQ ID NO: 736, SEQ ID NO: 417, SEQ ID NO: 716, SEQ ID NO: 762, SEQ ID NO: 395, SEQ ID NO: 587, SEQ ID NO: 669, SEQ ID NO: 758, SEQ ID NO: 593, SEQ ID NO: 451, SEQ ID NO: 827,

SEQ ID NO: 502, SEQ ID NO: 719, SEQ ID NO: 469, SEQ ID NO: 715, SEQ ID NO: 847, SEQ ID NO: 453, SEQ ID NO: 527, SEQ ID NO: 652, SEQ ID NO: 745, SEQ ID NO: 567, SEQ ID NO: 848, SEQ ID NO: 430, SEQ ID NO: 748, SEQ ID NO: 396, SEQ ID NO: 588, SEQ ID NO: 795, SEQ ID NO: 523, SEQ ID NO: 791, SEQ ID NO: 714, 5 SEQ ID NO: 481, and SEQ ID NO: 765.

In another embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* outer membrane polypeptide or a fragment thereof selected from the group consisting of SEQ ID NO: 1624, SEQ ID NO: 1856, SEQ ID NO: 1857, SEQ ID NO: 1861, SEQ ID NO: 1537, SEQ ID NO: 1773, SEQ ID NO: 1717, SEQ ID NO: 1733, 10 SEQ ID NO: 1722, SEQ ID NO: 1659, SEQ ID NO: 1577, SEQ ID NO: 1721, SEQ ID NO: 1729, SEQ ID NO: 1870, SEQ ID NO: 1576, SEQ ID NO: 1632, SEQ ID NO: 1867, SEQ ID NO: 1547, SEQ ID NO: 1533, SEQ ID NO: 1597, SEQ ID NO: 1596, SEQ ID NO: 1559, SEQ ID NO: 1599, SEQ ID NO: 1788, SEQ ID NO: 1789, SEQ ID NO: 1875, SEQ ID NO: 1451, SEQ ID NO: 1478, SEQ ID NO: 1626, SEQ ID NO: 1781, SEQ ID NO: 837, SEQ ID NO: 833, SEQ ID NO: 585, SEQ ID NO: 865, SEQ ID NO: 764, SEQ ID NO: 440, SEQ ID NO: 465, SEQ ID NO: 555, SEQ ID NO: 526, SEQ ID NO: 687, 15 SEQ ID NO: 692, SEQ ID NO: 693, SEQ ID NO: 677, SEQ ID NO: 649, and SEQ ID NO: 812.

Particularly preferred is a purified or isolated *H. pylori* cytoplasmic polypeptide or a fragment thereof, wherein the polypeptide is selected from the group consisting of SEQ ID NO: 1598, SEQ ID NO: 1739, SEQ ID NO: 1775, SEQ ID NO: 1814, SEQ ID NO: 1448, SEQ ID NO: 1466, SEQ ID NO: 1535, SEQ ID NO: 1545, SEQ ID NO: 1550, SEQ ID NO: 1680, SEQ ID NO: 1701, SEQ ID NO: 1719, SEQ ID NO: 1744, SEQ ID NO: 1790, SEQ ID NO: 1859, SEQ ID NO: 1880, SEQ ID NO: 1885, SEQ ID NO: 1679, SEQ ID NO: 1482, SEQ ID NO: 1485, SEQ ID NO: 1459, SEQ ID NO: 1512, SEQ ID NO: 1515, 25 SEQ ID NO: 1642, SEQ ID NO: 1668, SEQ ID NO: 1816, SEQ ID NO: 1845, SEQ ID NO: 1865, SEQ ID NO: 1866, SEQ ID NO: 1886, SEQ ID NO: 1509, SEQ ID NO: 1510, SEQ ID NO: 1531, SEQ ID NO: 1579, SEQ ID NO: 1584, SEQ ID NO: 1662, SEQ ID NO: 1703, SEQ ID NO: 1704, SEQ ID NO: 1737, SEQ ID NO: 1740, SEQ ID NO: 1742, SEQ ID NO: 1754, SEQ ID NO: 1847, SEQ ID NO: 1447, SEQ ID NO: 1546, SEQ ID NO: 1607, SEQ ID NO: 1609, SEQ ID NO: 1610, SEQ ID NO: 1728, SEQ ID NO: 1489, SEQ ID NO: 1708, SEQ ID NO: 1808, SEQ ID NO: 1887, SEQ ID NO: 1498, SEQ ID NO: 1506, SEQ ID NO: 1592, SEQ ID NO: 1678, SEQ ID NO: 1778, SEQ ID NO: 1863, SEQ ID NO: 1454, SEQ ID NO: 1538, SEQ ID NO: 1567, SEQ ID NO: 1581, SEQ ID NO: 1583, SEQ ID NO: 1636, SEQ ID NO: 1639, SEQ ID NO: 1649, SEQ ID NO: 1669, 30 SEQ ID NO: 1695, SEQ ID NO: 1757, SEQ ID NO: 1776, SEQ ID NO: 1848, SEQ ID NO: 1849, SEQ ID NO: 1858, SEQ ID NO: 1884, SEQ ID NO: 1667, SEQ ID NO: 1690, SEQ ID NO: 1813, SEQ ID NO: 1468, SEQ ID NO: 1470, SEQ ID NO: 1811, SEQ ID NO: 1874, SEQ ID NO: 1876, SEQ ID NO: 1825, SEQ ID NO: 1479, SEQ ID NO: 1488,

SEQ ID NO: 1528, SEQ ID NO: 1566, SEQ ID NO: 1683, SEQ ID NO: 1692, SEQ ID
NO: 1718, SEQ ID NO: 1614, SEQ ID NO: 1519, SEQ ID NO: 1476, SEQ ID NO: 1493,
SEQ ID NO: 1497, SEQ ID NO: 1507, SEQ ID NO: 1490, SEQ ID NO: 1523, SEQ ID
NO: 1524, SEQ ID NO: 1543, SEQ ID NO: 1551, SEQ ID NO: 1553, SEQ ID NO: 1554,
5 SEQ ID NO: 1555, SEQ ID NO: 1562, SEQ ID NO: 1570, SEQ ID NO: 1587, SEQ ID
NO: 1588, SEQ ID NO: 1591, SEQ ID NO: 1593, SEQ ID NO: 1684, SEQ ID NO: 1689,
SEQ ID NO: 1694, SEQ ID NO: 1696, SEQ ID NO: 1698, SEQ ID NO: 1700, SEQ ID
NO: 1712, SEQ ID NO: 1720, SEQ ID NO: 1730, SEQ ID NO: 1735, SEQ ID NO: 1741,
SEQ ID NO: 1748, SEQ ID NO: 1779, SEQ ID NO: 1821, SEQ ID NO: 1823, SEQ ID
10 NO: 1828, SEQ ID NO: 1834, SEQ ID NO: 1835, SEQ ID NO: 1836, SEQ ID NO: 1839,
SEQ ID NO: 1852, SEQ ID NO: 1853, SEQ ID NO: 1869, SEQ ID NO: 1871, SEQ ID
NO: 1878, SEQ ID NO: 1521, SEQ ID NO: 1602, SEQ ID NO: 1627, SEQ ID NO: 1450,
SEQ ID NO: 1457, SEQ ID NO: 1463, SEQ ID NO: 1469, SEQ ID NO: 1481, SEQ ID
NO: 1484, SEQ ID NO: 1492, SEQ ID NO: 1500, SEQ ID NO: 1505, SEQ ID NO: 1508,
15 SEQ ID NO: 1541, SEQ ID NO: 1548, SEQ ID NO: 1580, SEQ ID NO: 1590, SEQ ID
NO: 1594, SEQ ID NO: 1603, SEQ ID NO: 1604, SEQ ID NO: 1606, SEQ ID NO: 1612,
SEQ ID NO: 1613, SEQ ID NO: 1620, SEQ ID NO: 1621, SEQ ID NO: 1622, SEQ ID
NO: 1631, SEQ ID NO: 1645, SEQ ID NO: 1646, SEQ ID NO: 1650, SEQ ID NO: 1651,
SEQ ID NO: 1652, SEQ ID NO: 1653, SEQ ID NO: 1656, SEQ ID NO: 1763, SEQ ID
20 NO: 1787, SEQ ID NO: 1800, SEQ ID NO: 1806, SEQ ID NO: 1810, SEQ ID NO: 1864,
SEQ ID NO: 1877, SEQ ID NO: 1881, SEQ ID NO: 390, SEQ ID NO: 876, SEQ ID NO:
547, SEQ ID NO: 678, SEQ ID NO: 729, SEQ ID NO: 786, SEQ ID NO: 654, SEQ ID
NO: 734, SEQ ID NO: 646, SEQ ID NO: 522, SEQ ID NO: 696, SEQ ID NO: 807, SEQ
ID NO: 683, SEQ ID NO: 790, SEQ ID NO: 763, SEQ ID NO: 806, SEQ ID NO: 799,
25 SEQ ID NO: 434, SEQ ID NO: 743, SEQ ID NO: 804, SEQ ID NO: 733, SEQ ID NO:
826, SEQ ID NO: 562, SEQ ID NO: 420, SEQ ID NO: 664, SEQ ID NO: 850, SEQ ID
NO: 857, SEQ ID NO: 861, SEQ ID NO: 872, SEQ ID NO: 544, SEQ ID NO: 830, SEQ
ID NO: 446, SEQ ID NO: 397, SEQ ID NO: 699, SEQ ID NO: 459, SEQ ID NO: 509,
SEQ ID NO: 818, SEQ ID NO: 488, SEQ ID NO: 438, SEQ ID NO: 831, SEQ ID NO:
30 667, SEQ ID NO: 429, SEQ ID NO: 680, SEQ ID NO: 597, SEQ ID NO: 460, SEQ ID
NO: 709, SEQ ID NO: 822, SEQ ID NO: 466, SEQ ID NO: 584, SEQ ID NO: 388, SEQ
ID NO: 631, SEQ ID NO: 787, SEQ ID NO: 532, SEQ ID NO: 619, SEQ ID NO: 723,
SEQ ID NO: 641, SEQ ID NO: 698, SEQ ID NO: 630, SEQ ID NO: 869, SEQ ID NO:
601, SEQ ID NO: 415, SEQ ID NO: 542, SEQ ID NO: 704, SEQ ID NO: 572, SEQ ID
35 NO: 467, SEQ ID NO: 399, SEQ ID NO: 579, SEQ ID NO: 739, SEQ ID NO: 849, SEQ
ID NO: 824, SEQ ID NO: 871, SEQ ID NO: 547, SEQ ID NO: 633, SEQ ID NO: 695,
SEQ ID NO: 405, SEQ ID NO: 394, SEQ ID NO: 761, SEQ ID NO: 574, SEQ ID NO:
596, SEQ ID NO: 832, SEQ ID NO: 651, SEQ ID NO: 867, SEQ ID NO: 614, SEQ ID
NO: 401, SEQ ID NO: 393, SEQ ID NO: 413, SEQ ID NO: 835, SEQ ID NO: 863, SEQ

ID NO: 458, SEQ ID NO: 701, SEQ ID NO: 531, SEQ ID NO: 550, SEQ ID NO: 439, SEQ ID NO: 516, SEQ ID NO: 802, SEQ ID NO: 581, SEQ ID NO: 535, SEQ ID NO: 578, SEQ ID NO: 492, SEQ ID NO: 858, SEQ ID NO: 720, SEQ ID NO: 813, SEQ ID NO: 426, SEQ ID NO: 834, SEQ ID NO: 609, SEQ ID NO: 489, SEQ ID NO: 480, SEQ ID NO: 406, SEQ ID NO: 392, SEQ ID NO: 456, SEQ ID NO: 707, SEQ ID NO: 533, SEQ ID NO: 728, SEQ ID NO: 769, SEQ ID NO: 671, SEQ ID NO: 602, SEQ ID NO: 618, SEQ ID NO: 618, SEQ ID NO: 682, SEQ ID NO: 524, SEQ ID NO: 802, SEQ ID NO: 785, SEQ ID NO: 457, SEQ ID NO: 781, SEQ ID NO: 473, SEQ ID NO: 384, SEQ ID NO: 726, SEQ ID NO: 817, SEQ ID NO: 498, SEQ ID NO: 436, SEQ ID NO: 815, SEQ ID NO: 856, SEQ ID NO: 650, SEQ ID NO: 844, SEQ ID NO: 580, SEQ ID NO: 783, SEQ ID NO: 416, SEQ ID NO: 741, SEQ ID NO: 442, SEQ ID NO: 803, SEQ ID NO: 520, SEQ ID NO: 566, SEQ ID NO: 557, SEQ ID NO: 706, SEQ ID NO: 710, SEQ ID NO: 487, SEQ ID NO: 603, SEQ ID NO: 472, SEQ ID NO: 476, SEQ ID NO: 770, SEQ ID NO: 841, SEQ ID NO: 768, SEQ ID NO: 839, SEQ ID NO: 560, SEQ ID NO: 796, SEQ ID NO: 483, SEQ ID NO: 634, SEQ ID NO: 445, SEQ ID NO: 853, SEQ ID NO: 525, SEQ ID NO: 798, SEQ ID NO: 549, SEQ ID NO: 836, SEQ ID NO: 589, SEQ ID NO: 760, SEQ ID NO: 462, SEQ ID NO: 789, SEQ ID NO: 507, SEQ ID NO: 828, SEQ ID NO: 866, SEQ ID NO: 754, SEQ ID NO: 730, SEQ ID NO: 617, SEQ ID NO: 455, SEQ ID NO: 873, SEQ ID NO: 435, SEQ ID NO: 766, SEQ ID NO: 793, SEQ ID NO: 742, SEQ ID NO: 599, SEQ ID NO: 854, and SEQ ID NO: 632.

In one embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in energy conversion selected from the group consisting of SEQ ID NO: 1598, SEQ ID NO: 1739, SEQ ID NO: 1775, SEQ ID NO: 1814, SEQ ID NO: 390, SEQ ID NO: 876, SEQ ID NO: 547, and SEQ ID NO: 678.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in amino acid metabolism selected from the group consisting of SEQ ID NO: 1448, SEQ ID NO: 1466, SEQ ID NO: 1535, SEQ ID NO: 1545, SEQ ID NO: 1550, SEQ ID NO: 1680, SEQ ID NO: 1701, SEQ ID NO: 1719, SEQ ID NO: 1744, SEQ ID NO: 1790, SEQ ID NO: 1859, SEQ ID NO: 1880, SEQ ID NO: 1885, SEQ ID NO: 1679, SEQ ID NO: 1482, SEQ ID NO: 1485, SEQ ID NO: 1459, SEQ ID NO: 729, SEQ ID NO: 786, SEQ ID NO: 654, SEQ ID NO: 734, SEQ ID NO: 646, SEQ ID NO: 522, SEQ ID NO: 696, SEQ ID NO: 807, SEQ ID NO: 683, SEQ ID NO: 790, SEQ ID NO: 763, SEQ ID NO: 806, SEQ ID NO: 799, SEQ ID NO: 434, SEQ ID NO: 743, SEQ ID NO: 804, and SEQ ID NO: 733.

In yet another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in nucleotide metabolism selected from the group consisting of SEQ ID NO: 1512, SEQ ID NO: 1515, SEQ ID NO: 1642, SEQ ID NO: 1668, SEQ ID NO: 1816, SEQ ID NO: 1845, SEQ ID NO: 1865, SEQ ID NO: 1866, SEQ ID NO: 1886, SEQ ID NO: 1509, SEQ ID NO: 1510, SEQ ID NO: 826,

SEQ ID NO: 562, SEQ ID NO: 420, SEQ ID NO: 664, SEQ ID NO: 850, SEQ ID NO: 857, SEQ ID NO: 861, SEQ ID NO: 872, SEQ ID NO: 544, SEQ ID NO: 830, and SEQ ID NO: 446.

In yet a further embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in carbohydrate metabolism selected from the group consisting of SEQ ID NO: 1531, SEQ ID NO: 1579, SEQ ID NO: 1584, SEQ ID NO: 1662, SEQ ID NO: 1703, SEQ ID NO: 1704, SEQ ID NO: 1737, SEQ ID NO: 1740, SEQ ID NO: 1742, SEQ ID NO: 1754, SEQ ID NO: 1847, SEQ ID NO: 1447, SEQ ID NO: 397, SEQ ID NO: 699, SEQ ID NO: 459, SEQ ID NO: 509, SEQ ID NO: 818, SEQ ID NO: 488, SEQ ID NO: 438, SEQ ID NO: 831, SEQ ID NO: 667, SEQ ID NO: 429, SEQ ID NO: 680, and SEQ ID NO: 597.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in cofactor metabolism selected from the group consisting of SEQ ID NO: 1546, SEQ ID NO: 1607, SEQ ID NO: 1609, SEQ ID NO: 1610, SEQ ID NO: 1728, SEQ ID NO: 1489, SEQ ID NO: 460, SEQ ID NO: 709, SEQ ID NO: 822, SEQ ID NO: 466, SEQ ID NO: 584, and SEQ ID NO: 388.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in lipid metabolism selected from the group consisting of SEQ ID NO: 1708, SEQ ID NO: 1808, SEQ ID NO: 1887, SEQ ID NO: 631, SEQ ID NO: 787, and SEQ ID NO: 532.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in mRNA translation and ribosome biogenesis selected from the group consisting of SEQ ID NO: 1498, SEQ ID NO: 1506, SEQ ID NO: 1592, SEQ ID NO: 1678, SEQ ID NO: 1778, SEQ ID NO: 1863, SEQ ID NO: 619, SEQ ID NO: 723, SEQ ID NO: 641, SEQ ID NO: 698, SEQ ID NO: 630, and SEQ ID NO: 869.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in genome replication, transcription, recombination and repair selected from the group consisting of SEQ ID NO: 1454, SEQ ID NO: 1538, SEQ ID NO: 1567, SEQ ID NO: 1581, SEQ ID NO: 1583, SEQ ID NO: 1636, SEQ ID NO: 1639, SEQ ID NO: 1649, SEQ ID NO: 1669, SEQ ID NO: 1695, SEQ ID NO: 1757, SEQ ID NO: 1776, SEQ ID NO: 1848, SEQ ID NO: 1849, SEQ ID NO: 1858, SEQ ID NO: 1884, SEQ ID NO: 601, SEQ ID NO: 415, SEQ ID NO: 542, SEQ ID NO: 704, SEQ ID NO: 572, SEQ ID NO: 467, SEQ ID NO: 399, SEQ ID NO: 579, SEQ ID NO: 739, SEQ ID NO: 849, SEQ ID NO: 824, SEQ ID NO: 871, SEQ ID NO: 547, SEQ ID NO: 633, SEQ ID NO: 695, SEQ ID NO: 405, SEQ ID NO: 394, and SEQ ID NO: 761.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in outer membrane or cell wall

biosynthesis selected from the group consisting of SEQ ID NO: 1667, SEQ ID NO: 1690, SEQ ID NO: 1813, SEQ ID NO: 1468, SEQ ID NO: 1470, SEQ ID NO: 1811, SEQ ID NO: 574, SEQ ID NO: 596, SEQ ID NO: 832, SEQ ID NO: 651, SEQ ID NO: 867, SEQ ID NO: 614, SEQ ID NO: 401, and SEQ ID NO: 393.

- 5 In yet another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* chaperone polypeptide or a fragment thereof selected from the group consisting of SEQ ID NO: 1874, SEQ ID NO: 1876, SEQ ID NO: 1825, SEQ ID NO: 413, SEQ ID NO: 835, and SEQ ID NO: 863.

- 10 Particularly preferred is a purified or isolated *H. pylori* secreted or periplasmic polypeptide or a fragment thereof, wherein the polypeptide is selected from the group consisting of SEQ ID NO: 1455, SEQ ID NO: 1589, SEQ ID NO: 1518, SEQ ID NO: 1529, SEQ ID NO: 1765, SEQ ID NO: 1770, SEQ ID NO: 1829, SEQ ID NO: 1556, SEQ ID NO: 1565, SEQ ID NO: 1569, SEQ ID NO: 1571, SEQ ID NO: 1574, SEQ ID NO: 1578, SEQ ID NO: 1663, SEQ ID NO: 1674, SEQ ID NO: 1676, SEQ ID NO: 1697, SEQ ID NO: 1699, SEQ ID NO: 1710, SEQ ID NO: 1715, SEQ ID NO: 1716, SEQ ID NO: 1732, SEQ ID NO: 1736, SEQ ID NO: 1745, SEQ ID NO: 1749, SEQ ID NO: 1750, SEQ ID NO: 1766, SEQ ID NO: 1767, SEQ ID NO: 1768, SEQ ID NO: 1769, SEQ ID NO: 1795, SEQ ID NO: 1802, SEQ ID NO: 1804, SEQ ID NO: 1824, SEQ ID NO: 1831, SEQ ID NO: 1838, SEQ ID NO: 1840, SEQ ID NO: 1844, SEQ ID NO: 1862, SEQ ID NO: 1879, SEQ ID NO: 1882, SEQ ID NO: 1890, SEQ ID NO: 1494, SEQ ID NO: 1634, SEQ ID NO: 1635, SEQ ID NO: 1647, SEQ ID NO: 1648, SEQ ID NO: 1654, SEQ ID NO: 1446, SEQ ID NO: 1449, SEQ ID NO: 1452, SEQ ID NO: 1473, SEQ ID NO: 1474, SEQ ID NO: 1480, SEQ ID NO: 1491, SEQ ID NO: 1502, SEQ ID NO: 1513, SEQ ID NO: 1605, SEQ ID NO: 1771, SEQ ID NO: 1526, SEQ ID NO: 1557, SEQ ID NO: 1560, SEQ ID NO: 1585, SEQ ID NO: 1672, SEQ ID NO: 1677, SEQ ID NO: 1686, SEQ ID NO: 1752, SEQ ID NO: 1762, SEQ ID NO: 1777, SEQ ID NO: 1792, SEQ ID NO: 1805, SEQ ID NO: 1815, SEQ ID NO: 1817, SEQ ID NO: 1827, SEQ ID NO: 1842, SEQ ID NO: 1846, SEQ ID NO: 1896, SEQ ID NO: 1530, SEQ ID NO: 1637, SEQ ID NO: 1461, SEQ ID NO: 1467, SEQ ID NO: 1623, SEQ ID NO: 1625, SEQ ID NO: 530, SEQ ID NO: 708, SEQ ID NO: 414, SEQ ID NO: 694, SEQ ID NO: 703, SEQ ID NO: 721, SEQ ID NO: 749, SEQ ID NO: 685, SEQ ID NO: 444, SEQ ID NO: 606, SEQ ID NO: 582, SEQ ID NO: 621, SEQ ID NO: 868, SEQ ID NO: 666, SEQ ID NO: 408, SEQ ID NO: 538, SEQ ID NO: 573, SEQ ID NO: 639, SEQ ID NO: 668, SEQ ID NO: 524, SEQ ID NO: 422, SEQ ID NO: 819, SEQ ID NO: 611, SEQ ID NO: 674, SEQ ID NO: 577, SEQ ID NO: 663, SEQ ID NO: 558, SEQ ID NO: 794, SEQ ID NO: 564, SEQ ID NO: 592, SEQ ID NO: 814, SEQ ID NO: 398, SEQ ID NO: 767, SEQ ID NO: 425, SEQ ID NO: 659, SEQ ID NO: 517, SEQ ID NO: 539, SEQ ID NO: 475, SEQ ID NO: 615, SEQ ID NO: 665, SEQ ID NO: 607, SEQ ID NO: 598, SEQ ID NO: 759, SEQ ID NO: 752, SEQ ID NO: 595, SEQ ID NO: 686, SEQ ID NO: 528, SEQ ID NO: 705, SEQ ID NO: 828, SEQ ID

-28-

NO: 403, SEQ ID NO: 561, SEQ ID NO: 500, SEQ ID NO: 491, SEQ ID NO: 846, SEQ ID NO: 732, SEQ ID NO: 778, SEQ ID NO: 751, SEQ ID NO: 744, SEQ ID NO: 504, SEQ ID NO: 419, SEQ ID NO: 792, SEQ ID NO: 825, SEQ ID NO: 756, SEQ ID NO: 519, SEQ ID NO: 870, SEQ ID NO: 777, SEQ ID NO: 808, SEQ ID NO: 506, SEQ ID NO: 864, SEQ ID NO: 655, SEQ ID NO: 407, SEQ ID NO: 427, SEQ ID NO: 774, SEQ ID NO: 797, SEQ ID NO: 688, SEQ ID NO: 815, SEQ ID NO: 718, SEQ ID NO: 859, SEQ ID NO: 775, SEQ ID NO: 874, SEQ ID NO: 543, SEQ ID NO: 878, SEQ ID NO: 594, SEQ ID NO: 610, and SEQ ID NO: 600.

Particularly preferred is a purified or isolated *H. pylori* surface or membrane polypeptide or a fragment thereof, wherein the polypeptide is selected from the group consisting of SEQ ID NO: 1511, SEQ ID NO: 1561, SEQ ID NO: 1563, SEQ ID NO: 1681, SEQ ID NO: 1711, SEQ ID NO: 1731, SEQ ID NO: 1743, SEQ ID NO: 1747, SEQ ID NO: 1758, SEQ ID NO: 1893, SEQ ID NO: 1895, SEQ ID NO: 1573, SEQ ID NO: 1705, SEQ ID NO: 1707, SEQ ID NO: 1723, SEQ ID NO: 1726, SEQ ID NO: 1760, SEQ ID NO: 1764, SEQ ID NO: 1798, SEQ ID NO: 1803, SEQ ID NO: 1807, SEQ ID NO: 1889, SEQ ID NO: 1892, SEQ ID NO: 1460, SEQ ID NO: 1477, SEQ ID NO: 1499, SEQ ID NO: 1514, SEQ ID NO: 1641, SEQ ID NO: 1534, SEQ ID NO: 1564, SEQ ID NO: 1673, SEQ ID NO: 1746, SEQ ID NO: 1794, SEQ ID NO: 1843, SEQ ID NO: 1894, SEQ ID NO: 1536, SEQ ID NO: 1544, SEQ ID NO: 1568, SEQ ID NO: 1572, SEQ ID NO: 1582, SEQ ID NO: 1738, SEQ ID NO: 1891, SEQ ID NO: 1660, SEQ ID NO: 1793, SEQ ID NO: 1832, SEQ ID NO: 1841, SEQ ID NO: 1860, SEQ ID NO: 1486, SEQ ID NO: 1465, SEQ ID NO: 1539, SEQ ID NO: 1693, SEQ ID NO: 1629, SEQ ID NO: 1540, SEQ ID NO: 1791, SEQ ID NO: 1525, SEQ ID NO: 1558, SEQ ID NO: 1655, SEQ ID NO: 1517, SEQ ID NO: 875, SEQ ID NO: 676, SEQ ID NO: 801, SEQ ID NO: 860, SEQ ID NO: 747, SEQ ID NO: 529, SEQ ID NO: 387, SEQ ID NO: 391, SEQ ID NO: 515, SEQ ID NO: 625, SEQ ID NO: 568, SEQ ID NO: 454, SEQ ID NO: 800, SEQ ID NO: 499, SEQ ID NO: 779, SEQ ID NO: 648, SEQ ID NO: 643, SEQ ID NO: 537, SEQ ID NO: 511, SEQ ID NO: 616, SEQ ID NO: 829, SEQ ID NO: 546, SEQ ID NO: 780, SEQ ID NO: 553, SEQ ID NO: 549, SEQ ID NO: 410, SEQ ID NO: 608, SEQ ID NO: 513, SEQ ID NO: 656, SEQ ID NO: 845, SEQ ID NO: 563, SEQ ID NO: 570, SEQ ID NO: 805, SEQ ID NO: 851, SEQ ID NO: 423, SEQ ID NO: 810, SEQ ID NO: 604, SEQ ID NO: 636, SEQ ID NO: 757, SEQ ID NO: 412, SEQ ID NO: 816, SEQ ID NO: 771, SEQ ID NO: 418, SEQ ID NO: 662, SEQ ID NO: 512, SEQ ID NO: 679, SEQ ID NO: 605, SEQ ID NO: 421, SEQ ID NO: 552, SEQ ID NO: 576, SEQ ID NO: 571, SEQ ID NO: 725, SEQ ID NO: 565, SEQ ID NO: 717, SEQ ID NO: 536, SEQ ID NO: 647, SEQ ID NO: 501, SEQ ID NO: 838, SEQ ID NO: 428, SEQ ID NO: 494, SEQ ID NO: 479, SEQ ID NO: 711, SEQ ID NO: 722, SEQ ID NO: 645, SEQ ID NO: 670, SEQ ID NO: 746, SEQ ID NO: 493, SEQ ID NO: 540, SEQ ID NO: 612, SEQ ID NO: 629, SEQ ID NO: 484, SEQ ID NO: 485, SEQ ID NO: 486, SEQ ID NO: 433, SEQ ID NO: 385, and SEQ ID NO: 409.

In one embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least one membrane spanning region selected from the group consisting of SEQ ID NO: 1511, SEQ ID NO: 1561, SEQ ID NO: 1563, SEQ ID NO: 1681, SEQ ID NO: 1711, SEQ ID NO: 1731, SEQ ID NO: 1743, SEQ ID NO: 1747, SEQ ID NO: 1758, SEQ ID NO: 1893, SEQ ID NO: 1895, SEQ ID NO: 875, SEQ ID NO: 676, SEQ ID NO: 801, SEQ ID NO: 860, SEQ ID NO: 747, SEQ ID NO: 529, SEQ ID NO: 387, SEQ ID NO: 391, SEQ ID NO: 515, SEQ ID NO: 625, SEQ ID NO: 568, SEQ ID NO: 454, SEQ ID NO: 800, SEQ ID NO: 499, SEQ ID NO: 779, and SEQ ID NO: 385.

In another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least two membrane spanning regions selected from the group consisting of SEQ ID NO: 1573, SEQ ID NO: 1705, SEQ ID NO: 1707, SEQ ID NO: 1723, SEQ ID NO: 1726, SEQ ID NO: 1760, SEQ ID NO: 1764, SEQ ID NO: 1798, SEQ ID NO: 1803, SEQ ID NO: 1807, SEQ ID NO: 1889, SEQ ID NO: 1892, SEQ ID NO: 1460, SEQ ID NO: 1477, SEQ ID NO: 1499, SEQ ID NO: 1514, SEQ ID NO: 1641, SEQ ID NO: 648, SEQ ID NO: 643, SEQ ID NO: 537, SEQ ID NO: 511, SEQ ID NO: 616, SEQ ID NO: 829, SEQ ID NO: 546, SEQ ID NO: 780, SEQ ID NO: 553, SEQ ID NO: 549, SEQ ID NO: 410, SEQ ID NO: 608, SEQ ID NO: 513, SEQ ID NO: 656, SEQ ID NO: 845, SEQ ID NO: 563, SEQ ID NO: 570, SEQ ID NO: 805, and SEQ ID NO: 851.

In yet another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least three membrane spanning regions selected from the group consisting of SEQ ID NO: 1534, SEQ ID NO: 1564, SEQ ID NO: 1673, SEQ ID NO: 1746, SEQ ID NO: 1794, SEQ ID NO: 1843, SEQ ID NO: 1894, SEQ ID NO: 423, SEQ ID NO: 810, SEQ ID NO: 604, SEQ ID NO: 636, SEQ ID NO: 757, SEQ ID NO: 412, and SEQ ID NO: 816.

In yet a further embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least four membrane spanning regions selected from the group consisting of SEQ ID NO: 1536, SEQ ID NO: 1544, SEQ ID NO: 1568, SEQ ID NO: 1572, SEQ ID NO: 1582, SEQ ID NO: 1738, SEQ ID NO: 1891, SEQ ID NO: 1660, SEQ ID NO: 771, SEQ ID NO: 418, SEQ ID NO: 662, SEQ ID NO: 512, SEQ ID NO: 679, SEQ ID NO: 605, SEQ ID NO: 421, SEQ ID NO: 552, SEQ ID NO: 576, SEQ ID NO: 571.

In another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least five membrane spanning regions selected from the group consisting of SEQ ID NO: 1793, SEQ ID NO: 1832, SEQ ID NO: 1841, SEQ ID NO: 1860, SEQ ID NO: 1486, SEQ ID NO: 725, SEQ ID NO: 565, SEQ ID NO: 717, SEQ ID NO: 536, SEQ ID NO: 647, and SEQ ID NO: 409.

In another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least six membrane spanning regions selected from the group consisting of SEQ ID NO: 1465, SEQ ID NO: 1539, SEQ ID NO: 1693, SEQ ID NO: 1629, SEQ ID NO: 501, SEQ ID NO: 838, SEQ ID NO: 428, SEQ ID NO: 494, SEQ ID NO: 479, SEQ ID NO: 711, and SEQ ID NO: 722.

In yet another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least seven membrane spanning regions selected from the group consisting of SEQ ID NO: 1540, SEQ ID NO: 1791, SEQ ID NO: 1525, SEQ ID NO: 1558, SEQ ID NO: 1655, SEQ ID NO: 1517, SEQ ID NO: 645, SEQ ID NO: 670, SEQ ID NO: 746, SEQ ID NO: 493, SEQ ID NO: 540, SEQ ID NO: 612, SEQ ID NO: 629, SEQ ID NO: 484, SEQ ID NO: 485, SEQ ID NO: 486, and SEQ ID NO: 433.

In another aspect, the invention pertains to any individual *H. pylori* polypeptide member or nucleic acid encoding such a member from the above-identified groups of *H. pylori* polypeptides.

In another aspect, the invention features nucleic acids capable of binding mRNA of *H. pylori*. Such nucleic acid is capable of acting as antisense nucleic acid to control the translation of mRNA of *H. pylori*. A further aspect features a nucleic acid which is capable of binding specifically to an *H. pylori* nucleic acid. These nucleic acids are also referred to herein as complements and have utility as probes and as capture reagents.

In another aspect, the invention features an expression system comprising an open reading frame corresponding to *H. pylori* nucleic acid. The nucleic acid further comprises a control sequence compatible with an intended host. The expression system is useful for making polypeptides corresponding to *H. pylori* nucleic acid.

In another aspect, the invention features a cell transformed with the expression system to produce *H. pylori* polypeptides.

In another aspect, the invention features a method of generating antibodies against *H. pylori* polypeptides which are capable of binding specifically to *H. pylori* polypeptides. Such antibodies have utility as reagents for immunoassays to evaluate the abundance and distribution of *H. pylori*-specific antigens.

In another aspect, the invention features a method of generating vaccines for immunizing an individual against *H. pylori*. The method includes: immunizing a subject with an *H. pylori* polypeptide, e.g., a surface or secreted polypeptide, or active portion thereof, and a pharmaceutically acceptable carrier. Such vaccines have therapeutic and prophylactic utilities.

In another aspect, the invention provides a method for generating a vaccine comprising a modified immunogenic *H. pylori* polypeptide, e.g., a surface or secreted polypeptide, or active portion thereof, and a pharmacologically acceptable carrier.

In another aspect, the invention features a method of evaluating a compound, e.g. a polypeptide, e.g., a fragment of a host cell polypeptide, for the ability to bind an *H. pylori* polypeptide. The method includes: contacting the candidate compound with an *H. pylori* polypeptide and determining if the compound binds or otherwise interacts with an *H. pylori* polypeptide. Compounds which bind *H. pylori* are candidates as activators or inhibitors of the bacterial life cycle. These assays can be performed *in vitro* or *in vivo*.

In another aspect, the invention features a method of evaluating a compound, e.g. a polypeptide, e.g., a fragment of a host cell polypeptide, for the ability to bind an *H. pylori* nucleic acid, e.g., DNA or RNA. The method includes: contacting the candidate compound with an *H. pylori* nucleic acid and determining if the compound binds or otherwise interacts with an *H. pylori* polypeptide. Compounds which bind *H. pylori* are candidates as activators or inhibitors of the bacterial life cycle. These assays can be performed *in vitro* or *in vivo*.

The invention features *H. pylori* polypeptides, preferably a substantially pure preparation of an *H. pylori* polypeptide, or a recombinant *H. pylori* polypeptide. In preferred embodiments: the polypeptide has biological activity; the polypeptide has an amino acid sequence at least 60%, 70%, 80%, 90%, 95%, 98%, or 99% identical to an amino acid sequence of the invention contained in the Sequence Listing, preferably it has about 65% sequence identity with an amino acid sequence of the invention contained in the Sequence Listing, and most preferably it has about 92% to about 99% sequence identity with an amino acid sequence of the invention contained in the Sequence Listing; the polypeptide has an amino acid sequence essentially the same as an amino acid sequence of the invention contained in the Sequence Listing; the polypeptide is at least 5, 10, 20, 50, 100, or 150 amino acid residues in length; the polypeptide includes at least 5, preferably at least 10, more preferably at least 20, more preferably at least 50, 100, or 150 contiguous amino acid residues of the invention contained in the Sequence Listing. In yet another preferred embodiment, the amino acid sequence which differs in sequence identity by about 7% to about 8% from the *H. pylori* amino acid sequences of the invention contained in the Sequence Listing is also encompassed by the invention.

In preferred embodiments: the *H. pylori* polypeptide is encoded by a nucleic acid of the invention contained in the Sequence Listing, or by a nucleic acid having at least 60%, 70%, 80%, 90%, 95%, 98%, or 99% homology with a nucleic acid of the invention contained in the Sequence Listing.

In a preferred embodiment, the subject *H. pylori* polypeptide differs in amino acid sequence at 1, 2, 3, 5, 10 or more residues from a sequence of the invention contained in the Sequence Listing. The differences, however, are such that the *H. pylori* polypeptide exhibits an *H. pylori* biological activity, e.g., the *H. pylori* polypeptide retains a biological activity of a naturally occurring *H. pylori* enzyme.

-32-

In preferred embodiments, the polypeptide includes all or a fragment of an amino acid sequence of the invention contained in the Sequence Listing; fused, in reading frame, to additional amino acid residues, preferably to residues encoded by genomic DNA 5' or 3' to the genomic DNA which encodes a sequence of the invention contained in the Sequence Listing.

In yet other preferred embodiments, the *H. pylori* polypeptide is a recombinant fusion protein having a first *H. pylori* polypeptide portion and a second polypeptide portion, e.g., a second polypeptide portion having an amino acid sequence unrelated to *H. pylori*. The second polypeptide portion can be, e.g., any of glutathione-S-transferase, a DNA binding domain, or a polymerase activating domain. In preferred embodiment the fusion protein can be used in a two-hybrid assay.

Polypeptides of the invention include those which arise as a result of alternative transcription events, alternative RNA splicing events, and alternative translational and postranslational events.

The invention also encompasses an immunogenic component which includes an *H. pylori* polypeptide in an immunogenic preparation; the immunogenic component being capable of eliciting an immune response specific for the *H. pylori* polypeptide, e.g., a humoral response, an antibody response, or a cellular response. In preferred embodiments, the immunogenic component comprises at least one antigenic determinant from a polypeptide of the invention contained in the Sequence Listing.

In another aspect, the invention provides a substantially pure nucleic acid having a nucleotide sequence which encodes an *H. pylori* polypeptide. In preferred embodiments: the encoded polypeptide has biological activity; the encoded polypeptide has an amino acid sequence at least 60%, 70%, 80%, 90%, 95%, 98%, or 99% homologous to an amino acid sequence of the invention contained in the Sequence Listing; the encoded polypeptide has an amino acid sequence essentially the same as an amino acid sequence of the invention contained in the Sequence Listing; the encoded polypeptide is at least 5, 10, 20, 50, 100, or 150 amino acids in length; the encoded polypeptide comprises at least 5, preferably at least 10, more preferably at least 20, more preferably at least 50, 100, or 150 contiguous amino acids of the invention contained in the Sequence Listing.

In preferred embodiments: the nucleic acid of the invention is that contained in the Sequence Listing; the nucleic acid is at least 60%, 70%, 80%, 90%, 95%, 98%, or 99% homologous with a nucleic acid sequence of the invention contained in the Sequence Listing.

In a preferred embodiment, the encoded *H. pylori* polypeptide differs (e.g., by amino acid substitution, addition or deletion of at least one amino acid residue) in amino acid sequence at 1, 2, 3, 5, 10 or more residues, from a sequence of the invention contained in the Sequence Listing. The differences, however, are such that: the *H. pylori* encoded

polypeptide exhibits a *H. pylori* biological activity, e.g., the encoded *H. pylori* enzyme retains a biological activity of a naturally occurring *H. pylori*.

5 In preferred embodiments, the encoded polypeptide includes all or a fragment of an amino acid sequence of the invention contained in the Sequence Listing; fused, in reading frame, to additional amino acid residues, preferably to residues encoded by genomic DNA 5' or 3' to the genomic DNA which encodes a sequence of the invention contained in the Sequence Listing.

10 In preferred embodiments, the subject *H. pylori* nucleic acid will include a transcriptional regulatory sequence, e.g. at least one of a transcriptional promoter or transcriptional enhancer sequence, operably linked to the *H. pylori* gene sequence, e.g., to render the *H. pylori* gene sequence suitable for expression in a recombinant host cell.

15 In yet a further preferred embodiment, the nucleic acid which encodes an *H. pylori* polypeptide of the invention, hybridizes under stringent conditions to a nucleic acid probe corresponding to at least 8 consecutive nucleotides of the invention contained in the Sequence Listing; more preferably to at least 12 consecutive nucleotides of the invention contained in the Sequence Listing; more preferably to at least 20 consecutive nucleotides of the invention contained in the Sequence Listing; more preferably to at least 40 consecutive nucleotides of the invention contained in the Sequence Listing.

20 In a preferred embodiment, the nucleic acid encodes a peptide which differs by at least one amino acid residue from the sequences of the invention contained in the Sequence Listing.

In a preferred embodiment, the nucleic acid differs by at least one nucleotide from a nucleotide sequence of the invention contained in the Sequence Listing which encodes amino acids of the invention contained in the Sequence Listing.

25 In another aspect, the invention encompasses: a vector including a nucleic acid which encodes an *H. pylori* polypeptide or an *H. pylori* polypeptide variant as described herein; a host cell transfected with the vector; and a method of producing a recombinant *H. pylori* polypeptide or *H. pylori* polypeptide variant; including culturing the cell, e.g., in a cell culture medium, and isolating the *H. pylori* or *H. pylori* polypeptide variant, e.g., from the cell or from the cell culture medium.

30 In another aspect, the invention features, a purified recombinant nucleic acid having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, or 99% homology with a sequence of the invention contained in the Sequence Listing.

35 The invention also provides a probe or primer which includes a substantially purified oligonucleotide. The oligonucleotide includes a region of nucleotide sequence which hybridizes under stringent conditions to at least 10 consecutive nucleotides of sense or antisense sequence of the invention contained in the Sequence Listing, or naturally occurring mutants thereof. In preferred embodiments, the probe or primer further includes a label group attached thereto. The label group can be, e.g., a radioisotope, a fluorescent

compound, an enzyme, and/or an enzyme co-factor. Preferably the oligonucleotide is at least 10 and less than 20, 30, 50, 100, or 150 nucleotides in length.

The invention further provides nucleic acids, e.g., RNA or DNA, encoding a polypeptide of the invention. This includes double stranded nucleic acids as well as coding and antisense single strands.

The *H. pylori* strain, from which genomic sequences have been sequenced, has been deposited in the American Type Culture Collection(ATCC # 55679) as strain HP-J99.

Included in the invention are: allelic variations; natural mutants; induced mutants; proteins encoded by DNA that hybridizes under high or low stringency conditions to a nucleic acid which encodes a polypeptide of the invention contained in the Sequence Listing (for definitions of high and low stringency see Current Protocols in Molecular Biology, John Wiley & Sons, New York, 1989, 6.3.1 - 6.3.6, hereby incorporated by reference); and, polypeptides specifically bound by antisera to *H. pylori* polypeptides, especially by antisera to an active site or binding domain of *H. pylori* polypeptide. The invention also includes fragments, preferably biologically active fragments. These and other polypeptides are also referred to herein as *H. pylori* polypeptide analogs or variants.

Putative functions have been determined for several of the *H. pylori* polypeptides of the invention, as shown in Table 1.

Accordingly, uses of the claimed *H. pylori* polypeptides in these identified functions are also within the scope of the invention.

In addition, the present invention encompasses *H. pylori* polypeptides characterized as shown in Table 1 below, including: *H. pylori* cell envelope proteins, *H. pylori* periplasmic/secreted proteins, *H. pylori* cytoplasmic proteins, and other *H. pylori* surface and membrane proteins. Members of these groups were identified by BLAST homology searches and by searches for secretion signal or transmembrane protein motifs. (Polypeptides in the same row of Table 1, i.e., rows 1 and 3, or rows 2 and 4, are related to one another as described in Table 3 below.)

TABLE 1

TABLE OF FUNCTIONAL GROUPS					
ORF Name	nt	aa	ORF Name	nt	aa
	SeqID	SeqID		SeqID	SeqID
	#	#		#	#
Row	1	2		3	4
A. CELL ENVELOPE					
A.1. Flagella-associated					
01gp10401orf1	1020	1471	26588588.aa	217	660
01gp10401orf5	1021	1472	26588588.aa	217	660
02ae11612orf21	1036	1487	6288949.aa	367	855
02ce10213orf7	1050	1501	22692187.aa	911	534
02ge20116orf34	1071	1522	29454837.aa	944	675
04ge11713orf5	1101	1552	1171928.aa	18	404
04ge11713orf5	1101	1552	21699087.aa	107	518
05ep20322orf11	1135	1586	16219090.aa	894	464
12ge20305orf11	1276	1727	29298130.aa	943	672
06cp20302orf12	1150	1601	25525277.aa	203	640
07ge20415orf27	1187	1638	19557055.aa	85	490
07ge20415orf27	1187	1638	36111066.aa	290	755
07ge31107orf2	1192	1643	104792.aa	5	389
29zp10241orf6	1361	1812	24882763.aa	199	635
hp2el0911orf5	1379	1830	917152.aa	992	877
hp3el1122orf1	1399	1850	25478375.aa	934	637
hp3el1168orf2	1403	1854	16984442.aa	899	477
hpe11122orf5	1400	1851	3942217.aa	302	772
07ge20415orf34	1189	1640	26380318.aa	215	658
A.2. Inner membrane proteins					
01cel11016orf1	1002	1453			
09ap11406orf14	1213	1664	16131887.aa	893	463
09ap11406orf15	1214	1665	6093906.aa	984	852
09ap11406orf5	1215	1666	2082012.aa	97	503
11cel1603orf16	1234	1685	1204418.aa	22	411
11cel1603orf16	1234	1685	14455461.aa	49	441
11cel1603orf25	1236	1687	4035783.aa	309	782
11cel1603orf6	1237	1688	23915877.aa	150	575
09cp10502orf22	1224	1675	30730068.aa	240	691
09cp10502orf22	1224	1675	3385833.aa	957	724
11gp10904orf29	1251	1702	14713512.aa	57	452
12ap10324orf2	1262	1713	10353192.aa	2	386
06cp20302orf10	1149	1600	203192.aa	92	497
09ap20802orf5	1220	1671	32704686.aa	255	712
11gel0309orf14	1240	1691	24222885.aa	164	591
11gel0309orf14	1240	1691	2548562.aa	201	638
06gp10409orf7	1164	1615	34666680.aa	278	740
06gp10409orf8	1165	1616	3203142.aa	245	697

-36-

hp3e11168orf29	1404	1855	23853165.aa	921	569
06cp11118orf6	1144	1595	16412593.aa	896	470
06cp11118orf6	1144	1595	32236462.aa	248	700
07ee20513orf28	1182	1633	24132293.aa	159	586
07ee20513orf28	1182	1633	486075.aa	979	823
06ep10306orf12	1157	1608	24651083.aa	194	627
06ep10306orf3	1160	1611	24651083.aa	194	627
06ep10306orf3	1160	1611	30089217.aa	946	684
13ep12003orf20	1300	1751	23493756.aa	916	551
14ge10705orf11	1321	1772	17086587.aa	76	478
14ge10705orf11	1321	1772	21486677.aa	905	508
14ge10705orf11	1321	1772	23468781.aa	914	545
14ge10705orf11	1321	1772	24708129.aa	931	628
14gp11820orf13	1323	1774	14494077.aa	50	443
14gp11820orf13	1323	1774	3242337.aa	250	702
14gp11820orf13	1323	1774	3962777.aa	969	776
14gp12015orf12	1329	1780	15824052.aa	66	461
14gp12015orf12	1329	1780	34489543.aa	275	737
14gp12015orf16	1332	1783	4698838.aa	330	809
27ze10351orf17	1345	1796	25605166.aa	204	642
29zp10241orf14	1358	1809	9776562.aa	383	879
hplp13947orf2	1375	1826	3953143.aa	303	773
hp4p11352orf4	1417	1868	16406265.aa	70	468
13ap11517orf20	1283	1734	5267037.aa	983	842
16ae10113orf1	1335	1786	423131.aa	972	788
hplp13922orf22	1368	1819	24611590.aa	929	624
07ee11620orf2	1179	1630	423131.aa	972	788
12ae10622orf9	1255	1706	259665.aa	936	644
12ae10622orf9	1255	1706	34097707.aa	267	727
12ae11404orf15	1258	1709	24806290.aa	197	631
02ce10213orf14	1044	1495	14645905.aa	55	450
12ge10305orf15	1273	1724	14642202.aa	54	448
01xe21717orf18	1024	1475	26261040.aa	210	653
A.3. Transporters					
09ap20802orf27	1219	1670	20032561.aa	90	495
12ge10305orf16	1274	1725	11132778.aa	15	400
09ae11601orf14	1210	1661	23439633.aa	913	541
09ae11601orf14	1210	1661	29302003.aa	227	673
hp5e11726orf7	1422	1873	179677.aa	79	482
14ce11113orf1	1302	1753	24609593.aa	191	622
14cp10119orf12	1308	1759	30662792.aa	238	689
14cp10119orf15	1310	1761	34427317.aa	274	736
14gp12015orf14	1331	1782	12617677.aa	27	417
hp5e15440orf16	1432	1883	33203192.aa	258	716
hp5e15440orf16	1432	1883	36573502.aa	295	762
02ce11022orf7	1052	1503	1071890.aa	10	395
04ep10811orf4	1091	1542	24215.aa	160	587

-37-

04ep10811orf4	1091	1542	289711.aa	225	669
hp5e11726orf4	1421	1872	36203402.aa	964	758
02ge20116orf28	1069	1520	24238762.aa	166	593
01ce11513orf21	1005	1456	1464715.aa	56	451
01ce11513orf21	1005	1456	4882763.aa	980	827
01ce11618orf10	1007	1458	207817.aa	903	502
06gp11202orf7	1166	1617	33399142.aa	261	719
07cp21714orf13	1177	1628	16406581.aa	71	469
07gp11807orf25	1193	1644	3319687.aa	955	715
07gp11807orf8	1206	1657	5875152.aa	361	847
07gp11807orf9	1207	1658	14714687.aa	58	453
14ce20219orf1	1304	1755	22441050.aa	114	527
14ce20219orf2	1305	1756	26258562.aa	940	652
27ze10351orf18	1346	1797	35345228.aa	960	745
27ze10351orf24	1348	1799	23728388.aa	144	567
27ze10351orf29	1350	1801	5878208.aa	362	848
02ae11611orf11	1032	1483	13726562.aa	40	430
02ae11611orf11	1032	1483	35428912.aa	285	748
02ce11022orf8	1053	1504	10723412.aa	11	396
02ce11022orf8	1053	1504	24218968.aa	161	588
02ce11022orf8	1053	1504	4455467.aa	974	795
03ee11215orf29	1081	1532	22265691.aa	111	523
05cp11911orf41	1124	1575	4338438.aa	316	791
hp2p10625orf28	1382	1833	32952.aa	257	714
hp5p15641orf12	1437	1888	17787558.aa	78	481
12ap10324orf3	1263	1714	3906712.aa	966	765
A.4. Outer membrane proteins					
07ap80601orf8	1173	1624	5083193.aa	352	837
hp3e11168orf30	1405	1856	4960952.aa	981	833
hp3p10156orf12	1406	1857	24104558.aa	158	585
hp4e13394orf2	1410	1861	7116626.aa	989	865
04ce11617orf2	1086	1537	36126938.aa	963	764
14ge10705orf5	1322	1773	1431462.aa	48	440
14ge10705orf5	1322	1773	16225006.aa	68	465
12ap10324orf7	1266	1717	23531562.aa	135	555
13ae10712orf9	1282	1733	22379952.aa	910	526
12ge10305orf1	1271	1722	30478562.aa	236	687
12ge10305orf1	1271	1722	31250333.aa	241	692
07gp31516orf4	1208	1659	31262.aa	949	693
05cp20518orf33	1126	1577	29479681.aa	945	677
12ap11614orf8	1270	1721	26054702.aa	207	649
12ge20305orf2	1278	1729	4721061.aa	977	812
A.5. Other cell envelope proteins					
hp4p11352orf9	1419	1870	4821082.aa	978	820
05cp20518orf3	1125	1576	978477.aa	994	880
07ee20513orf14	1181	1632	24220627.aa	163	590
hp4p11352orf2	1416	1867	32705252.aa	256	713

-38-

hp4p11352orf2	1416	1867	35445843.aa	287	750
04ge11713orf11	1096	1547	24427340.aa	184	613
03ee11215orf30	1082	1533	1416312.aa	45	437
06cp11722orf15	1146	1597	23535937.aa	136	556
06cp11722orf15	1146	1597	26366312.aa	214	657
06cp11722orf12	1145	1596	114505.aa	16	402
05ae20220orf32	1108	1559	2461062.aa	192	623
06cp11722orf21	1148	1599	6828218.aa	373	862
16ae10508orf13	1337	1788	14642217.aa	892	449
16ae10508orf14	1338	1789	30703183.aa	239	690
hp5e12982orf14	1424	1875	1365943.aa	34	424
01ae22001orf2	1000	1451	4826401.aa	340	821
01xe21717orf5	1027	1478	1385937.aa	41	432
01xe21717orf5	1027	1478	4714375.aa	332	811
07ce10203orf22	1175	1626	23526667.aa	134	554
14gp12015orf13	1330	1781	4698838.aa	330	809
B. CYTOPLASAMIC PROTEINS					
B.1. Proteins involved in energy conversion					
06cp11722orf16	1147	1598	10553192.aa	882	390
13ee10216orf55	1288	1739	914087.aa	382	876
14gp11820orf20	1324	1775	23475342.aa	130	547
hplp11244orf7	1363	1814	29500075.aa	230	678
B.2. Proteins involved in amino acid metabolism					
01ae12021orf1	997	1448	34109763.aa	269	729
01ee11621orf6	1015	1466	4177212.aa	312	786
03ge31106orf1	1084	1535	26301059.aa	211	654
04ep71403orf15	1094	1545	34194093.aa	959	734
04ge11713orf37	1099	1550	25992137.aa	938	646
09gp10903orf3	1229	1680	21976637.aa	110	522
11gp10904orf27	1250	1701	31681556.aa	244	696
12ap11614orf4	1268	1719	45914063.aa	328	807
13ee12016orf10	1293	1744	30082267.aa	235	683
16ae10508orf21	1339	1790	429192.aa	315	790
hp3p10349orf16	1408	1859	36594167.aa	296	763
hp5e15211orf22	1429	1880	4578469.aa	976	806
hp5e15440orf19	1434	1885	4492217.aa	321	799
09cp10713orf29	1228	1679	1408.aa	43	434
02ae11611orf1	1031	1482	35269000.aa	281	743
02ae11612orf13	1034	1485	4570262.aa	326	804
01ce11618orf18	1008	1459	34189716.aa	272	733
B.3. Proteins involved in nucleotide metabolism					
02cp20821orf10	1061	1512	4882652.aa	344	826
02ep30607orf10	1064	1515	23598962.aa	139	562
07ge20415orf6	1191	1642	12897656.aa	30	420
09ap20802orf1	1217	1668	2738378.aa	220	664
hplp13852orf5	1365	1816	598933.aa	364	850
hp3e11024orf24	1394	1845	6517040.aa	369	857

-39-

hp4e14535orf3	1414	1865	677088.aa	372	861
hp4e14535orf4	1415	1866	867183.aa	991	872
hp5e15440orf21	1435	1886	23442642.aa	128	544
02cp11822orf22	1058	1509	4895327.aa	347	830
02cp11822orf26	1059	1510	14574201.aa	52	446
B.4. Proteins involved in carbohydrate metabolism					
03ee11215orf26	1080	1531	10737627.aa	12	397
05cp20518orf5	1128	1579	32144532.aa	247	699
05cp20518orf64	1133	1584	15807794.aa	64	459
09ae11601orf3	1211	1662	2149041.aa	101	509
11gp11422orf1	1252	1703	4787562.aa	338	818
11gp11422orf2	1253	1704	19541302.aa	83	488
13ee10216orf43	1286	1737	14257751.aa	46	438
13ee10216orf56	1289	1740	4897177.aa	348	831
13ee10216orf9	1291	1742	2855006.aa	223	667
14ce11519orf2	1303	1754	13723593.aa	39	429
hp3e11060orf11	1396	1847	29557266.aa	232	680
01ae11421orf1	996	1447	24300682.aa	168	597
B.5. Proteins involved in cofactor metabolism					
04ge10816orf2	1095	1546	1581937.aa	65	460
06ee10709orf5	1156	1607	3261306.aa	952	709
06ep10306orf13	1158	1609	485375.aa	341	822
06ep10306orf14	1159	1610	16251627.aa	69	466
12ge20305orf14	1277	1728	24089437.aa	924	584
02ae11612orf26	1038	1489	10407625.aa	4	388
B.6. Proteins involved in lipid metabolism					
12ae11404orf14	1257	1708	24806290.aa	197	631
29zp10241orf11	1357	1808	422937.aa	313	787
hp5e15440orf22	1436	1887	22667967.aa	119	532
B.7. Proteins involved in mRNA translation and ribosome biogenesis					
02ce10213orf2	1047	1498	24500088.aa	188	619
02cp11404orf11	1055	1506	33601578.aa	956	723
06ce10515orf4	1141	1592	25595387.aa	935	641
09cp10713orf28	1227	1678	32036462.aa	246	698
14gp11820orf5	1327	1778	24803280.aa	196	630
hp4e14522orf11	1412	1863	785437.aa	376	869
B.8. Proteins involved in genome replication, transcription, recombination& repair					
01ce11016orf14	1003	1454	24396937.aa	172	601
04ce11617orf27	1087	1538	12520952.aa	25	415
05ap11505orf1	1116	1567	23440814.aa	126	542
05cp20518orf56	1130	1581	32431687.aa	951	704
05cp20518orf63	1132	1583	23880087.aa	147	572
07ge11504orf4	1185	1636	16305252.aa	895	467
07ge20415orf30	1188	1639	10745275.aa	14	399
07gp11807orf35	1198	1649	24036302.aa	154	579

-40-

09ap20802orf22	1218	1669	34574062.aa	277	739
09ap20802orf22	1218	1669	5879160.aa	363	849
11ge10309orf51	1244	1695	487750.aa	342	824
14ce21516orf1	1306	1757	85786.aa	378	871
14gp11820orf27	1325	1776	23475342.aa	130	547
hp3e11060orf2	1397	1848	24818802.aa	198	633
hp3e11060orf9	1398	1849	3166040.aa	243	695
hp3p10156orf8	1407	1858	11719687.aa	19	405
hp5e15440orf18	1433	1884	10677187.aa	9	394
hp5e15440orf18	1433	1884	36523442.aa		761
B.9. Proteins involved in outer membrane or					
cell wall biosynthesis					
09ap11406orf8	1216	1667	23912807.aa	149	574
09ap11406orf8	1216	1667	24298127.aa	167	596
11ep12011orf9	1239	1690	495312.aa	349	832
29zp10241orf7	1362	1813	26197187.aa	209	651
01ep30520orf16	1017	1468	7225666.aa	990	867
01ep30520orf27	1019	1470	24441412.aa	185	614
01ep30520orf27	1019	1470	11253.aa	883	401
29zp10241orf4	1360	1811	10675632.aa	8	393
B.10. Chaperones					
hp5e12982orf13	1423	1874	12343763.aa	887	413
hp5e15211orf10	1425	1876	50253.aa	350	835
hplp13947orf1	1374	1825	6845425.aa	987	863
B.11 Other cytoplasmic proteins					
01xe21717orf9	1028	1479	156587.aa	63	458
02ae11612orf25	1037	1488	32422343.aa	249	701
03ee11215orf10	1077	1528	22542803.aa	118	531
05ae20220orf99	1115	1566	23492181.aa	132	550
11ce10917orf14	1232	1683	14313885.aa	47	439
11ge10309orf15	1241	1692	21647676.aa	106	516
12ap11614orf2	1267	1718	4562712.aa	324	802
06ge10115orf15	1163	1614	24070250.aa	155	581
02ge20116orf22	1068	1519	22704567.aa	121	535
02ge20116orf22	1068	1519	24003758.aa	153	578
02ge20116orf22	1068	1519	19626250.aa	87	492
02cp11404orf9	1056	1507	6517192.aa	986	858
03ae10516orf11	1072	1523	33476715.aa	262	720
03ae10516orf11	1072	1523	4726503.aa	333	813
03ap21820orf10	1073	1524	13673328.aa	36	426
04ep71403orf10	1092	1543	50062.aa	982	834
04gp11213orf36	1102	1553	24414687.aa	180	609
04gp11213orf60	1103	1554	19556290.aa	84	489
05ae10307orf1	1104	1555	17497107.aa	900	480
05ae20220orf54	1111	1562	1179838.aa	20	406
05cp11911orf11	1119	1570	10664078.aa	7	392
05gp11901orf20	1136	1587	15039062.aa	61	456

-41-

05gp11901orf24	1137	1588	32600912.aa	253	707
06ael1405orf10	1140	1591	22687687.aa	120	533
06cel1002orf2	1142	1593	34099062.aa	268	728
11cel0917orf9	1233	1684	391313.aa	299	769
11cp12006orf17	1238	1689	291700.aa	942	671
11gel0309orf25	1243	1694	24406401.aa	173	602
11gel0309orf56	1245	1696	24495312.aa	187	618
11gel0309orf66	1247	1698	24495312.aa	187	618
11gp10904orf12	1249	1700	29844512.aa	234	682
12ael1404orf9	1261	1712	22303918.aa	112	524
12apl1614orf6	1269	1720	4562712.aa	324	802
12ge20305orf30	1279	1730	4095342.aa	971	785
13apl1517orf31	1284	1735	15126875.aa	62	457
13eel0216orf82	1290	1741	4035262.aa	308	781
13eel2016orf24	1297	1748	16459375.aa	74	473
14gp12015orf1	1328	1779	10009666.aa	1	384
hplp13922orf30	1370	1821	34089087.aa	266	726
hplp13939orf13	1372	1823	4766691.aa	337	817
hp2e10911orf25	1377	1828	2035936.aa	93	498
hp2p10625orf30	1383	1834	1411681.aa	44	436
hp2p10625orf7	1384	1835	4740887.aa	335	815
hp2p10625orf8	1385	1836	6495137.aa	368	856
hp3e10349orf18	1388	1839	260941.aa	208	650
hp3e11168orf14	1401	1852	5325005.aa	358	844
hp3e11168orf15	1402	1853	24039587.aa	923	580
hp4p11352orf8	1418	1869	4040928.aa	310	783
hp4p13402orf1	1420	1871	1256885.aa	26	416
hp5e15211orf15	1427	1878	35156938.aa	279	741
02ge20116orf33	1070	1521	14480927.aa	890	442
06cp20302orf8	1151	1602	4569693.aa	325	803
07cel1409orf4	1176	1627	21742157.aa	109	520
01ael2021orf8	999	1450	23646885.aa	143	566
01cel1513orf24	1006	1457	23539006.aa	918	557
01cp11710orf27	1012	1463	32595137.aa	252	706
01ep30520orf20	1018	1469	32627125.aa	953	710
02ael1211orf19	1030	1481	19537968.aa	902	487
02ael1611orf5	1033	1484	24407533.aa	174	603
02cel0114orf1	1041	1492	16440842.aa	73	472
02cel0213orf32	1049	1500	16839562.aa	898	476
02cel1220orf2	1054	1505	3930468.aa	300	770
02cp11721orf13	1057	1508	5265957.aa	356	841
04ep10811orf1	1090	1541	3907042.aa	298	768
04gel1713orf27	1097	1548	5111308.aa	354	839
05cp20518orf50	1129	1580	23573294.aa	138	560
06ael1020orf2	1139	1590	4486092.aa	319	796
06cel1002orf8	1143	1594	194415.aa	80	483
06cp30603orf11	1152	1603	24824087.aa	933	634

-42-

06ee10207orf2	1153	1604	14572133.aa	891	445
06ee10709orf17	1155	1606	6136430.aa	366	853
06ep11108orf20	1161	1612	22370182.aa	113	525
06ge10115orf12	1162	1613	4491093.aa	320	798
07ap11111orf3	1169	1620	23490686.aa	915	549
07ap80601orf10	1170	1621	5078593.aa	351	836
07ap80601orf12	1171	1622	24219012.aa	162	589
07ee20513orf1	1180	1631	36520792.aa	965	760
07gp11807orf28	1194	1645	16100038.aa	67	462
07gp11807orf29	1195	1646	42683.aa	314	789
07gp11807orf38	1199	1650	214812.aa	904	507
07gp11807orf41	1200	1651	4882842.aa	345	828
07gp11807orf42	1201	1652	719606.aa	374	866
07gp11807orf44	1202	1653	35949212.aa	962	754
07gp11807orf54	1205	1656	34161500.aa	270	730
14cp10923orf1	1312	1763	24492192.aa	186	617
16ae10508orf10	1336	1787	14864452.aa	60	455
27ze10351orf25	1349	1800	875042.aa	379	873
29gp10119orf6	1355	1806	14094816.aa	889	435
29zp10241orf18	1359	1810	3906937.aa	967	766
hp4e14535orf2	1413	1864	43490713.aa	973	793
hp5e15211orf13	1426	1877	35163962.aa	280	742
hp5e15211orf29	1430	1881	24329712.aa	170	599
			625277.aa	985	854
			24816915.aa	932	632
C. SECRETED OR PERIPLASMIC PROTEINS					
C.1. Secreted or periplasmic proteins					
01ce11016orf19	1004	1455	22460468.aa	117	530
05gp11901orf25	1138	1589	32609403.aa	254	708
02ge20116orf20	1067	1518	12505125.aa	24	414
03ee11215orf15	1078	1529	3157067.aa	242	694
14cp10923orf3	1314	1765	3242952.aa	950	703
14ee11217orf1	1319	1770	33595708.aa	263	721
14ee11217orf1	1319	1770	35442513.aa	286	749
hp2e10911orf30	1378	1829	30100332.aa	947	685
05ae20220orf124	1105	1556	14570443.aa	51	444
05ae20220orf92	1114	1565	24410643.aa	177	606
05ap21216orf7	1118	1569	24078837.aa	156	582
05cp11911orf12	1120	1571	24609431.aa	190	621
05cp11911orf27	1123	1574	783432.aa	375	868
05cp20518orf41	1127	1578	2843912.aa	222	666
09ae11601orf4	1212	1663	11876471.aa	21	408
09cp10502orf17	1223	1674	23438887.aa	912	538
09cp10713orf25	1225	1676	23912707.aa	148	573
11ge10309orf63	1246	1697	25501501.aa	202	639
11ge10309orf9	1248	1699	289077.aa	224	668
12ae11404orf3	1259	1710	22303918.aa	112	524

-43-

12ap10324orf4	1264	1715	13178562.aa	32	422
12ap10324orf5	1265	1716	4805318.aa	339	819
13ae10712orf4	1281	1732	24416083.aa	182	611
13ap11517orf7	1285	1736	29386577.aa	228	674
13ee12016orf15	1294	1745	23958179.aa	152	577
13ee12016orf5	1298	1749	272058.aa	219	663
13ee12016orf8	1299	1750	23564012.aa	137	558
14cp10923orf8	1315	1766	4414000.aa	318	794
14cp11121orf6	1316	1767	23631292.aa	141	564
14ee10308orf8	1317	1768	24230058.aa	165	592
14ee10308orf9	1318	1769	4728193.aa	334	814
16ep10117orf8	1344	1795	10742963.aa	13	398
27ze10351orf5	1351	1802	3906963.aa	297	767
29ge10111orf1	1353	1804	1367157.aa	35	425
hp1p13939orf9	1373	1824	26423583.aa	216	659
hp2e11858orf5	1380	1831	21687842.aa	908	517
hp3e10349orf17	1387	1838	23439055.aa	124	539
hp3e10349orf24	1389	1840	16603418.aa	75	475
hp3e11024orf22	1393	1844	2445812.aa	927	615
hp3e11024orf22	1393	1844	2774062.aa	221	665
hp4e13394orf5	1411	1862	24411011.aa	178	607
hp5e15211orf21	1428	1879	24328910.aa	169	598
hp5e15276orf14	1431	1882	36335436.aa	293	759
hp5p15641orf8	1439	1890	35837767.aa	289	752
02ce10213orf11	1043	1494	24276587.aa	926	595
07ge11504orf2	1183	1634	30283516.aa	948	686
07ge11504orf3	1184	1635	22447252.aa	115	528
07gp11807orf32	1196	1647	32462543.aa	251	705
07gp11807orf33	1197	1648	4882842.aa	345	828
07gp11807orf48	1203	1654	116018.aa	17	403
01ae11403orf1	995	1446	23594838.aa	920	561
01ae12021orf7	998	1449	20415937.aa	95	500
01ce10516orf2	1001	1452	1962590.aa	86	491
01gp11016orf14	1022	1473	5869090.aa	360	846
01xe21717orf12	1023	1474	34179577.aa	271	732
02ae11211orf10	1029	1480	3987580.aa	970	778
02ae11612orf4	1040	1491	35704718.aa	288	751
02ce10216orf1	1051	1502	35336707.aa	282	744
02cp20821orf12	1062	1513	20836042.aa	98	504
02cp20821orf12	1062	1513	12698442.aa	29	419
06ee10709orf16	1154	1605	4339708.aa	317	792
14ep11115orf1	1320	1771	4882318.aa	343	825
C.2. Proteins likely to be secreted or periplasmic					
03ap21820orf5	1075	1526	36131282.aa	291	756
05ae20220orf24	1106	1557	21720017.aa	108	519
05ae20220orf50	1109	1560	80257.aa	377	870
05cp20518orf9	1134	1585	3964593.aa	305	777

-44-

05cp20518orf9	1134	1585	4687507.aa	305	808
09cp10502orf14	1221	1672	2111040.aa	100	506
09cp10713orf26	1226	1677	7031343.aa	988	864
11ce11603orf22	1235	1686	26306340.aa	212	655
14ce10720orf2	1301	1752	1181418.aa	884	407
14cp10119orf7	1311	1762	1370202.aa	37	427
14gp11820orf4	1326	1777	3953952.aa	968	774
16cp30109orf6	1341	1792	4490717.aa	975	797
29gp10119orf5	1354	1805	30603402.aa	237	688
hplp11256orf7	1364	1815	4740887.aa	335	815
hplp13868orf24	1366	1817	33397538.aa	260	718
hplp14013orf4	1376	1827	663530.aa	370	859
hp3e11024orf16	1391	1842	20173437.aa	91	496
hp3e11024orf16	1391	1842	34573431.aa	276	738
hp3e11024orf6	1395	1846	4062813.aa	311	784
hp6p10723orf7	1445	1896	24406401.aa	173	602
03ee11215orf20	1079	1530	2150290.aa	102	510
07ge20415orf22	1186	1637	3958537.aa	304	775
01ce11618orf20	1010	1461	882827.aa	380	874
01ep10216orf6	1016	1467	23441078.aa	127	543
07ap80601orf5	1172	1623	917200.aa	993	878
04ge11713orf35	1098	1549	24256572.aa	925	594
03ap21820orf9	1076	1527	24415917.aa	181	610
07ce10203orf14	1174	1625	24395801.aa	171	600
D. OTHER SURFACE AND MEMBRANE PROTEINS					
D.1. Proteins likely to contain a single membrane					
spanning region					
02cp11822orf8	1060	1511	907827.aa	381	875
05ae20220orf51	1110	1561	29458178.aa	229	676
05ae20220orf6	1112	1563	4548792.aa	323	801
11ae10305orf4	1230	1681	6696887.aa	371	860
12ae11404orf8	1260	1711	35417942.aa	284	747
12ge20305orf35	1280	1731	22453166.aa	116	529
13ee11718orf2	1292	1743	1038312.aa	3	387
13ee12016orf19	1296	1747	10580417.aa	6	391
13ee12016orf19	1296	1747	21618785.aa	907	515
14ce21516orf3	1307	1758	24634750.aa	193	625
hp6p10723orf20	1442	1893	23831562.aa	145	568
hp6p10723orf5	1444	1895	14726542.aa	59	454
02ce10213orf1	1042	1493	4531568.aa	322	800
02ae11612orf36	1039	1490	2040717.aa	94	499
04ge11713orf41	1100	1551	3991067.aa	306	779
			10037799.aa	881	385
D.2. Proteins likely to contain two membrane spans					
05cp11911orf15	1122	1573	26052137.aa	939	648
12ae10622orf16	1254	1705	25925.aa	205	643
12ae11404orf12	1256	1707	23438840.aa	123	537

-45-

12ge10305orf10	1272	1723	21503772.aa	906	511
12ge10305orf10	1272	1723	24488537.aa	928	616
12ge10305orf21	1275	1726	489057.aa	346	829
14cp10119orf14	1309	1760	23473437.aa	129	546
14cp10119orf14	1309	1760	40339452.aa	307	780
14cp10923orf14	1313	1764	23515833.aa	133	553
27ze10351orf22	1347	1798	23486342.aa	131	548
27ze10351orf7	1352	1803	11924177.aa	886	410
29gp10119orf7	1356	1807	24413512.aa	179	608
hp5p15641orf5	1438	1889	21563752.aa	104	513
hp6p10723orf13	1441	1892	26351567.aa	213	656
01ce11618orf19	1009	1460	55843.aa	359	845
01xe21717orf40	1026	1477	23610905.aa	140	563
02ce10213orf23	1048	1499	23867207.aa	146	570
02cp20821orf8	1063	1514	4572168.aa	327	805
07ge20415orf39	1190	1641	5993958.aa	365	851
D.3. Proteins likely to contain 3 membrane spanning regions					
03ge10505orf14	1083	1534	1364378.aa	33	423
05ae20220orf88	1113	1564	4708337.aa	331	810
09cp10502orf16	1222	1673	24409577.aa	175	604
13ee12016orf18	1295	1746	25398250.aa	200	636
16ep10117orf7	1343	1794	36134661.aa	292	757
hp3e11024orf17	1392	1843	1206675.aa	23	412
hp6p10723orf43	1443	1894	4744128.aa	336	816
D.4. Proteins likely to contain 4 membrane spanning regions					
03xe11215orf5	1085	1536	3933437.aa	301	771
04ep71403orf12	1093	1544	12694087.aa	28	418
05ap11505orf10	1117	1568	26758437.aa	941	662
05cp11911orf13	1121	1572	21511555.aa	103	512
05cp11911orf13	1121	1572	29531590.aa	231	679
05cp20518orf61	1131	1582	24409641.aa	176	605
13ee10216orf5	1287	1738	12969218.aa	31	421
13ee10216orf5	1287	1738	23494043.aa	917	552
hp5p15641orf9	1440	1891	23945317.aa	151	576
09ae11601orf11	1209	1660	23867687.aa	922	571
D.5. Proteins likely to contain 5 membrane spanning regions					
16ep10117orf6	1342	1793			
hp2p10625orf14	1381	1832	33986087.aa	265	725
hp3e10349orf25	1390	1841	23631317.aa	142	565
hp3p10349orf32	1409	1860	33218912.aa	259	717
02ae11612orf14	1035	1486	23437502.aa	122	536
			25995917.aa	206	647
			11878127.aa	885	409
D.6. Proteins likely to contain 6 membrane spanning regions					
01cp11710orf34	1014	1465	2042312.aa	96	501
01cp11710orf34	1014	1465	5083577.aa	353	838
04ep10206orf22	1088	1539	13704718.aa	38	428

04ep10206orf22	1088	1539	20023400.aa	89	494
11ge10309orf18	1242	1693	17089217.aa	77	479
07cp21714orf14	1178	1629	32663212.aa	954	711
07cp21714orf14	1178	1629	3360130.aa	264	722
D.7. Proteins likely to contain 7 or more membrane spanning regions					
04ep10206orf23	1089	1540	25976418.aa	937	645
04ep10206orf23	1089	1540	2915903.aa	226	670
16ae10508orf3	1340	1791	35360843.aa	283	746
03ap21820orf13	1074	1525	197166.aa	88	493
03ap21820orf13	1074	1525	234391.aa	125	540
03ap21820orf13	1074	1525	24417212.aa	183	612
05ae20220orf31	1107	1558	24798427.aa	195	629
07gp11807orf49	1204	1655	19531291.aa	81	484
07gp11807orf49	1204	1655	19536375.aa	901	485
02ep30607orf31	1066	1517	19536458.aa	82	486
02ep30607orf31	1066	1517	13865928.aa	42	433

[In Table 1, "nt" represents nucleotide Seq. ID number and "aa" represents amino Seq. ID number]

Definitions

- 5 A purified or isolated polypeptide or a substantially pure preparation of a polypeptide are used interchangeably herein and, as used herein, mean a polypeptide that has been separated from other proteins, lipids, and nucleic acids with which it naturally occurs. Preferably, the polypeptide is also separated from substances, e.g., antibodies or gel matrix, e.g., polyacrylamide, which are used to purify it. Preferably, the polypeptide
- 10 constitutes at least 10, 20, 50 70, 80 or 95% dry weight of the purified preparation. Preferably, the preparation contains: sufficient polypeptide to allow protein sequencing; at least 1, 10, or 100 µg of the polypeptide; at least 1, 10, or 100 mg of the polypeptide.

- A purified preparation of cells refers to, in the case of plant or animal cells, an *in vitro* preparation of cells and not an entire intact plant or animal. In the case of cultured
- 15 cells or microbial cells, it consists of a preparation of at least 10% and more preferably 50% of the subject cells.

- A purified or isolated or a substantially pure nucleic acid, e.g., a substantially pure DNA, (are terms used interchangeably herein) is a nucleic acid which is one or both of the following: not immediately contiguous with both of the coding sequences with which it is
- 20 immediately contiguous (i.e., one at the 5' end and one at the 3' end) in the naturally-occurring genome of the organism from which the nucleic acid is derived; or which is substantially free of a nucleic acid with which it occurs in the organism from which the nucleic acid is derived. The term includes, for example, a recombinant DNA which is incorporated into a vector, e.g., into an autonomously replicating plasmid or virus, or into
- 25 the genomic DNA of a prokaryote or eukaryote, or which exists as a separate molecule (e.g., a cDNA or a genomic DNA fragment produced by PCR or restriction endonuclease treatment) independent of other DNA sequences. Substantially pure DNA also includes a

recombinant DNA which is part of a hybrid gene encoding additional *H. pylori* DNA sequence.

A "contig" as used herein is a nucleic acid representing a continuous stretch of genomic sequence of an organism.

- 5 An "open reading frame", also referred to herein as ORF, is a region of nucleic acid which encodes a polypeptide. This region may represent a portion of a coding sequence or a total sequence and can be determined from a stop to stop codon or from a start to stop codon.

- 10 As used herein, a "coding sequence" is a nucleic acid which is transcribed into messenger RNA and/or translated into a polypeptide when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a translation start codon at the five prime terminus and a translation stop code at the three prime terminus. A coding sequence can include but is not limited to messenger RNA, synthetic DNA, and recombinant nucleic acid sequences.

- 15 A "complement" of a nucleic acid as used herein refers to an anti-parallel or antisense sequence that participates in Watson-Crick base-pairing with the original sequence.

A "gene product" is a protein or structural RNA which is specifically encoded by a gene.

- 20 As used herein, the term "probe" refers to a nucleic acid, peptide or other chemical entity which specifically binds to a molecule of interest. Probes are often associated with or capable of associating with a label. A label is a chemical moiety capable of detection. Typical labels comprise dyes, radioisotopes, luminescent and chemiluminescent moieties, fluorophores, enzymes, precipitating agents, amplification sequences, and the like.
- 25 Similarly, a nucleic acid, peptide or other chemical entity which specifically binds to a molecule of interest and immobilizes such molecule is referred herein as a "capture ligand". Capture ligands are typically associated with or capable of associating with a support such as nitro-cellulose, glass, nylon membranes, beads, particles and the like. The specificity of hybridization is dependent on conditions such as the base pair composition of the
- 30 nucleotides, and the temperature and salt concentration of the reaction. These conditions are readily discernable to one of ordinary skill in the art using routine experimentation.

- Homologous refers to the sequence similarity or sequence identity between two polypeptides or between two nucleic acid molecules. When a position in both of the two compared sequences is occupied by the same base or amino acid monomer subunit, e.g., if
- 35 a position in each of two DNA molecules is occupied by adenine, then the molecules are homologous at that position. The percent of homology between two sequences is a function of the number of matching or homologous positions shared by the two sequences divided by the number of positions compared x 100. For example, if 6 of 10 of the positions in two sequences are matched or homologous then the two sequences are 60%

homologous. By way of example, the DNA sequences ATTGCC and TATGGC share 50% homology. Generally, a comparison is made when two sequences are aligned to give maximum homology.

5 Nucleic acids are hybridizable to each other when at least one strand of a nucleic acid can anneal to the other nucleic acid under defined stringency conditions. Stringency of hybridization is determined by: (a) the temperature at which hybridization and/or washing is performed; and (b) the ionic strength and polarity of the hybridization and washing solutions. Hybridization requires that the two nucleic acids contain complementary sequences; depending on the stringency of hybridization, however, mismatches may be
10 tolerated. Typically, hybridization of two sequences at high stringency (such as, for example, in a solution of 0.5X SSC, at 65° C) requires that the sequences be essentially completely homologous. Conditions of intermediate stringency (such as, for example, 2X SSC at 65° C) and low stringency (such as, for example 2X SSC at 55° C), require correspondingly less overall complementarity between the hybridizing sequences. (1X
15 SSC is 0.15 M NaCl, 0.015 M Na citrate).

The terms peptides, proteins, and polypeptides are used interchangeably herein.

As used herein, the term "surface protein" refers to all surface accessible proteins, e.g. inner and outer membrane proteins, proteins adhering to the cell wall, and secreted proteins.

20 A polypeptide has *H. pylori* biological activity if it has one, two and preferably more of the following properties: (1) if when expressed in the course of an *H. pylori* infection, it can promote, or mediate the attachment of *H. pylori* to a cell; (2) it has an enzymatic activity, structural or regulatory function characteristic of an *H. pylori* protein; (3) or the gene which encodes it can rescue a lethal mutation in an *H. pylori* gene. A
25 polypeptide has biological activity if it is an antagonist, agonist, or super-agonist of a polypeptide having one of the above-listed properties.

A biologically active fragment or analog is one having an *in vivo* or *in vitro* activity which is characteristic of the *H. pylori* polypeptides of the invention contained in the Sequence Listing, or of other naturally occurring *H. pylori* polypeptides, e.g., one or more
30 of the biological activities described herein. Especially preferred are fragments which exist *in vivo*, e.g., fragments which arise from post transcriptional processing or which arise from translation of alternatively spliced RNA's. Fragments include those expressed in native or endogenous cells as well as those made in expression systems, e.g., in CHO cells. Because peptides such as *H. pylori* polypeptides often exhibit a range of physiological properties
35 and because such properties may be attributable to different portions of the molecule, a useful *H. pylori* fragment or *H. pylori* analog is one which exhibits a biological activity in any biological assay for *H. pylori* activity. Most preferably the fragment or analog possesses 10%, preferably 40%, more preferably 60%, 70%, 80% or 90% or greater of the activity of *H. pylori*, in any *in vivo* or *in vitro* assay.

5 Analogues can differ from naturally occurring *H. pylori* polypeptides in amino acid sequence or in ways that do not involve sequence, or both. Non-sequence modifications include changes in acetylation, methylation, phosphorylation, carboxylation, or glycosylation. Preferred analogues include *H. pylori* polypeptides (or biologically active fragments thereof) whose sequences differ from the wild-type sequence by one or more conservative amino acid substitutions or by one or more non-conservative amino acid substitutions, deletions, or insertions which do not substantially diminish the biological activity of the *H. pylori* polypeptide. Conservative substitutions typically include the substitution of one amino acid for another with similar characteristics, e.g., substitutions within the following groups: valine, glycine; glycine, alanine; valine, isoleucine, leucine; aspartic acid, glutamic acid; asparagine, glutamine; serine, threonine; lysine, arginine; and phenylalanine, tyrosine. Other conservative substitutions can be made in view of the table below.

15

TABLE 2
CONSERVATIVE AMINO ACID REPLACEMENTS

For Amino Acid	Code	Replace with any of
Alanine	A	D-Ala, Gly, beta-Ala, L-Cys, D-Cys
Arginine	R	D-Arg, Lys, D-Lys, homo-Arg, D-homo-Arg, Met, Ile, D-Met, D-Ile, Orn, D-Orn
Asparagine	N	D-Asn, Asp, D-Asp, Glu, D-Glu, Gln, D-Gln
Aspartic Acid	D	D-Asp, D-Asn, Asn, Glu, D-Glu, Gln, D-Gln
Cysteine	C	D-Cys, S-Me-Cys, Met, D-Met, Thr, D-Thr
Glutamine	Q	D-Gln, Asn, D-Asn, Glu, D-Glu, Asp, D-Asp
Glutamic Acid	E	D-Glu, D-Asp, Asp, Asn, D-Asn, Gln, D-Gln
Glycine	G	Ala, D-Ala, Pro, D-Pro, β -Ala, Acp
Isoleucine	I	D-Ile, Val, D-Val, Leu, D-Leu, Met, D-Met
Leucine	L	D-Leu, Val, D-Val, Leu, D-Leu, Met, D-Met
Lysine	K	D-Lys, Arg, D-Arg, homo-Arg, D-homo-Arg, Met, D-Met, Ile, D-Ile, Orn, D-Orn
Methionine	M	D-Met, S-Me-Cys, Ile, D-Ile, Leu, D-Leu, Val, D-Val
Phenylalanine	F	D-Phe, Tyr, D-Thr, L-Dopa, His, D-His, Trp, D-Trp, Trans-3,4, or 5-phenylproline, cis-3,4, or 5-phenylproline

-50-

Proline	P	D-Pro, L-I-thioazolidine-4-carboxylic acid, D-or L-l-oxazolidine-4-carboxylic acid
Serine	S	D-Ser, Thr, D-Thr, allo-Thr, Met, D-Met, Met(O), D-Met(O), L-Cys, D-Cys
Threonine	T	D-Thr, Ser, D-Ser, allo-Thr, Met, D-Met, Met(O), D-Met(O), Val, D-Val
Tyrosine	Y	D-Tyr, Phe, D-Phe, L-Dopa, His, D-His
Valine	V	D-Val, Leu, D-Leu, Ile, D-Ile, Met, D-Met

Other analogs within the invention are those with modifications which increase peptide stability; such analogs may contain, for example, one or more non-peptide bonds (which replace the peptide bonds) in the peptide sequence. Also included are: analogs that include residues other than naturally occurring L-amino acids, e.g., D-amino acids or non-naturally occurring or synthetic amino acids, e.g., β or γ amino acids; and cyclic analogs.

As used herein, the term "fragment", as applied to an *H. pylori* analog, will ordinarily be at least about 20 residues, more typically at least about 40 residues, preferably at least about 60 residues in length. Fragments of *H. pylori* polypeptides can be generated by methods known to those skilled in the art. The ability of a candidate fragment to exhibit a biological activity of *H. pylori* polypeptide can be assessed by methods known to those skilled in the art as described herein. Also included are *H. pylori* polypeptides containing residues that are not required for biological activity of the peptide or that result from alternative mRNA splicing or alternative protein processing events.

An "immunogenic component" as used herein is a moiety, such as an *H. pylori* polypeptide, analog or fragment thereof, that is capable of eliciting a humoral and/or cellular immune response in a host animal.

An "antigenic component" as used herein is a moiety, such as an *H. pylori* polypeptide, analog or fragment thereof, that is capable of binding to a specific antibody with sufficiently high affinity to form a detectable antigen-antibody complex.

As used herein, the term "transgene" means a nucleic acid (encoding, e.g., one or more polypeptides), which is partly or entirely heterologous, i.e., foreign, to the transgenic animal or cell into which it is introduced, or, is homologous to an endogenous gene of the transgenic animal or cell into which it is introduced, but which is designed to be inserted, or is inserted, into the cell's genome in such a way as to alter the genome of the cell into which it is inserted (e.g., it is inserted at a location which differs from that of the natural gene or its insertion results in a knockout). A transgene can include one or more transcriptional regulatory sequences and any other nucleic acid, such as introns, that may be necessary for optimal expression of the selected nucleic acid, all operably linked to the selected nucleic acid, and may include an enhancer sequence.

-51-

As used herein, the term "transgenic cell" refers to a cell containing a transgene.

As used herein, a "transgenic animal" is any animal in which one or more, and preferably essentially all, of the cells of the animal includes a transgene. The transgene can be introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate genetic manipulation, such as by a process of transformation of competent cells or by microinjection or by infection with a recombinant virus. This molecule may be integrated within a chromosome, or it may be extrachromosomally replicating DNA.

The term "antibody" as used herein is intended to include fragments thereof which are specifically reactive with *H. pylori* polypeptides.

As used herein, the term "cell-specific promoter" means a DNA sequence that serves as a promoter, i.e., regulates expression of a selected DNA sequence operably linked to the promoter, and which effects expression of the selected DNA sequence in specific cells of a tissue. The term also covers so-called "leaky" promoters, which regulate expression of a selected DNA primarily in one tissue, but cause expression in other tissues as well.

Misexpression, as used herein, refers to a non-wild type pattern of gene expression. It includes: expression at non-wild type levels, i.e., over or under expression; a pattern of expression that differs from wild type in terms of the time or stage at which the gene is expressed, e.g., increased or decreased expression (as compared with wild type) at a predetermined developmental period or stage; a pattern of expression that differs from wild type in terms of decreased expression (as compared with wild type) in a predetermined cell type or tissue type; a pattern of expression that differs from wild type in terms of the splicing size, amino acid sequence, post-translational modification, or biological activity of the expressed polypeptide; a pattern of expression that differs from wild type in terms of the effect of an environmental stimulus or extracellular stimulus on expression of the gene, e.g., a pattern of increased or decreased expression (as compared with wild type) in the presence of an increase or decrease in the strength of the stimulus.

As used herein, "host cells" and other such terms denoting microorganisms or higher eukaryotic cell lines cultured as unicellular entities refers to cells which can become or have been used as recipients for a recombinant vector or other transfer DNA, and include the progeny of the original cell which has been transfected. It is understood by individuals skilled in the art that the progeny of a single parental cell may not necessarily be completely identical in genomic or total DNA complement to the original parent, due to accident or deliberate mutation.

As used herein, the term "control sequence" refers to a nucleic acid having a base sequence which is recognized by the host organism to effect the expression of encoded sequences to which they are ligated. The nature of such control sequences differs depending upon the host organism; in prokaryotes, such control sequences generally include a

-52-

promoter, ribosomal binding site, terminators, and in some cases operators; in eukaryotes, generally such control sequences include promoters, terminators and in some instances, enhancers. The term control sequence is intended to include at a minimum, all components whose presence is necessary for expression, and may also include additional components whose presence is advantageous, for example, leader sequences.

As used herein, the term "operably linked" refers to sequences joined or ligated to function in their intended manner. For example, a control sequence is operably linked to coding sequence by ligation in such a way that expression of the coding sequence is achieved under conditions compatible with the control sequence and host cell.

The metabolism of a substance, as used herein, means any aspect of the, expression, function, action, or regulation of the substance. The metabolism of a substance includes modifications, e.g., covalent or non-covalent modifications of the substance. The metabolism of a substance includes modifications, e.g., covalent or non-covalent modification, the substance induces in other substances. The metabolism of a substance also includes changes in the distribution of the substance. The metabolism of a substance includes changes the substance induces in the distribution of other substances.

A "sample" as used herein refers to a biological sample, such as, for example, tissue or fluid isolated from an individual (including without limitation plasma, serum, cerebrospinal fluid, lymph, tears, saliva and tissue sections) or from *in vitro* cell culture constituents, as well as samples from the environment.

The practice of the invention will employ, unless otherwise indicated, conventional techniques of chemistry, molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. See e.g., Sambrook, Fritsch, and Maniatis, *Molecular Cloning; Laboratory Manual* 2nd ed. (1989); *DNA Cloning*, Volumes I and II (D.N Glover ed. 1985); *Oligonucleotide Synthesis* (M.J. Gait ed, 1984); *Nucleic Acid Hybridization* (B.D. Hames & S.J. Higgins eds. 1984); the series, *Methods in Enzymology* (Academic Press, Inc.), particularly Vol. 154 and Vol. 155 (Wu and Grossman, eds.) and *PCR-A Practical Approach* (McPherson, Quirke, and Taylor, eds., 1991).

30

I. Isolation of Nucleic Acids of *H. pylori* and Uses Therefor

H. pylori Genomic Sequence

This invention provides nucleotide sequences of the genome of *H. pylori* which thus comprises a DNA sequence library of *H. pylori* genomic DNA. The detailed description that follows provides nucleotide sequences of *H. pylori*, and also describes how the sequences were obtained and how ORFs and protein-coding sequences were identified. Also described are methods of using the disclosed *H. pylori* sequences in methods including diagnostic and therapeutic applications. Furthermore, the library can be used as a

database for identification and comparison of medically important sequences in this and other strains of *H. pylori*.

To determine the genomic sequence of *H. pylori*, DNA was isolated from a strain of *H. pylori* (ATCC # 55679) and mechanically sheared by nebulization to a median size of 2 kb. Following size fractionation by gel electrophoresis, the fragments were blunt-ended, ligated to adapter oligonucleotides, and cloned into each of 20 different pMPX vectors (Rice et al., abstracts of Meeting of Genome Mapping and Sequencing, Cold Spring Harbor, NY, 5/11-5/15, 1994, p. 225) to construct a series of "shotgun" subclone libraries.

DNA sequencing was achieved using multiplex sequencing procedures essentially as disclosed in Church et al., 1988, *Science* 240:185; U.S. Patents No. 4,942,124 and 5,149,625). DNA was extracted from pooled cultures and subjected to chemical or enzymatic sequencing. Sequencing reactions were resolved by electrophoresis, and the products were transferred and covalently bound to nylon membranes. Finally, the membranes were sequentially hybridized with a series of labelled oligonucleotides complimentary to "tag" sequences present in the different shotgun cloning vectors. In this manner, a large number of sequences could be obtained from a single set of sequencing reactions. The cloning and sequencing procedures are described in more detail in the Exemplification.

Individual sequence reads obtained in this manner were assembled using the FALCON™ program (Church et al., 1994, *Automated DNA Sequencing and Analysis*, J.C. Venter, ed., Academic Press) and PHRAP (P. Green, Abstracts of DOE Human Genome Program Contractor-Grantee Workshop V, Jan. 1996, p.157). The average contig length was about 3-4 kb.

A variety of approaches are used to order the contigs so as to obtain a continuous sequence representing the entire *H. pylori* genome. Synthetic oligonucleotides are designed that are complementary to sequences at the end of each contig. These oligonucleotides may be hybridized to libraries of *H. pylori* genomic DNA in, for example, lambda phage vectors or plasmid vectors to identify clones that contain sequences corresponding to the junctional regions between individual contigs. Such clones are then used to isolate template DNA and the same oligonucleotides are used as primers in polymerase chain reaction (PCR) to amplify junctional fragments, the nucleotide sequence of which is then determined.

The *H. pylori* sequences were analyzed for the presence of open reading frames (ORFs) comprising at least 180 nucleotides. As a result of the analysis of ORFs based on stop-to-stop codon reads, it should be understood that these ORFs may not correspond to the ORF of a naturally-occurring *H. pylori* polypeptide. These ORFs may contain start codons which indicate the initiation of protein synthesis of a naturally-occurring *H. pylori* polypeptide. Such start codons within the ORFs provided herein can be identified by those of ordinary skill in the relevant art, and the resulting ORF and the encoded *H. pylori* polypeptide is within the scope of this invention. For example, within the ORFs a codon

-54-

such as AUG or GUG (encoding methionine or valine) which is part of the initiation signal for protein synthesis can be identified and the ORF modified to correspond to a naturally-occurring *H. pylori* polypeptide. The predicted coding regions were defined by evaluating the coding potential of such sequences with the program GENEMARK™ (Borodovsky and
5 McNinch, 1993, *Comp. Chem.* 17:123).

Other *H. pylori* Nucleic Acids

The nucleic acids of this invention may be obtained directly from the DNA of the above referenced *H. pylori* strain by using the polymerase chain reaction (PCR). See "*PCR, A Practical Approach*" (McPherson, Quirke, and Taylor, eds., IRL Press, Oxford, UK,
10 1991) for details about the PCR. High fidelity PCR can be used to ensure a faithful DNA copy prior to expression. In addition, the authenticity of amplified products can be checked by conventional sequencing methods. Clones carrying the desired sequences described in this invention may also be obtained by screening the libraries by means of the PCR or by
15 hybridization of synthetic oligonucleotide probes to filter lifts of the library colonies or plaques as known in the art (see, e.g., Sambrook et al., *Molecular Cloning, A Laboratory Manual* 2nd edition, 1989, Cold Spring Harbor Press, NY).

It is also possible to obtain nucleic acids encoding *H. pylori* polypeptides from a cDNA library in accordance with protocols herein described. A cDNA encoding an *H.*
20 *pylori* polypeptide can be obtained by isolating total mRNA from an appropriate strain. Double stranded cDNAs can then be prepared from the total mRNA. Subsequently, the cDNAs can be inserted into a suitable plasmid or viral (e.g., bacteriophage) vector using any one of a number of known techniques. Genes encoding *H. pylori* polypeptides can also be cloned using established polymerase chain reaction techniques in accordance with the
25 nucleotide sequence information provided by the invention. The nucleic acids of the invention can be DNA or RNA. Preferred nucleic acids of the invention are contained in the Sequence Listing.

The nucleic acids of the invention can also be chemically synthesized using standard techniques. Various methods of chemically synthesizing polydeoxynucleotides
30 are known, including solid-phase synthesis which, like peptide synthesis, has been fully automated in commercially available DNA synthesizers (See e.g., Itakura *et al.* U.S. Patent No. 4,598,049; Caruthers *et al.* U.S. Patent No. 4,458,066; and Itakura U.S. Patent Nos. 4,401,796 and 4,373,071, incorporated by reference herein).

Nucleic acids isolated or synthesized in accordance with features of the present
35 invention are useful, by way of example, without limitation, as probes, primers, capture ligands, antisense genes and for developing expression systems for the synthesis of proteins and peptides corresponding to such sequences. As probes, primers, capture ligands and antisense agents, the nucleic acid normally consists of all or part (approximately twenty or more nucleotides for specificity as well as the ability to form stable hybridization products)

of the nucleic acids of the invention contained in the Sequence Listing. These uses are described in further detail below.

Probes

5 A nucleic acid isolated or synthesized in accordance with the sequence of the invention contained in the Sequence Listing can be used as a probe to specifically detect *H. pylori*. With the sequence information set forth in the present application, sequences of twenty or more nucleotides are identified which provide the desired inclusivity and exclusivity with respect to *H. pylori*, and extraneous nucleic acids likely to be encountered
10 during hybridization conditions. More preferably, the sequence will comprise at least twenty to thirty nucleotides to convey stability to the hybridization product formed between the probe and the intended target molecules.

Sequences larger than 1000 nucleotides in length are difficult to synthesize but can be generated by recombinant DNA techniques. Individuals skilled in the art will readily
15 recognize that the nucleic acids, for use as probes, can be provided with a label to facilitate detection of a hybridization product.

Nucleic acid isolated and synthesized in accordance with the sequence of the invention contained in the Sequence Listing can also be useful as probes to detect homologous regions (especially homologous genes) of other *Helicobacter* species using
20 appropriate stringency hybridization conditions as described herein.

Capture Ligand

For use as a capture ligand, the nucleic acid selected in the manner described above with respect to probes, can be readily associated with a support. The manner in which nucleic acid is associated with supports is well known. Nucleic acid having twenty or more
25 nucleotides in a sequence of the invention contained in the Sequence Listing have utility to separate *H. pylori* nucleic acid from the nucleic acid of each other and other organisms. Nucleic acid having twenty or more nucleotides in a sequence of the invention contained in the Sequence Listing can also have utility to separate other *Helicobacter* species from each other and from other organisms. Preferably, the sequence will comprise at least twenty
30 nucleotides to convey stability to the hybridization product formed between the probe and the intended target molecules. Sequences larger than 1000 nucleotides in length are difficult to synthesize but can be generated by recombinant DNA techniques.

Primers

Nucleic acid isolated or synthesized in accordance with the sequences described
35 herein have utility as primers for the amplification of *H. pylori* nucleic acid. These nucleic acids may also have utility as primers for the amplification of nucleic acids in other *Helicobacter* species. With respect to polymerase chain reaction (PCR) techniques, nucleic acid sequences of ≥ 10 -15 nucleotides of the invention contained in the Sequence Listing have utility in conjunction with suitable enzymes and reagents to create copies of *H. pylori*

-56-

nucleic acid. More preferably, the sequence will comprise twenty or more nucleotides to convey stability to the hybridization product formed between the primer and the intended target molecules. Binding conditions of primers greater than 100 nucleotides are more difficult to control to obtain specificity. High fidelity PCR can be used to ensure a faithful DNA copy prior to expression. In addition, amplified products can be checked by conventional sequencing methods.

The copies can be used in diagnostic assays to detect specific sequences, including genes from *H. pylori* and/or other *Helicobacter* species. The copies can also be incorporated into cloning and expression vectors to generate polypeptides corresponding to the nucleic acid synthesized by PCR, as is described in greater detail herein.

Antisense

Nucleic acid or nucleic acid-hybridizing derivatives isolated or synthesized in accordance with the sequences described herein have utility as antisense agents to prevent the expression of *H. pylori* genes. These sequences also have utility as antisense agents to prevent expression of genes of other *Helicobacter* species.

In one embodiment, nucleic acid or derivatives corresponding to *H. pylori* nucleic acids is loaded into a suitable carrier such as a liposome or bacteriophage for introduction into bacterial cells. For example, a nucleic acid having twenty or more nucleotides is capable of binding to bacteria nucleic acid or bacteria messenger RNA. Preferably, the antisense nucleic acid is comprised of 20 or more nucleotides to provide necessary stability of a hybridization product of non-naturally occurring nucleic acid and bacterial nucleic acid and/or bacterial messenger RNA. Nucleic acid having a sequence greater than 1000 nucleotides in length is difficult to synthesize but can be generated by recombinant DNA techniques. Methods for loading antisense nucleic acid in liposomes is known in the art as exemplified by U.S. Patent 4,241,046 issued December 23, 1980 to Papahadjopoulos et al.

II. Expression of *H. pylori* Nucleic Acids

Nucleic acid isolated or synthesized in accordance with the sequences described herein have utility to generate polypeptides. The nucleic acid of the invention exemplified in the Sequence Listing or fragments of said nucleic acid encoding active portions of *H. pylori* polypeptides can be cloned into suitable vectors or used to isolate nucleic acid. The isolated nucleic acid is combined with suitable DNA linkers and cloned into a suitable vector.

The function of a specific gene or operon can be ascertained by expression in a bacterial strain under conditions where the activity of the gene product(s) specified by the gene or operon in question can be specifically measured. Alternatively, a gene product may be produced in large quantities in an expressing strain for use as an antigen, an industrial reagent, for structural studies, etc. This expression can be accomplished in a mutant strain which lacks the activity of the gene to be tested, or in a strain that does not produce the

same gene product(s). This includes, but is not limited to other *Helicobacter* strains, or other bacterial strains such as *E. coli*, *Nocardia*, *Corynebacterium*, *Campylobacter*, and *Streptomyces* species. In some cases the expression host will utilize the natural *Helicobacter* promoter whereas in others, it will be necessary to drive the gene with a promoter sequence derived from the expressing organism (e.g., an *E. coli* beta-galactosidase promoter for expression in *E. coli*).

To express a gene product using the natural *H. pylori* promoter, a procedure such as the following can be used. A restriction fragment containing the gene of interest, together with its associated natural promoter element and regulatory sequences (identified using the DNA sequence data) is cloned into an appropriate recombinant plasmid containing an origin of replication that functions in the host organism and an appropriate selectable marker. This can be accomplished by a number of procedures known to those skilled in the art. It is most preferably done by cutting the plasmid and the fragment to be cloned with the same restriction enzyme to produce compatible ends that can be ligated to join the two pieces together. The recombinant plasmid is introduced into the host organism by, for example, electroporation and cells containing the recombinant plasmid are identified by selection for the marker on the plasmid. Expression of the desired gene product is detected using an assay specific for that gene product.

In the case of a gene that requires a different promoter, the body of the gene (coding sequence) is specifically excised and cloned into an appropriate expression plasmid. This subcloning can be done by several methods, but is most easily accomplished by PCR amplification of a specific fragment and ligation into an expression plasmid after treating the PCR product with a restriction enzyme or exonuclease to create suitable ends for cloning.

A suitable host cell for expression of a gene can be any procaryotic or eucaryotic cell. For example, an *H. pylori* polypeptide can be expressed in bacterial cells such as *E. coli*, insect cells (baculovirus), yeast, or mammalian cells such as Chinese hamster ovary cell (CHO). Other suitable host cells are known to those skilled in the art.

Expression in eucaryotic cells such as mammalian, yeast, or insect cells can lead to partial or complete glycosylation and/or formation of relevant inter- or intra-chain disulfide bonds of a recombinant peptide product. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, et al., (1987) *Embo J.* 6:229-234), pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz et al., (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Baculovirus vectors available for expression of proteins in cultured insect cells (SF 9 cells) include the pAc series (Smith et al., (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow, V.A., and Summers, M.D., (1989) *Virology* 170:31-39). Generally, COS cells (Gluzman, Y., (1981) *Cell* 23:175-182) are used in conjunction with such vectors as pCDM 8 (Aruffo, A. and Seed, B., (1987) *Proc. Natl. Acad. Sci. USA* 84:8573-8577) for transient

amplification/expression in mammalian cells, while CHO (dhfr⁻ Chinese Hamster Ovary) cells are used with vectors such as pMT2PC (Kaufman et al. (1987), *EMBO J.* 6:187-195) for stable amplification/expression in mammalian cells. Vector DNA can be introduced into mammalian cells via conventional techniques such as calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, or electroporation. Suitable methods for transforming host cells can be found in Sambrook et al. (Molecular Cloning: A Laboratory Manual, 2nd Edition, Cold Spring Harbor Laboratory press (1989)), and other laboratory textbooks.

Expression in procaryotes is most often carried out in *E. coli* with either fusion or non-fusion inducible expression vectors. Fusion vectors usually add a number of NH₂ terminal amino acids to the expressed target gene. These NH₂ terminal amino acids often are referred to as a reporter group. Such reporter groups usually serve two purposes: 1) to increase the solubility of the target recombinant protein; and 2) to aid in the purification of the target recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the reporter group and the target recombinant protein to enable separation of the target recombinant protein from the reporter group subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Amrad Corp., Melbourne, Australia), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase, maltose E binding protein, or protein A, respectively, to the target recombinant protein. A preferred reporter group is poly(His), which may be fused to the amino or carboxy terminus of the protein and which renders the recombinant fusion protein easily purifiable by metal chelate chromatography.

Inducible non-fusion expression vectors include pTrc (Amann et al., (1988) *Gene* 69:301-315) and pET11d (Studier et al., Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, California (1990) 60-89). While target gene expression relies on host RNA polymerase transcription from the hybrid trp-lac fusion promoter in pTrc, expression of target genes inserted into pET11d relies on transcription from the T7 gn10-lac 0 fusion promoter mediated by coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7 gn1 under the transcriptional control of the lacUV 5 promoter.

For example, a host cell transfected with a nucleic acid vector directing expression of a nucleotide sequence encoding an *H. pylori* polypeptide can be cultured under appropriate conditions to allow expression of the polypeptide to occur. The polypeptide may be secreted and isolated from a mixture of cells and medium containing the peptide. Alternatively, the polypeptide may be retained cytoplasmically and the cells harvested, lysed and the protein isolated. A cell culture includes host cells, media and other

byproducts. Suitable media for cell culture are well known in the art. Polypeptides of the invention can be isolated from cell culture medium, host cells, or both using techniques known in the art for purifying proteins including ion-exchange chromatography, gel filtration chromatography, ultrafiltration, electrophoresis, and immunoaffinity purification
5 with antibodies specific for such polypeptides. Additionally, in many situations, polypeptides can be produced by chemical cleavage of a native protein (e.g., tryptic digestion) and the cleavage products can then be purified by standard techniques.

In the case of membrane bound proteins, these can be isolated from a host cell by contacting a membrane-associated protein fraction with a detergent forming a solubilized
10 complex, where the membrane-associated protein is no longer entirely embedded in the membrane fraction and is solubilized at least to an extent which allows it to be chromatographically isolated from the membrane fraction. Several different criteria are used for choosing a detergent suitable for solubilizing these complexes. For example, one property considered is the ability of the detergent to solubilize the *H. pylori* protein within
15 the membrane fraction at minimal denaturation of the membrane-associated protein allowing for the activity or functionality of the membrane-associated protein to return upon reconstitution of the protein. Another property considered when selecting the detergent is the critical micelle concentration (CMC) of the detergent in that the detergent of choice preferably has a high CMC value allowing for ease of removal after reconstitution. A third
20 property considered when selecting a detergent is the hydrophobicity of the detergent. Typically, membrane-associated proteins are very hydrophobic and therefore detergents which are also hydrophobic, e.g., the triton series, would be useful for solubilizing the hydrophobic proteins. Another property important to a detergent can be the capability of the detergent to remove the *H. pylori* protein with minimal protein-protein interaction
25 facilitating further purification. A fifth property of the detergent which should be considered is the charge of the detergent. For example, if it is desired to use ion exchange resins in the purification process then preferably detergent should be an uncharged detergent. Chromatographic techniques which can be used in the final purification step are known in the art and include hydrophobic interaction, lectin affinity, ion exchange, dye
30 affinity and immunoaffinity.

One strategy to maximize recombinant *H. pylori* peptide expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, California (1990) 119-128). Another
35 strategy would be to alter the nucleic acid encoding an *H. pylori* peptide to be inserted into an expression vector so that the individual codons for each amino acid would be those preferentially utilized in highly expressed *E. coli* proteins (Wada et al., (1992) *Nuc. Acids Res.* 20:2111-2118). Such alteration of nucleic acids of the invention can be carried out by standard DNA synthesis techniques.

-60-

The nucleic acids of the invention can also be chemically synthesized using standard techniques. Various methods of chemically synthesizing polydeoxynucleotides are known, including solid-phase synthesis which, like peptide synthesis, has been fully automated in commercially available DNA synthesizers (See, e.g., Itakura et al. U.S. Patent No. 4,598,049; Caruthers et al. U.S. Patent No. 4,458,066; and Itakura U.S. Patent Nos. 4,401,796 and 4,373,071, incorporated by reference herein).

III. *H. pylori* Polypeptides

This invention encompasses isolated *H. pylori* polypeptides encoded by the disclosed *H. pylori* genomic sequences, including the polypeptides of the invention contained in the Sequence Listing. Polypeptides of the invention are preferably at least 5 amino acid residues in length. Using the DNA sequence information provided herein, the amino acid sequences of the polypeptides encompassed by the invention can be deduced using methods well-known in the art. It will be understood that the sequence of an entire nucleic acid encoding an *H. pylori* polypeptide can be isolated and identified based on an ORF that encodes only a fragment of the cognate protein-coding region. This can be achieved, for example, by using the isolated nucleic acid encoding the ORF, or fragments thereof, to prime a polymerase chain reaction with genomic *H. pylori* DNA as template; this is followed by sequencing the amplified product.

The polypeptides of the invention can be isolated from wild-type or mutant *H. pylori* cells or from heterologous organisms or cells (including, but not limited to, bacteria, yeast, insect, plant and mammalian cells) into which an *H. pylori* nucleic acid has been introduced and expressed. In addition, the polypeptides can be part of recombinant fusion proteins.

H. pylori polypeptides of the invention can be chemically synthesized using commercially automated procedures such as those referenced herein.

Many of the polypeptides of the invention are related to one another. Some of these relationships are described in Table 3 below. Most polypeptides described in Table 3 are over 90% identical to one another as noted in the last two columns; some are between 70% and 90% identical to one another; and very few share between 60% and 70% identity with each other. The polypeptides represented by the sequence identification numbers in the third column of Table 3 result from translations carried out from stop codon to stop codon in the genomic nucleotide sequence of the invention, while those in the first column result from translations carried out from the first methionine or valine codon following the prior stop codon and proceeding to the final stop codon in the nucleotide sequence. In some cases, the nucleotide sequence encoding the related polypeptides is slightly different, resulting in some differences in amino acid residues of the related polypeptides. In many cases, the related polypeptides differ significantly in length, with one polypeptide containing amino acid residues in addition to those in common between the two

polypeptides. In all cases, the relationships described in Table 3 are highly significant, and the nucleotide sequences encoding these related polypeptides are also very similar to one another. For example, the nucleotide probes derived from the coding sequence of the polypeptides in column one can be used in PCR or hybridization experiments to identify clones carrying the nucleotide sequence encoding the polypeptides of column three.

The relationships between the polypeptides shown in Table 3 can be classified in five broad categories as follows. First, for many polypeptides (designated "A" in the last column of the Table 3), the polypeptide denoted in column one is identical to the polypeptide denoted in column three except for an occasional addition of a few putative amino acid residues at the N-terminus which result from the fact that the polypeptides of column three were derived by translating from stop codon to stop codon instead of from a predicted start codon (i.e., Met or Val) to a stop codon as was done for the polypeptides in column one.

Second, for most polypeptides (designated "B" in the last column of the Table 3), the polypeptide of column one is at least 95% identical to the polypeptide of column three except that the polypeptide in column three is longer (at either or both ends) by one or more amino acid residues which do not result from the difference between reading from stop to stop instead of from start to stop.

Third, for some polypeptides (designated "C" in the last column of Table 3), the converse is true, the polypeptide of column one is at least 95% identical to the polypeptide of column three except that the polypeptide in column three is shorter (at either or both ends).

Fourth, for some polypeptides (designated "D" in the last column of Table 3), the polypeptide of column one shares a high level of amino acid identity (i.e., at least 95%) with the polypeptide of column three in the region in which they overlap, but shares little or no identity (i.e., less than 95%) at one or both ends. The level of identity of the polypeptides in columns one and three in categories "B", "C" and "D" is highly significant. For example, a typical *H. pylori* gene product will exhibit amino acid sequence identities of between 92% to 100% among strains of *H. pylori* isolated from human patients (see Table 10 below).

Finally, a fifth class of polypeptides in column one (designated "E" in the last column of Table 3) are closely related but differ significantly (i.e., less than 95% identical) from the polypeptide of column three. These polypeptides are likely "paralogs," members of related gene families in *H. pylori*.

TABLE 3					
SeqID #	Length (aa)	SeqID #	Length (aa)	% Identity: Overlap Length	Category
384	509	1779	593	100.0 : 504 aa	B
386	133	1713	205	99.2 : 127 aa	B
387	158	1743	340	98.7 : 155 aa	B
388	112	1489	330	100.0 : 105 aa	B
389	650	1643	369	95.4 : 65 aa	D
390	62	1598	327	90.2 : 61 aa	E
391	619	1747	991	99.3 : 608 aa	B
392	110	1570	183	93.1 : 101 aa	E
393	68	1811	85	97.1 : 68 aa	B
394	446	1884	594	99.5 : 433 aa	B
395	84	1503	347	100.0 : 84 aa	B
396	40	1504	519	88.2 : 34 aa	E
397	300	1531	273	98.9 : 267 aa	C
398	214	1795	197	99.0 : 192 aa	C
399	137	1639	199	96.4 : 137 aa	B
400	272	1725	285	99.3 : 271 aa	B
401	287	1470	455	98.9 : 277 aa	D
402	106	1596	302	99.1 : 106 aa	B
403	157	1654	197	99.3 : 150 aa	B
404	278	1552	362	100.0 : 277 aa	B
405	120	1858	529	100.0 : 116 aa	B
406	226	1562	297	100.0 : 216 aa	B
407	62	1752	157	77.6 : 58 aa	E
408	50	1663	74	97.9 : 47 aa	B
410	188	1803	351	87.1 : 155 aa	E
411	130	1685	497	100.0 : 129 aa	B
412	183	1843	185	100.0 : 183 aa	A
413	194	1874	508	97.6 : 169 aa	D
414	235	1518	246	100.0 : 235 aa	B
415	88	1538	676	97.5 : 80 aa	B
416	109	1871	335	99.1 : 109 aa	B
417	107	1782	593	94.4 : 90 aa	E
418	136	1544	441	100.0 : 135 aa	B
419	54	1513	175	97.0 : 33 aa	E
420	125	1642	539	96.7 : 122 aa	B
421	249	1738	346	99.6 : 249 aa	B
422	86	1715	128	97.5 : 79 aa	B
423	128	1534	149	100.0 : 128 aa	B
424	93	1875	178	100.0 : 93 aa	B
425	88	1804	105	97.7 : 88 aa	B
426	128	1524	116	62.4 : 117 aa	E
427	108	1762	109	100.0 : 108 aa	A
428	118	1539	276	100.0 : 118 aa	B
429	54	1754	113	89.6 : 48 aa	E
430	288	1483	377	95.5 : 286 aa	B
431	303	1785	248	98.2 : 170 aa	D
431	303	1784	148	96.4 : 138 aa	D
432	192	1478	408	99.5 : 192 aa	B
433	168	1517	426	99.3 : 151 aa	D

-63-

434	153	1679	403	100.0 : 153 aa	B
435	162	1806	173	98.1 : 161 aa	B
436	59	1834	80	37.5 : 24 aa	E
437	222	1533	288	100.0 : 221 aa	B
438	53	1737	260	93.5 : 31 aa	E
439	109	1683	121	100.0 : 109 aa	B
440	73	1773	280	100.0 : 73 aa	B
441	237	1685	497	96.0 : 198 aa	D
442	92	1521	646	100.0 : 84 aa	D
443	97	1774	327	100.0 : 96 aa	B
444	280	1556	284	100.0 : 280 aa	A
445	187	1604	253	95.5 : 155 aa	D
446	58	1510	198	96.4 : 55 aa	B
447	85	1496	155	100.0 : 85 aa	B
448	90	1724	90	100.0 : 90 aa	A
449	105	1788	141	98.0 : 100 aa	D
450	172	1495	239	100.0 : 172 aa	B
451	212	1456	139	81.7 : 126 aa	E
452	182	1702	192	97.0 : 166 aa	D
453	224	1658	228	100.0 : 224 aa	A
454	131	1895	159	100.0 : 131 aa	B
455	73	1787	370	100.0 : 54 aa	D
456	92	1587	295	96.6 : 87 aa	B
457	205	1735	310	100.0 : 195 aa	B
458	41	1479	144	97.6 : 41 aa	B
459	219	1584	297	100.0 : 219 aa	B
460	188	1546	375	89.3 : 187 aa	E
461	231	1780	438	97.3 : 225 aa	B
462	63	1645	71	100.0 : 63 aa	B
463	183	1664	242	97.8 : 182 aa	B
464	117	1586	234	99.1 : 113 aa	B
465	153	1773	280	98.0 : 153 aa	B
466	43	1610	308	100.0 : 43 aa	B
467	240	1636	255	97.0 : 237 aa	B
468	209	1868	240	96.6 : 206 aa	B
469	95	1628	321	98.5 : 65 aa	D
470	229	1595	375	96.5 : 228 aa	B
471	92	1713	205	90.1 : 71 aa	E
472	96	1492	352	95.4 : 87 aa	B
473	1178	1748	1183	100.0 : 1178 aa	A
474	163	1822	113	92.7 : 109 aa	E
474	163	1820	88	93.1 : 58 aa	E
475	466	1840	467	100.0 : 466 aa	A
476	60	1500	90	97.0 : 33 aa	D
477	249	1854	254	100.0 : 248 aa	B
478	44	1772	528	100.0 : 44 aa	B
479	421	1693	421	99.8 : 421 aa	A
480	167	1555	340	98.1 : 162 aa	B
481	89	1888	236	100.0 : 89 aa	B
482	237	1873	461	97.5 : 236 aa	B
483	471	1594	428	99.3 : 301 aa	C
484	123	1655	366	87.9 : 107 aa	E
485	127	1655	366	99.2 : 127 aa	B
486	259	1517	259	100.0 : 259 aa	A
487	17	1481	101	93.3 : 15 aa	E
488	77	1704	246	100.0 : 77 aa	B

-64-

489	180	1554	180	100.0 : 180 aa	A
490	213	1638	577	92.3 : 209 aa	E
491	148	1452	157	100.0 : 148 aa	B
492	281	1519	849	99.6 : 281 aa	B
493	144	1525	377	94.9 : 118 aa	D
494	73	1539	276	95.8 : 71 aa	B
495	311	1670	446	99.0 : 311 aa	B
496	115	1842	384	99.1 : 114 aa	B
497	200	1600	459	100.0 : 200 aa	B
498	264	1828	458	100.0 : 264 aa	B
499	339	1490	362	99.7 : 339 aa	B
500	146	1449	430	94.4 : 142 aa	E
501	60	1465	240	98.3 : 58 aa	B
502	351	1458	532	98.6 : 346 aa	B
503	233	1666	296	94.3 : 230 aa	E
504	32	1513	175	100.0 : 32 aa	B
505	171	1462	452	91.8 : 171 aa	B
506	33	1672	121	100.0 : 24 aa	D
507	100	1650	192	80.0 : 90 aa	E
508	79	1772	528	80.8 : 78 aa	E
509	70	1662	88	96.2 : 53 aa	D
510	130	1530	131	100.0 : 130 aa	A
511	53	1723	163	91.8 : 49 aa	E
512	79	1572	189	98.5 : 65 aa	D
513	102	1889	114	99.0 : 100 aa	B
514	15	1516	407	100.0 : 12 aa	B
515	378	1747	991	97.9 : 377 aa	B
516	1027	1692	2440	100.0 : 1027 aa	B
517	155	1831	182	89.6 : 154 aa	E
518	62	1552	362	74.5 : 47 aa	E
519	237	1557	241	100.0 : 237 aa	A
520	83	1627	424	100.0 : 83 aa	B
522	64	1680	227	98.4 : 63 aa	B
523	228	1532	241	100.0 : 228 aa	B
524	273	1710	189	97.2 : 180 aa	C
524	273	1712	115	100.0 : 99 aa	C
525	15	1612	65	100.0 : 15 aa	B
526	115	1733	112	94.6 : 111 aa	C
527	67	1755	156	100.0 : 62 aa	D
528	323	1635	336	100.0 : 322 aa	B
529	10	1731	101	50.0 : 10 aa	B
530	12	1455	284	100.0 : 12 aa	B
531	79	1528	101	94.9 : 79 aa	B
532	95	1887	279	100.0 : 95 aa	B
533	154	1591	168	100.0 : 152 aa	B
534	68	1501	283	100.0 : 67 aa	B
535	313	1519	849	95.5 : 313 aa	B
536	319	1486	325	100.0 : 319 aa	A
537	118	1707	154	90.9 : 110 aa	E
538	89	1674	161	88.2 : 76 aa	E
539	92	1838	100	100.0 : 92 aa	A
540	138	1525	377	86.9 : 137 aa	B
541	277	1661	394	96.0 : 273 aa	D
542	254	1567	392	98.0 : 254 aa	B
543	185	1467	594	99.5 : 185 aa	B
544	37	1886	326	100.0 : 37 aa	B

-65-

545	94	1772	528	89.1 : 92 aa	E
546	182	1760	366	100.0 : 182 aa	B
547	247	1776	150	100.0 : 146 aa	C
547	247	1775	88	100.0 : 87 aa	C
548	422	1798	426	100.0 : 422 aa	A
549	61	1620	78	96.7 : 60 aa	B
550	54	1566	309	37.8 : 45 aa	E
551	298	1751	518	98.0 : 297 aa	B
552	91	1738	346	95.5 : 88 aa	D
553	111	1764	130	100.0 : 111 aa	B
554	137	1626	93	100.0 : 84 aa	D
555	124	1717	114	89.2 : 111 aa	E
556	86	1597	432	89.7 : 78 aa	E
557	87	1457	97	100.0 : 86 aa	B
558	108	1750	154	99.1 : 108 aa	B
559	142	1619	211	97.9 : 141 aa	B
560	231	1580	315	99.6 : 231 aa	B
561	186	1446	275	88.3 : 180 aa	E
562	183	1515	198	100.0 : 183 aa	B
563	154	1477	188	100.0 : 154 aa	B
564	288	1767	303	100.0 : 288 aa	B
565	420	1841	424	100.0 : 420 aa	A
566	72	1450	486	98.5 : 67 aa	D
567	205	1799	270	99.5 : 199 aa	D
568	328	1893	338	100.0 : 328 aa	B
569	140	1855	614	84.8 : 125 aa	E
570	76	1499	184	98.1 : 53 aa	D
571	194	1660	201	100.0 : 193 aa	B
572	140	1583	163	96.9 : 130 aa	D
573	308	1676	316	100.0 : 308 aa	B
574	339	1667	468	99.1 : 335 aa	B
575	207	1688	208	98.1 : 207 aa	A
576	251	1891	267	100.0 : 251 aa	B
577	69	1745	109	96.7 : 61 aa	D
578	112	1519	849	99.1 : 112 aa	B
579	152	1649	543	98.7 : 152 aa	B
580	130	1853	220	98.3 : 120 aa	D
581	113	1614	134	100.0 : 113 aa	B
582	174	1569	209	100.0 : 174 aa	B
583	35	1752	157	34.4 : 32 aa	E
584	308	1728	316	100.0 : 307 aa	B
585	702	1857	797	99.9 : 702 aa	B
586	293	1633	664	96.2 : 293 aa	B
587	52	1542	429	100.0 : 52 aa	B
588	182	1504	519	100.0 : 182 aa	B
589	251	1622	262	99.6 : 251 aa	B
590	40	1632	61	97.5 : 40 aa	B
591	122	1691	717	99.1 : 113 aa	D
592	113	1768	121	100.0 : 113 aa	B
593	437	1520	448	100.0 : 437 aa	A
594	146	1549	200	93.2 : 146 aa	E
595	128	1494	131	99.2 : 127 aa	B
596	95	1667	468	100.0 : 93 aa	B
597	102	1447	149	100.0 : 91 aa	D
598	127	1879	138	100.0 : 127 aa	B
599	502	1881	928	99.2 : 500 aa	B

SUBSTITUTE SHEET (RULE 26)

-66-

600	42	1625	91	100.0 : 42 aa	B
601	341	1454	381	99.7 : 341 aa	B
602	465	1694	442	98.2 : 433 aa	D
602	465	1896	259	99.6 : 238 aa	D
603	193	1484	229	99.4 : 170 aa	D
604	141	1673	130	97.6 : 126 aa	D
605	159	1582	358	83.3 : 156 aa	E
606	376	1565	382	100.0 : 376 aa	B
607	352	1862	363	99.1 : 352 aa	B
608	88	1807	144	98.7 : 77 aa	D
609	86	1553	181	72.0 : 82 aa	E
610	76	1527	77	100.0 : 76 aa	A
611	98	1732	118	98.9 : 95 aa	B
612	162	1525	377	91.3 : 161 aa	E
613	58	1547	152	98.3 : 58 aa	B
614	66	1470	455	85.2 : 61 aa	E
615	117	1844	982	95.5 : 111 aa	D
616	83	1723	163	96.3 : 82 aa	B
617	77	1763	275	89.6 : 77 aa	E
618	176	1696	149	93.6 : 125 aa	E
618	176	1698	231	92.3 : 65 aa	E
619	144	1498	577	96.0 : 124 aa	D
620	90	1516	407	98.9 : 90 aa	B
621	268	1571	275	100.0 : 268 aa	B
622	171	1753	206	99.4 : 171 aa	B
623	102	1559	256	100.0 : 84 aa	D
624	117	1819	640	94.2 : 104 aa	E
625	237	1758	842	99.6 : 233 aa	B
626	199	1464	200	100.0 : 198 aa	C
627	225	1611	347	97.7 : 221 aa	B
627	225	1608	97	97.8 : 91 aa	C
628	86	1772	528	90.4 : 83 aa	E
629	496	1558	539	100.0 : 496 aa	B
630	142	1778	332	99.1 : 116 aa	D
631	153	1709	111	76.9 : 108 aa	E
631	153	1708	76	60.9 : 46 aa	E
633	93	1848	106	100.0 : 93 aa	B
634	177	1603	531	98.9 : 175 aa	B
635	88	1812	93	100.0 : 88 aa	A
636	115	1746	122	100.0 : 115 aa	B
637	261	1850	304	98.5 : 260 aa	B
638	191	1691	717	99.5 : 185 aa	B
639	351	1697	373	99.7 : 351 aa	B
640	351	1601	355	100.0 : 342 aa	D
641	146	1592	320	96.6 : 145 aa	B
642	190	1796	376	100.0 : 190 aa	B
643	489	1705	957	99.4 : 468 aa	D
644	249	1706	249	100.0 : 248 aa	A
645	120	1540	269	100.0 : 104 aa	D
646	109	1550	350	100.0 : 108 aa	B
648	158	1573	237	95.5 : 155 aa	D
649	312	1721	312	100.0 : 312 aa	A
650	56	1839	242	98.1 : 52 aa	D
651	199	1813	261	99.5 : 196 aa	B
652	82	1756	99	96.3 : 81 aa	D
653	89	1475	227	100.0 : 89 aa	B

-67-

654	111	1535	119	98.2 : 111 aa	B
655	65	1686	276	98.3 : 59 aa	D
656	268	1892	272	100.0 : 268 aa	A
657	100	1597	432	100.0 : 84 aa	D
658	80	1640	276	97.2 : 72 aa	D
659	205	1824	217	100.0 : 205 aa	B
660	124	1471	67	98.4 : 64 aa	D
660	124	1472	186	96.7 : 60 aa	D
661	93	1618	95	98.9 : 93 aa	B
662	80	1568	170	98.7 : 79 aa	B
663	214	1749	224	100.0 : 214 aa	B
664	78	1668	214	97.3 : 75 aa	D
665	177	1844	982	78.6 : 173 aa	E
666	258	1578	275	94.1 : 254 aa	E
667	75	1742	360	100.0 : 75 aa	B
668	421	1699	421	99.5 : 421 aa	A
669	81	1542	429	100.0 : 81 aa	B
670	112	1540	269	76.1 : 113 aa	E
671	326	1689	246	92.8 : 208 aa	E
672	272	1727	279	100.0 : 271 aa	A
673	78	1661	394	100.0 : 78 aa	B
674	400	1736	419	100.0 : 400 aa	B
675	91	1522	273	95.5 : 88 aa	D
676	126	1561	131	100.0 : 126 aa	A
677	195	1577	301	76.5 : 196 aa	E
678	72	1814	90	98.6 : 72 aa	B
679	111	1572	189	100.0 : 111 aa	B
680	142	1847	207	92.6 : 135 aa	E
681	63	1516	407	96.4 : 56 aa	D
682	310	1700	446	99.3 : 301 aa	B
683	169	1744	219	100.0 : 169 aa	B
684	85	1611	347	88.1 : 84 aa	E
685	77	1829	251	97.3 : 75 aa	D
686	197	1634	425	99.0 : 194 aa	D
687	142	1722	197	100.0 : 136 aa	D
688	86	1805	87	100.0 : 86 aa	A
689	121	1759	356	97.5 : 118 aa	B
690	59	1789	77	84.6 : 52 aa	E
691	142	1675	420	97.1 : 140 aa	B
692	80	1722	197	83.3 : 60 aa	E
693	180	1659	187	100.0 : 179 aa	B
694	75	1529	159	100.0 : 75 aa	B
695	99	1849	119	100.0 : 99 aa	B
696	209	1701	430	99.5 : 205 aa	B
697	75	1616	196	100.0 : 75 aa	B
698	121	1678	460	100.0 : 121 aa	B
699	102	1579	139	99.0 : 100 aa	B
700	131	1595	375	99.2 : 131 aa	B
701	441	1488	444	96.9 : 426 aa	D
702	127	1774	327	99.1 : 116 aa	D
703	287	1765	327	93.9 : 279 aa	E
704	46	1581	111	95.2 : 21 aa	D
705	115	1647	117	100.0 : 115 aa	A
706	86	1463	111	100.0 : 86 aa	B
707	44	1588	68	100.0 : 44 aa	B
708	560	1589	1413	98.8 : 560 aa	B

-68-

709	125	1607	443	95.8 : 118 aa	D
710	96	1469	540	100.0 : 73 aa	D
711	81	1629	244	96.3 : 80 aa	D
712	141	1671	375	100.0 : 125 aa	D
713	51	1867	193	96.1 : 51 aa	B
714	233	1833	240	99.5 : 218 aa	D
715	266	1644	271	100.0 : 265 aa	B
716	158	1883	226	94.7 : 150 aa	E
717	191	1860	240	100.0 : 189 aa	B
718	243	1817	256	99.6 : 243 aa	B
719	236	1617	667	98.3 : 236 aa	B
720	175	1523	592	97.1 : 172 aa	B
721	226	1770	340	92.7 : 218 aa	E
722	79	1629	244	100.0 : 74 aa	D
723	65	1506	229	100.0 : 49 aa	D
724	138	1675	426	93.2 : 132 aa	E
725	210	1832	215	100.0 : 210 aa	A
726	296	1821	223	100.0 : 190 aa	D
726	296	1819	640	99.1 : 106 aa	D
727	94	1706	249	97.8 : 91 aa	D
728	83	1593	171	100.0 : 83 aa	B
729	203	1448	268	100.0 : 202 aa	B
730	220	1656	242	100.0 : 220 aa	B
731	116	1818	196	100.0 : 115 aa	B
732	248	1474	248	100.0 : 248 aa	A
733	150	1459	347	100.0 : 118 aa	D
734	228	1545	302	96.9 : 227 aa	B
735	187	1597	432	100.0 : 172 aa	D
736	198	1761	354	100.0 : 198 aa	B
737	208	1780	438	93.8 : 208 aa	E
738	201	1842	384	100.0 : 193 aa	D
739	127	1669	405	21.6 : 74 aa	E
740	79	1615	280	97.3 : 75 aa	D
741	49	1878	443	91.3 : 46 aa	E
742	412	1877	425	97.8 : 412 aa	B
743	89	1482	111	100.0 : 89 aa	B
744	192	1502	222	98.4 : 189 aa	B
745	109	1797	304	96.3 : 109 aa	B
746	116	1791	359	94.8 : 116 aa	B
747	163	1711	321	100.0 : 163 aa	B
748	40	1483	377	100.0 : 40 aa	B
749	45	1770	340	95.2 : 42 aa	D
750	118	1867	193	92.2 : 116 aa	E
751	200	1491	211	100.0 : 200 aa	B
752	79	1890	80	100.0 : 79 aa	A
753	98	1837	268	98.7 : 79 aa	D
754	146	1653	413	100.0 : 141 aa	B
755	206	1638	577	93.7 : 206 aa	B
756	97	1526	89	100.0 : 66 aa	D
757	197	1794	198	100.0 : 197 aa	A
758	149	1872	94	97.5 : 80 aa	D
759	68	1882	291	100.0 : 68 aa	B
760	135	1631	162	99.3 : 134 aa	B
761	93	1884	594	100.0 : 69 aa	D
762	73	1883	226	100.0 : 73 aa	B
763	268	1859	430	95.4 : 263 aa	B

-69-

764	274	1537	277	100.0 : 273 aa	B
765	134	1714	136	99.2 : 133 aa	A
766	72	1810	74	95.8 : 71 aa	A
767	147	1802	285	100.0 : 147 aa	B
768	144	1541	241	100.0 : 144 aa	B
769	47	1684	75	100.0 : 47 aa	B
770	129	1505	183	90.2 : 122 aa	E
771	242	1536	235	99.1 : 232 aa	C
772	97	1851	129	99.0 : 97 aa	B
773	143	1826	259	96.5 : 143 aa	B
774	218	1777	383	99.5 : 217 aa	B
775	84	1637	143	100.0 : 84 aa	B
776	76	1774	327	95.9 : 73 aa	D
777	155	1585	263	79.7 : 133 aa	E
778	192	1480	299	91.5 : 189 aa	E
779	171	1551	186	99.4 : 171 aa	B
780	141	1760	366	99.2 : 129 aa	D
781	70	1741	95	100.0 : 70 aa	B
782	153	1687	223	98.0 : 153 aa	B
783	183	1869	184	100.0 : 183 aa	A
784	67	1846	231	100.0 : 67 aa	B
785	254	1730	256	100.0 : 253 aa	B
786	173	1466	251	100.0 : 166 aa	D
787	259	1808	322	100.0 : 238 aa	D
788	294	1786	131	93.7 : 126 aa	E
788	294	1630	163	94.0 : 116 aa	E
789	194	1655	366	99.2 : 122 aa	D
789	194	1646	75	100.0 : 72 aa	C
790	132	1790	273	100.0 : 132 aa	B
791	213	1575	216	98.1 : 213 aa	A
792	47	1605	86	100.0 : 47 aa	B
793	143	1864	342	93.0 : 143 aa	E
794	69	1766	93	100.0 : 69 aa	B
795	144	1504	519	95.7 : 138 aa	D
796	190	1590	193	100.0 : 190 aa	A
797	84	1792	215	83.5 : 79 aa	E
798	135	1613	138	100.0 : 135 aa	A
799	255	1885	424	99.6 : 253 aa	B
800	243	1493	205	87.1 : 140 aa	E
800	243	1497	131	100.0 : 126 aa	C
801	252	1563	255	100.0 : 252 aa	A
802	165	1720	91	100.0 : 88 aa	C
802	165	1718	99	92.7 : 82 aa	E
803	171	1602	297	85.5 : 159 aa	E
804	62	1485	165	100.0 : 61 aa	B
805	199	1514	219	100.0 : 199 aa	B
806	131	1880	391	86.2 : 130 aa	E
807	101	1719	257	95.0 : 100 aa	B
808	80	1585	263	98.8 : 80 aa	B
809	447	1781	344	99.7 : 331 aa	D
809	447	1783	118	98.3 : 117 aa	C
810	218	1564	250	100.0 : 218 aa	B
811	192	1478	408	99.5 : 192 aa	B
812	341	1729	354	100.0 : 340 aa	B
813	201	1523	592	100.0 : 158 aa	D
814	130	1769	306	92.3 : 130 aa	E

SUBSTITUTE SHEET (RULE 26)

-70-

815	144	1835	548	78.4 : 116 aa	E
815	144	1815	377	84.3 : 121 aa	E
816	309	1894	310	100.0 : 309 aa	A
817	164	1823	156	96.7 : 153 aa	D
818	54	1703	87	100.0 : 53 aa	B
819	202	1716	215	99.5 : 202 aa	B
820	169	1870	115	100.0 : 110 aa	D
821	186	1451	254	100.0 : 186 aa	B
822	72	1609	180	96.6 : 58 aa	D
823	122	1633	664	94.9 : 118 aa	D
824	13	1695	70	100.0 : 13 aa	B
824	13	1567	392	100.0 : 13 aa	B
825	99	1771	144	100.0 : 86 aa	D
826	71	1512	154	98.6 : 71 aa	B
827	150	1456	139	93.7 : 127 aa	E
828	255	1651	155	100.0 : 155 aa	C
828	255	1648	109	98.0 : 102 aa	D
829	106	1726	147	99.1 : 106 aa	B
830	527	1509	567	99.8 : 524 aa	B
831	124	1740	214	99.2 : 123 aa	B
832	110	1690	400	98.2 : 110 aa	B
833	326	1856	325	100.0 : 325 aa	C
834	253	1543	191	96.7 : 184 aa	D
835	597	1876	638	100.0 : 594 aa	B
836	156	1621	345	99.4 : 154 aa	B
837	157	1624	253	97.4 : 155 aa	B
838	191	1465	241	96.8 : 190 aa	B
839	90	1548	231	92.9 : 85 aa	E
840	277	1682	298	99.6 : 277 aa	B
841	58	1508	270	98.1 : 54 aa	D
842	139	1734	139	88.4 : 129 aa	E
843	279	1476	276	100.0 : 269 aa	C
844	36	1852	83	94.4 : 36 aa	B
845	129	1460	196	100.0 : 129 aa	B
846	127	1473	172	100.0 : 105 aa	D
847	276	1657	319	100.0 : 276 aa	B
848	126	1801	187	98.4 : 126 aa	B
849	242	1669	405	97.0 : 236 aa	D
850	151	1816	217	100.0 : 151 aa	B
851	154	1641	194	100.0 : 154 aa	B
852	496	1665	327	97.5 : 314 aa	C
853	179	1606	272	97.2 : 179 aa	B
855	160	1487	198	96.9 : 160 aa	B
856	94	1836	420	100.0 : 93 aa	B
857	146	1845	371	99.3 : 146 aa	B
858	205	1507	366	98.5 : 202 aa	B
859	173	1827	198	100.0 : 149 aa	D
860	193	1681	294	100.0 : 175 aa	D
861	104	1865	253	100.0 : 104 aa	B
862	355	1599	358	100.0 : 355 aa	B
863	93	1825	236	97.8 : 92 aa	B
864	82	1677	315	97.5 : 81 aa	B
865	234	1861	249	99.1 : 233 aa	B
866	239	1652	405	99.2 : 238 aa	B
867	86	1468	201	77.4 : 84 aa	E
868	289	1574	395	94.4 : 284 aa	E

-71-

869	436	1863	662	100.0 : 436 aa	B
870	114	1560	121	100.0 : 114 aa	B
871	173	1757	362	98.8 : 173 aa	B
872	116	1866	145	98.1 : 105 aa	D
873	127	1797	304	63.9 : 83 aa	E
873	127	1799	270	89.7 : 58 aa	E
873	127	1800	62	97.4 : 38 aa	D
873	127	1801	187	82.0 : 50 aa	E
874	150	1461	179	100.0 : 150 aa	B
875	209	1511	339	98.9 : 188 aa	D
876	234	1739	615	99.6 : 230 aa	B
877	395	1830	879	99.7 : 379 aa	D
878	103	1623	413	97.0 : 99 aa	D
879	265	1809	566	89.8 : 265 aa	B
880	364	1576	442	98.6 : 346 aa	D

IV. Identification of Nucleic Acids Encoding Vaccine Components and Targets for Agents Effective Against *H. pylori*

The disclosed *H. pylori* genome sequence includes segments that direct the synthesis of ribonucleic acids and polypeptides, as well as origins of replication, promoters, other types of regulatory sequences, and intergenic nucleic acids. The invention encompasses nucleic acids encoding immunogenic components of vaccines and targets for agents effective against *H. pylori*. Identification of said immunogenic components involved in the determination of the function of the disclosed sequences, which can be achieved using a variety of approaches. Non-limiting examples of these approaches are described briefly below.

Homology to known sequences: Computer-assisted comparison of the disclosed *H. pylori* sequences with previously reported sequences present in publicly available databases is useful for identifying functional *H. pylori* nucleic acid and polypeptide sequences. It will be understood that protein-coding sequences, for example, may be compared as a whole, and that a high degree of sequence homology between two proteins (such as, for example, >80-90%) at the amino acid level indicates that the two proteins also possess some degree of functional homology, such as, for example, among enzymes involved in metabolism, DNA synthesis, or cell wall synthesis, and proteins involved in transport, cell division, etc. In addition, many structural features of particular protein classes have been identified and correlate with specific consensus sequences, such as, for example, binding domains for nucleotides, DNA, metal ions, and other small molecules; sites for covalent modifications such as phosphorylation, acylation, and the like; sites of protein:protein interactions, etc. These consensus sequences may be quite short and thus may represent only a fraction of the entire protein-coding sequence. Identification of such a feature in an *H. pylori* sequence is therefore useful in determining the function of the encoded protein and identifying useful targets of antibacterial drugs.

Of particular relevance to the present invention are structural features that are common to secretory, transmembrane, and surface proteins, including secretion signal

-72-

peptides and hydrophobic transmembrane domains. *H. pylori* proteins identified as containing putative signal sequences and/or transmembrane domains are useful as immunogenic components of vaccines.

5 Identification of essential genes: Nucleic acids that encode proteins essential for growth or viability of *H. pylori* are preferred drug targets. *H. pylori* genes can be tested for their biological relevance to the organism by examining the effect of deleting and/or disrupting the genes, i.e., by so-called gene "knockout", using techniques known to those skilled in the relevant art. In this manner, essential genes may be identified.

10 Strain-specific sequences: Because of the evolutionary relationship between different *H. pylori* strains, it is believed that the presently disclosed *H. pylori* sequences are useful for identifying, and/or discriminating between, previously known and new *H. pylori* strains. It is believed that other *H. pylori* strains will exhibit at least 70% sequence homology with the presently disclosed sequence. Systematic and routine analyses of DNA sequences derived from samples containing *H. pylori* strains, and comparison with the
15 present sequence allows for the identification of sequences that can be used to discriminate between strains, as well as those that are common to all *H. pylori* strains. In one embodiment, the invention provides nucleic acids, including probes, and peptide and polypeptide sequences that discriminate between different strains of *H. pylori*. Strain-specific components can also be identified functionally by their ability to elicit or react with
20 antibodies that selectively recognize one or more *H. pylori* strains.

In another embodiment, the invention provides nucleic acids, including probes, and peptide and polypeptide sequences that are common to all *H. pylori* strains but are *not* found in other bacterial species.

25 Specific Example: Determination Of Candidate Protein Antigens For Antibody And Vaccine Development

The selection of candidate protein antigens for vaccine development can be derived from the nucleic acids encoding *H. pylori* polypeptides. First, the ORF's can be analyzed for homology to other known exported or membrane proteins and analyzed using the
30 discriminant analysis described by Klein, et al. (Klein, P., Kanehsia, M., and DeLisi, C. (1985) *Biochimica et Biophysica Acta* 815, 468-476) for predicting exported and membrane proteins.

Homology searches can be performed using the BLAST algorithm contained in the Wisconsin Sequence Analysis Package (Genetics Computer Group, University Research
35 Park, 575 Science Drive, Madison, WI 53711) to compare each predicted ORF amino acid sequence with all sequences found in the current GenBank, SWISS-PROT and PIR databases. BLAST searches for local alignments between the ORF and the databank sequences and reports a probability score which indicates the probability of finding this sequence by chance in the database. ORF's with significant homology (e.g. probabilities

lower than 1×10^{-6} that the homology is only due to random chance) to membrane or exported proteins represent protein antigens for vaccine development. Possible functions can be provided to *H. pylori* genes based on sequence homology to genes cloned in other organisms.

- 5 Discriminant analysis (Klein, et al. supra) can be used to examine the ORF amino acid sequences. This algorithm uses the intrinsic information contained in the ORF amino acid sequence and compares it to information derived from the properties of known membrane and exported proteins. This comparison predicts which proteins will be exported, membrane associated or cytoplasmic. ORF amino acid sequences identified as
10 exported or membrane associated by this algorithm are likely protein antigens for vaccine development.

Infrequently it is not possible to distinguish between multiple possible nucleotides at a given position in the nucleic acid sequence. In those cases the ambiguities are denoted by an extended alphabet as follows:

- 15 These are the official IUPAC-IUB single-letter base codes

Code	Base Description	
G	Guanine	
A	Adenine	
T	Thymine	
C	Cytosine	
R	Purine	(A or G)
Y	Pyrimidine	(C or T or U)
M	Amino	(A or C)
K	Ketone	(G or T)
S	Strong interaction	(C or G)
W	Weak interaction	(A or T)
H	Not-G	(A or C or T)
B	Not-A	(C or G or T)
V	Not-T (not-U)	(A or C or G)
D	Not-C	(A or G or T)
N	Any	(A or C or G or T)

- The amino acid translations of this invention account for the ambiguity in the nucleic acid sequence by translating the ambiguous codon as the letter "X". In all cases, the
20 permissible amino acid residues at a position are clear from an examination of the nucleic acid sequence based on the standard genetic code.

V. Production of Fragments and Analogs of *H. pylori* Nucleic Acids and Polypeptides

Based on the discovery of the *H. pylori* gene products of the invention provided in the Sequence Listing, one skilled in the art can alter the disclosed structure (of *H. pylori* genes), e.g., by producing fragments or analogs, and test the newly produced structures for activity. Examples of techniques known to those skilled in the relevant art which allow the production and testing of fragments and analogs are discussed below. These, or analogous methods can be used to make and screen libraries of polypeptides, e.g., libraries of random peptides or libraries of fragments or analogs of cellular proteins for the ability to bind *H. pylori* polypeptides. Such screens are useful for the identification of inhibitors of *H. pylori*.

Generation of Fragments

Fragments of a protein can be produced in several ways, e.g., recombinantly, by proteolytic digestion, or by chemical synthesis. Internal or terminal fragments of a polypeptide can be generated by removing one or more nucleotides from one end (for a terminal fragment) or both ends (for an internal fragment) of a nucleic acid which encodes the polypeptide. Expression of the mutagenized DNA produces polypeptide fragments. Digestion with "end-nibbling" endonucleases can thus generate DNA's which encode an array of fragments. DNA's which encode fragments of a protein can also be generated by random shearing, restriction digestion or a combination of the above-discussed methods.

Fragments can also be chemically synthesized using techniques known in the art such as conventional Merrifield solid phase f-Moc or t-Boc chemistry. For example, peptides of the present invention may be arbitrarily divided into fragments of desired length with no overlap of the fragments, or divided into overlapping fragments of a desired length.

Alteration of Nucleic Acids and Polypeptides: Random Methods

Amino acid sequence variants of a protein can be prepared by random mutagenesis of DNA which encodes a protein or a particular domain or region of a protein. Useful methods include PCR mutagenesis and saturation mutagenesis. A library of random amino acid sequence variants can also be generated by the synthesis of a set of degenerate oligonucleotide sequences. (Methods for screening proteins in a library of variants are elsewhere herein).

(A) PCR Mutagenesis

In PCR mutagenesis, reduced Taq polymerase fidelity is used to introduce random mutations into a cloned fragment of DNA (Leung et al., 1989, *Technique* 1:11-15). The DNA region to be mutagenized is amplified using the polymerase chain reaction (PCR) under conditions that reduce the fidelity of DNA synthesis by Taq DNA polymerase, e.g., by using a dGTP/dATP ratio of five and adding Mn^{2+} to the PCR reaction. The pool of amplified DNA fragments are inserted into appropriate cloning vectors to provide random mutant libraries.

(B) Saturation Mutagenesis

Saturation mutagenesis allows for the rapid introduction of a large number of single base substitutions into cloned DNA fragments (Mayers et al., 1985, *Science* 229:242). This technique includes generation of mutations, e.g., by chemical treatment or irradiation of single-stranded DNA *in vitro*, and synthesis of a complimentary DNA strand. The mutation frequency can be modulated by modulating the severity of the treatment, and essentially all possible base substitutions can be obtained. Because this procedure does not involve a genetic selection for mutant fragments both neutral substitutions, as well as those that alter function, are obtained. The distribution of point mutations is not biased toward conserved sequence elements.

(C) Degenerate Oligonucleotides

A library of homologs can also be generated from a set of degenerate oligonucleotide sequences. Chemical synthesis of a degenerate sequences can be carried out in an automatic DNA synthesizer, and the synthetic genes then ligated into an appropriate expression vector. The synthesis of degenerate oligonucleotides is known in the art (see for example, Narang, SA (1983) *Tetrahedron* 39:3; Itakura et al. (1981) *Recombinant DNA, Proc 3rd Cleveland Sympos. Macromolecules*, ed. AG Walton, Amsterdam: Elsevier pp273-289; Itakura et al. (1984) *Annu. Rev. Biochem.* 53:323; Itakura et al. (1984) *Science* 198:1056; Ike et al. (1983) *Nucleic Acid Res.* 11:477. Such techniques have been employed in the directed evolution of other proteins (see, for example, Scott et al. (1990) *Science* 249:386-390; Roberts et al. (1992) *PNAS* 89:2429-2433; Devlin et al. (1990) *Science* 249: 404-406; Cwirla et al. (1990) *PNAS* 87: 6378-6382; as well as U.S. Patents Nos. 5,223,409, 5,198,346, and 5,096,815).

25 Alteration of Nucleic Acids and Polypeptides: Methods for Directed Mutagenesis

Non-random or directed, mutagenesis techniques can be used to provide specific sequences or mutations in specific regions. These techniques can be used to create variants which include, e.g., deletions, insertions, or substitutions, of residues of the known amino acid sequence of a protein. The sites for mutation can be modified individually or in series, e.g., by (1) substituting first with conserved amino acids and then with more radical choices depending upon results achieved, (2) deleting the target residue, or (3) inserting residues of the same or a different class adjacent to the located site, or combinations of options 1-3.

(A) Alanine Scanning Mutagenesis

Alanine scanning mutagenesis is a useful method for identification of certain residues or regions of the desired protein that are preferred locations or domains for mutagenesis, Cunningham and Wells (*Science* 244:1081-1085, 1989). In alanine scanning, a residue or group of target residues are identified (e.g., charged residues such as Arg, Asp, His, Lys, and Glu) and replaced by a neutral or negatively charged amino acid (most preferably alanine or polyalanine). Replacement of an amino acid can affect the interaction

-76-

of the amino acids with the surrounding aqueous environment in or outside the cell. Those domains demonstrating functional sensitivity to the substitutions are then refined by introducing further or other variants at or for the sites of substitution. Thus, while the site for introducing an amino acid sequence variation is predetermined, the nature of the mutation per se need not be predetermined. For example, to optimize the performance of a mutation at a given site, alanine scanning or random mutagenesis may be conducted at the target codon or region and the expressed desired protein subunit variants are screened for the optimal combination of desired activity.

(B) Oligonucleotide-Mediated Mutagenesis

Oligonucleotide-mediated mutagenesis is a useful method for preparing substitution, deletion, and insertion variants of DNA, see, e.g., Adelman et al., (*DNA* 2:183, 1983). Briefly, the desired DNA is altered by hybridizing an oligonucleotide encoding a mutation to a DNA template, where the template is the single-stranded form of a plasmid or bacteriophage containing the unaltered or native DNA sequence of the desired protein. After hybridization, a DNA polymerase is used to synthesize an entire second complementary strand of the template that will thus incorporate the oligonucleotide primer, and will code for the selected alteration in the desired protein DNA. Generally, oligonucleotides of at least 25 nucleotides in length are used. An optimal oligonucleotide will have 12 to 15 nucleotides that are completely complementary to the template on either side of the nucleotide(s) coding for the mutation. This ensures that the oligonucleotide will hybridize properly to the single-stranded DNA template molecule. The oligonucleotides are readily synthesized using techniques known in the art such as that described by Crea et al. (*Proc. Natl. Acad. Sci. USA*, 75: 5765[1978]).

(C) Cassette Mutagenesis

Another method for preparing variants, cassette mutagenesis, is based on the technique described by Wells et al. (*Gene*, 34:315[1985]). The starting material is a plasmid (or other vector) which includes the protein subunit DNA to be mutated. The codon(s) in the protein subunit DNA to be mutated are identified. There must be a unique restriction endonuclease site on each side of the identified mutation site(s). If no such restriction sites exist, they may be generated using the above-described oligonucleotide-mediated mutagenesis method to introduce them at appropriate locations in the desired protein subunit DNA. After the restriction sites have been introduced into the plasmid, the plasmid is cut at these sites to linearize it. A double-stranded oligonucleotide encoding the sequence of the DNA between the restriction sites but containing the desired mutation(s) is synthesized using standard procedures. The two strands are synthesized separately and then hybridized together using standard techniques. This double-stranded oligonucleotide is referred to as the cassette. This cassette is designed to have 3' and 5' ends that are comparable with the ends of the linearized plasmid, such that it can be directly ligated to

-77-

the plasmid. This plasmid now contains the mutated desired protein subunit DNA sequence.

(D) Combinatorial Mutagenesis

Combinatorial mutagenesis can also be used to generate mutants (Ladner et al., WO 88/06630). In this method, the amino acid sequences for a group of homologs or other related proteins are aligned, preferably to promote the highest homology possible. All of the amino acids which appear at a given position of the aligned sequences can be selected to create a degenerate set of combinatorial sequences. The variegated library of variants is generated by combinatorial mutagenesis at the nucleic acid level, and is encoded by a variegated gene library. For example, a mixture of synthetic oligonucleotides can be enzymatically ligated into gene sequences such that the degenerate set of potential sequences are expressible as individual peptides, or alternatively, as a set of larger fusion proteins containing the set of degenerate sequences.

Other Modifications of *H. pylori* Nucleic Acids and Polypeptides

It is possible to modify the structure of an *H. pylori* polypeptide for such purposes as increasing solubility, enhancing stability (e.g., shelf life *ex vivo* and resistance to proteolytic degradation *in vivo*). A modified *H. pylori* protein or peptide can be produced in which the amino acid sequence has been altered, such as by amino acid substitution, deletion, or addition as described herein.

An *H. pylori* peptide can also be modified by substitution of cysteine residues preferably with alanine, serine, threonine, leucine or glutamic acid residues to minimize dimerization via disulfide linkages. In addition, amino acid side chains of fragments of the protein of the invention can be chemically modified. Another modification is cyclization of the peptide.

In order to enhance stability and/or reactivity, an *H. pylori* polypeptide can be modified to incorporate one or more polymorphisms in the amino acid sequence of the protein resulting from any natural allelic variation. Additionally, D-amino acids, non-natural amino acids, or non-amino acid analogs can be substituted or added to produce a modified protein within the scope of this invention. Furthermore, an *H. pylori* polypeptide can be modified using polyethylene glycol (PEG) according to the method of A. Schon and co-workers (Wie et al., *supra*) to produce a protein conjugated with PEG. In addition, PEG can be added during chemical synthesis of the protein. Other modifications of *H. pylori* proteins include reduction/alkylation (Tarr, *Methods of Protein Microcharacterization*, J. E. Silver ed., Humana Press, Clifton NJ 155-194 (1986)); acylation (Tarr, *supra*); chemical coupling to an appropriate carrier (Mishell and Shiigi, eds, *Selected Methods in Cellular Immunology*, WH Freeman, San Francisco, CA (1980), U.S. Patent 4,939,239; or mild formalin treatment (Marsh, (1971) *Int. Arch. of Allergy and Appl. Immunol.*, 41: 199 - 215).

-78-

To facilitate purification and potentially increase solubility of an *H. pylori* protein or peptide, it is possible to add an amino acid fusion moiety to the peptide backbone. For example, hexa-histidine can be added to the protein for purification by immobilized metal ion affinity chromatography (Hochuli, E. et al., (1988) *Bio/Technology*, 6: 1321 - 1325). In addition, to facilitate isolation of peptides free of irrelevant sequences, specific endoprotease cleavage sites can be introduced between the sequences of the fusion moiety and the peptide.

To potentially aid proper antigen processing of epitopes within an *H. pylori* polypeptide, canonical protease sensitive sites can be engineered between regions, each comprising at least one epitope via recombinant or synthetic methods. For example, charged amino acid pairs, such as KK or RR, can be introduced between regions within a protein or fragment during recombinant construction thereof. The resulting peptide can be rendered sensitive to cleavage by cathepsin and/or other trypsin-like enzymes which would generate portions of the protein containing one or more epitopes. In addition, such charged amino acid residues can result in an increase in the solubility of the peptide.

Primary Methods for Screening Polypeptides and Analogs

Various techniques are known in the art for screening generated mutant gene products. Techniques for screening large gene libraries often include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the genes under conditions in which detection of a desired activity, e.g., in this case, binding to *H. pylori* polypeptide or an interacting protein, facilitates relatively easy isolation of the vector encoding the gene whose product was detected. Each of the techniques described below is amenable to high through-put analysis for screening large numbers of sequences created, e.g., by random mutagenesis techniques.

(A) Two Hybrid Systems

Two hybrid assays such as the system described above (as with the other screening methods described herein), can be used to identify polypeptides, e.g., fragments or analogs of a naturally-occurring *H. pylori* polypeptide, e.g., of cellular proteins, or of randomly generated polypeptides which bind to an *H. pylori* protein. (The *H. pylori* domain is used as the bait protein and the library of variants are expressed as fish fusion proteins.) In an analogous fashion, a two hybrid assay (as with the other screening methods described herein), can be used to find polypeptides which bind a *H. pylori* polypeptide.

(B) Display Libraries

In one approach to screening assays, the candidate peptides are displayed on the surface of a cell or viral particle, and the ability of particular cells or viral particles to bind an appropriate receptor protein via the displayed product is detected in a "panning assay". For example, the gene library can be cloned into the gene for a surface membrane protein of a bacterial cell, and the resulting fusion protein detected by panning (Ladner et al., WO

88/06630; Fuchs et al. (1991) *Bio/Technology* 9:1370-1371; and Goward et al. (1992) *TIBS* 18:136-140). In a similar fashion, a detectably labeled ligand can be used to score for potentially functional peptide homologs. Fluorescently labeled ligands, e.g., receptors, can be used to detect homologs which retain ligand-binding activity. The use of fluorescently labeled ligands, allows cells to be visually inspected and separated under a fluorescence microscope, or, where the morphology of the cell permits, to be separated by a fluorescence-activated cell sorter.

A gene library can be expressed as a fusion protein on the surface of a viral particle. For instance, in the filamentous phage system, foreign peptide sequences can be expressed on the surface of infectious phage, thereby conferring two significant benefits. First, since these phage can be applied to affinity matrices at concentrations well over 10^{13} phage per milliliter, a large number of phage can be screened at one time. Second, since each infectious phage displays a gene product on its surface, if a particular phage is recovered from an affinity matrix in low yield, the phage can be amplified by another round of infection. The group of almost identical *E. coli* filamentous phages M13, fd., and f1 are most often used in phage display libraries. Either of the phage gIII or gVIII coat proteins can be used to generate fusion proteins without disrupting the ultimate packaging of the viral particle. Foreign epitopes can be expressed at the NH₂-terminal end of pIII and phage bearing such epitopes recovered from a large excess of phage lacking this epitope (Ladner et al. PCT publication WO 90/02909; Garrard et al., PCT publication WO 92/09690; Marks et al. (1992) *J. Biol. Chem.* 267:16007-16010; Griffiths et al. (1993) *EMBO J* 12:725-734; Clackson et al. (1991) *Nature* 352:624-628; and Barbas et al. (1992) *PNAS* 89:4457-4461).

A common approach uses the maltose receptor of *E. coli* (the outer membrane protein, LamB) as a peptide fusion partner (Charbit et al. (1986) *EMBO* 5, 3029-3037). Oligonucleotides have been inserted into plasmids encoding the LamB gene to produce peptides fused into one of the extracellular loops of the protein. These peptides are available for binding to ligands, e.g., to antibodies, and can elicit an immune response when the cells are administered to animals. Other cell surface proteins, e.g., OmpA (Schorr et al. (1991) *Vaccines* 9, pp. 387-392), PhoE (Agterberg, et al. (1990) *Gene* 88, 37-45), and PAL (Fuchs et al. (1991) *Bio/Tech* 9, 1369-1372), as well as large bacterial surface structures have served as vehicles for peptide display. Peptides can be fused to pilin, a protein which polymerizes to form the pilus-a conduit for interbacterial exchange of genetic information (Thiry et al. (1989) *Appl. Environ. Microbiol.* 55, 984-993). Because of its role in interacting with other cells, the pilus provides a useful support for the presentation of peptides to the extracellular environment. Another large surface structure used for peptide display is the bacterial motive organ, the flagellum. Fusion of peptides to the subunit protein flagellin offers a dense array of many peptide copies on the host cells (Kuwayama et al. (1988) *Bio/Tech.* 6, 1080-1083). Surface proteins of other bacterial species have also served as peptide fusion partners. Examples include the *Staphylococcus*

-80-

protein A and the outer membrane IgA protease of *Neisseria* (Hansson et al. (1992) *J. Bacteriol.* 174, 4239-4245 and Klauser et al. (1990) *EMBO J.* 9, 1991-1999).

In the filamentous phage systems and the LamB system described above, the physical link between the peptide and its encoding DNA occurs by the containment of the DNA within a particle (cell or phage) that carries the peptide on its surface. Capturing the peptide captures the particle and the DNA within. An alternative scheme uses the DNA-binding protein LacI to form a link between peptide and DNA (Cull *et al.* (1992) *PNAS USA* 89:1865-1869). This system uses a plasmid containing the LacI gene with an oligonucleotide cloning site at its 3'-end. Under the controlled induction by arabinose, a LacI-peptide fusion protein is produced. This fusion retains the natural ability of LacI to bind to a short DNA sequence known as LacO operator (LacO). By installing two copies of LacO on the expression plasmid, the LacI-peptide fusion binds tightly to the plasmid that encoded it. Because the plasmids in each cell contain only a single oligonucleotide sequence and each cell expresses only a single peptide sequence, the peptides become specifically and stably associated with the DNA sequence that directed its synthesis. The cells of the library are gently lysed and the peptide-DNA complexes are exposed to a matrix of immobilized receptor to recover the complexes containing active peptides. The associated plasmid DNA is then reintroduced into cells for amplification and DNA sequencing to determine the identity of the peptide ligands. As a demonstration of the practical utility of the method, a large random library of dodecapeptides was made and selected on a monoclonal antibody raised against the opioid peptide dynorphin B. A cohort of peptides was recovered, all related by a consensus sequence corresponding to a six-residue portion of dynorphin B. (Cull et al. (1992) *Proc. Natl. Acad. Sci. U.S.A.* 89-1869)

This scheme, sometimes referred to as peptides-on-plasmids, differs in two important ways from the phage display methods. First, the peptides are attached to the C-terminus of the fusion protein, resulting in the display of the library members as peptides having free carboxy termini. Both of the filamentous phage coat proteins, pIII and pVIII, are anchored to the phage through their C-termini, and the guest peptides are placed into the outward-extending N-terminal domains. In some designs, the phage-displayed peptides are presented right at the amino terminus of the fusion protein. (Cwirla, et al. (1990) *Proc. Natl. Acad. Sci. U.S.A.* 87, 6378-6382) A second difference is the set of biological biases affecting the population of peptides actually present in the libraries. The LacI fusion molecules are confined to the cytoplasm of the host cells. The phage coat fusions are exposed briefly to the cytoplasm during translation but are rapidly secreted through the inner membrane into the periplasmic compartment, remaining anchored in the membrane by their C-terminal hydrophobic domains, with the N-termini, containing the peptides, protruding into the periplasm while awaiting assembly into phage particles. The peptides in the LacI and phage libraries may differ significantly as a result of their exposure to different proteolytic activities. The phage coat proteins require transport across the inner

membrane and signal peptidase processing as a prelude to incorporation into phage. Certain peptides exert a deleterious effect on these processes and are underrepresented in the libraries (Gallop et al. (1994) *J. Med. Chem.* 37(9):1233-1251). These particular biases are not a factor in the LacI display system.

- 5 The number of small peptides available in recombinant random libraries is enormous. Libraries of 10^7 - 10^9 independent clones are routinely prepared. Libraries as large as 10^{11} recombinants have been created, but this size approaches the practical limit for clone libraries. This limitation in library size occurs at the step of transforming the DNA containing randomized segments into the host bacterial cells. To circumvent this
- 10 limitation, an *in vitro* system based on the display of nascent peptides in polysome complexes has recently been developed. This display library method has the potential of producing libraries 3-6 orders of magnitude larger than the currently available phage/phagemid or plasmid libraries. Furthermore, the construction of the libraries, expression of the peptides, and screening, is done in an entirely cell-free format.
- 15 In one application of this method (Gallop et al. (1994) *J. Med. Chem.* 37(9):1233-1251), a molecular DNA library encoding 10^{12} decapeptides was constructed and the library expressed in an *E. coli* S30 *in vitro* coupled transcription/translation system. Conditions were chosen to stall the ribosomes on the mRNA, causing the accumulation of a
- 20 substantial proportion of the RNA in polysomes and yielding complexes containing nascent peptides still linked to their encoding RNA. The polysomes are sufficiently robust to be affinity purified on immobilized receptors in much the same way as the more conventional recombinant peptide display libraries are screened. RNA from the bound complexes is recovered, converted to cDNA, and amplified by PCR to produce a template for the next
- 25 round of synthesis and screening. The polysome display method can be coupled to the phage display system. Following several rounds of screening, cDNA from the enriched pool of polysomes was cloned into a phagemid vector. This vector serves as both a peptide expression vector, displaying peptides fused to the coat proteins, and as a DNA sequencing vector for peptide identification. By expressing the polysome-derived peptides on phage, one can either continue the affinity selection procedure in this format or assay the peptides
- 30 on individual clones for binding activity in a phage ELISA, or for binding specificity in a completion phage ELISA (Barret, et al. (1992) *Anal. Biochem* 204,357-364). To identify the sequences of the active peptides one sequences the DNA produced by the phagemid host.

35 Secondary Screening of Polypeptides and Analogs

The high through-put assays described above can be followed by secondary screens in order to identify further biological activities which will, e.g., allow one skilled in the art to differentiate agonists from antagonists. The type of a secondary screen used will depend on the desired activity that needs to be tested. For example, an assay can be developed in

-82-

which the ability to inhibit an interaction between a protein of interest and its respective ligand can be used to identify antagonists from a group of peptide fragments isolated though one of the primary screens described above.

Therefore, methods for generating fragments and analogs and testing them for activity are known in the art. Once the core sequence of interest is identified, it is routine for one skilled in the art to obtain analogs and fragments.

Peptide Mimetics of *H. pylori* Polypeptides

The invention also provides for reduction of the protein binding domains of the subject *H. pylori* polypeptides to generate mimetics, e.g. peptide or non-peptide agents. The peptide mimetics are able to disrupt binding of a polypeptide to its counter ligand, e.g., in the case of an *H. pylori* polypeptide binding to a naturally occurring ligand. The critical residues of a subject *H. pylori* polypeptide which are involved in molecular recognition of a polypeptide can be determined and used to generate *H. pylori*-derived peptidomimetics which competitively or noncompetitively inhibit binding of the *H. pylori* polypeptide with an interacting polypeptide (see, for example, European patent applications EP-412,762A and EP-B31,080A).

For example, scanning mutagenesis can be used to map the amino acid residues of a particular *H. pylori* polypeptide involved in binding an interacting polypeptide, peptidomimetic compounds (e.g. diazepine or isoquinoline derivatives) can be generated which mimic those residues in binding to an interacting polypeptide, and which therefore can inhibit binding of an *H. pylori* polypeptide to an interacting polypeptide and thereby interfere with the function of *H. pylori* polypeptide. For instance, non-hydrolyzable peptide analogs of such residues can be generated using benzodiazepine (e.g., see Freidinger et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), azepine (e.g., see Huffman et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), substituted gamma lactam rings (Garvey et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), keto-methylene pseudopeptides (Ewenson et al. (1986) *J Med Chem* 29:295; and Ewenson et al. in *Peptides: Structure and Function* (Proceedings of the 9th American Peptide Symposium) Pierce Chemical Co. Rockland, IL, 1985), β -turn dipeptide cores (Nagai et al. (1985) *Tetrahedron Lett* 26:647; and Sato et al. (1986) *J Chem Soc Perkin Trans* 1:1231), and β -aminoalcohols (Gordon et al. (1985) *Biochem Biophys Res Commun* 126:419; and Dann et al. (1986) *Biochem Biophys Res Commun* 134:71).

VI. Vaccine Formulations for *H. pylori* Nucleic Acids and Polypeptides

This invention also features vaccine compositions for protection against infection by *H. pylori* or for treatment of *H. pylori* infection, a gram-negative spiral microaerophilic bacterium. In one embodiment, the vaccine compositions contain one or more
5 immunogenic components such as a surface protein from *H. pylori*, or portion thereof, and a pharmaceutically acceptable carrier. Nucleic acids within the scope of the invention are exemplified by the nucleic acids of the invention contained in the Sequence Listing which encode *H. pylori* surface proteins. For example, the preferred nucleic acid for a vaccine composition of the invention is isolated from the group of nucleic acids which encode cell
10 envelope proteins as outlined in Table 1. More specifically, the amino acids of SEQ ID NO:812, SEQ ID NO:820, SEQ ID NO:880, SEQ ID NO:658, SEQ ID NO:865, SEQ ID NO:1729, SEQ ID NO:1861, or fragments thereof, can be used alone or in combination for the formulation of vaccine compositions of the invention, as well as, their corresponding nucleic acids of SEQ ID NO:977, SEQ ID NO:978, SEQ ID NO:994, SEQ ID NO:215,
15 SEQ ID NO:989, SEQ ID NO:1278, and SEQ ID NO:1410. However, any nucleic acid encoding an immunogenic *H. pylori* protein, or portion thereof, which is capable of expression in a cell, can be used in the present invention. These vaccines have therapeutic and prophylactic utilities.

One aspect of the invention provides a vaccine composition for protection against
20 infection by *H. pylori* which contains at least one immunogenic fragment of an *H. pylori* protein and a pharmaceutically acceptable carrier. Preferred fragments include peptides of at least about 10 amino acid residues in length, preferably about 10-20 amino acid residues in length, and more preferably about 12-16 amino acid residues in length.

Immunogenic components of the invention can be obtained, for example, by
25 screening polypeptides recombinantly produced from the corresponding fragment of the nucleic acid encoding the full-length *H. pylori* protein. In addition, fragments can be chemically synthesized using techniques known in the art such as conventional Merrifield solid phase f-Moc or t-Boc chemistry.

In one embodiment, immunogenic components are identified by the ability of the
30 peptide to stimulate T cells. Peptides which stimulate T cells, as determined by, for example, T cell proliferation or cytokine secretion are defined herein as comprising at least one T cell epitope. T cell epitopes are believed to be involved in initiation and perpetuation of the immune response to the protein allergen which is responsible for the clinical symptoms of allergy. These T cell epitopes are thought to trigger early events at the level
35 of the T helper cell by binding to an appropriate HLA molecule on the surface of an antigen presenting cell, thereby stimulating the T cell subpopulation with the relevant T cell receptor for the epitope. These events lead to T cell proliferation, lymphokine secretion, local inflammatory reactions, recruitment of additional immune cells to the site of antigen/T cell interaction, and activation of the B cell cascade, leading to the production of

antibodies. A T cell epitope is the basic element, or smallest unit of recognition by a T cell receptor, where the epitope comprises amino acids essential to receptor recognition (e.g., approximately 6 or 7 amino acid residues). Amino acid sequences which mimic those of the T cell epitopes are within the scope of this invention.

5 Screening immunogenic components can be accomplished using one or more of several different assays. For example, *in vitro*, peptide T cell stimulatory activity is assayed by contacting a peptide known or suspected of being immunogenic with an antigen presenting cell which presents appropriate MHC molecules in a T cell culture. Presentation of an immunogenic *H. pylori* peptide in association with appropriate MHC molecules to T
10 cells in conjunction with the necessary costimulation has the effect of transmitting a signal to the T cell that induces the production of increased levels of cytokines, particularly of interleukin-2 and interleukin-4. The culture supernatant can be obtained and assayed for interleukin-2 or other known cytokines. For example, any one of several conventional assays for interleukin-2 can be employed, such as the assay described in *Proc. Natl. Acad.*
15 *Sci USA*, 86: 1333 (1989) the pertinent portions of which are incorporated herein by reference. A kit for an assay for the production of interferon is also available from Genzyme Corporation (Cambridge, MA).

 Alternatively, a common assay for T cell proliferation entails measuring tritiated thymidine incorporation. The proliferation of T cells can be measured *in vitro* by
20 determining the amount of ³H-labeled thymidine incorporated into the replicating DNA of cultured cells. Therefore, the rate of DNA synthesis and, in turn, the rate of cell division can be quantified.

 Vaccine compositions of the invention containing immunogenic components (e.g., *H. pylori* polypeptide or fragment thereof or nucleic acid encoding an *H. pylori* polypeptide
25 or fragment thereof) preferably include a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier that does not cause an allergic reaction or other untoward effect in patients to whom it is administered. Suitable pharmaceutically acceptable carriers include, for example, one or more of water, saline, phosphate buffered saline, dextrose, glycerol, ethanol and the like, as well as combinations
30 thereof. Pharmaceutically acceptable carriers may further comprise minor amounts of auxiliary substances such as wetting or emulsifying agents, preservatives or buffers, which enhance the shelf life or effectiveness of the antibody. For vaccines of the invention containing *H. pylori* polypeptides, the polypeptide is coadministered with a suitable adjuvant.

35 It will be apparent to those of skill in the art that the therapeutically effective amount of DNA or protein of this invention will depend, *inter alia*, upon the administration schedule, the unit dose of antibody administered, whether the protein or DNA is administered in combination with other therapeutic agents, the immune status and health of the patient, and the therapeutic activity of the particular protein or DNA.

- Vaccine compositions are conventionally administered parenterally, e.g., by injection, either subcutaneously or intramuscularly. Methods for intramuscular immunization are described by Wolff et al. (1990) *Science* 247: 1465-1468 and by Sedegah et al. (1994) *Immunology* 91: 9866-9870. Other modes of administration include oral and pulmonary formulations, suppositories, and transdermal applications. Oral immunization is preferred over parenteral methods for inducing protection against infection by *H. pylori*. Czinn et. al. (1993) *Vaccine* 11: 637-642. Oral formulations include such normally employed excipients as, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, and the like.
- 10 The vaccine compositions of the invention can include an adjuvant, including, but not limited to aluminum hydroxide; N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP); N-acetyl-nor-muramyl-L-alanyl-D-isoglutamine (CGP 11637, referred to as nor-MDP); N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine (CGP 19835A, referred to as MTP-PE);
- 15 RIBI, which contains three components from bacteria; monophosphoryl lipid A; trehalose dimycolate; cell wall skeleton (MPL + TDM + CWS) in a 2% squalene/Tween 80 emulsion; and cholera toxin. Others which may be used are non-toxic derivatives of cholera toxin, including its B subunit, and/or conjugates or genetically engineered fusions of the *H. pylori* polypeptide with cholera toxin or its B subunit, procholeraenoid, fungal polysaccharides, including schizophyllan, muramyl dipeptide, muramyl dipeptide derivatives, phorbol esters, labile toxin of *E. coli*, non-*H. pylori* bacterial lysates, block polymers or saponins.

- Other suitable delivery methods include biodegradable microcapsules or immunostimulating complexes (ISCOMs), cochleates, or liposomes, genetically engineered
- 25 attenuated live vectors such as viruses or bacteria, and recombinant (chimeric) virus-like particles, e.g., bluetongue. The amount of adjuvant employed will depend on the type of adjuvant used. For example, when the mucosal adjuvant is cholera toxin, it is suitably used in an amount of 5 µg to 50 µg, for example 10 µg to 35 µg. When used in the form of microcapsules, the amount used will depend on the amount employed in the matrix of the
- 30 microcapsule to achieve the desired dosage. The determination of this amount is within the skill of a person of ordinary skill in the art.

- Carrier systems in humans may include enteric release capsules protecting the antigen from the acidic environment of the stomach, and including *H. pylori* polypeptide in an insoluble form as fusion proteins. Suitable carriers for the vaccines of the invention are
- 35 enteric coated capsules and polylactide-glycolide microspheres. Suitable diluents are 0.2 N NaHCO₃ and/or saline.

Vaccines of the invention can be administered as a primary prophylactic agent in adults or in children, as a secondary prevention, after successful eradication of *H. pylori* in an infected host, or as a therapeutic agent in the aim to induce an immune response in a

susceptible host to prevent infection by *H. pylori*. The vaccines of the invention are administered in amounts readily determined by persons of ordinary skill in the art. Thus, for adults a suitable dosage will be in the range of 10 µg to 10 g, preferably 10 µg to 100 mg, for example 50 µg to 50 mg. A suitable dosage for adults will also be in the range of 5 µg to 500 mg. Similar dosage ranges will be applicable for children. Those skilled in the art will recognize that the optimal dose may be more or less depending upon the patient's body weight, disease, the route of administration, and other factors. Those skilled in the art will also recognize that appropriate dosage levels can be obtained based on results with known oral vaccines such as, for example, a vaccine based on an *E. coli* lysate (6 mg dose daily up to total of 540 mg) and with an enterotoxigenic *E. coli* purified antigen (4 doses of 1 mg) (Schulman et al., *J. Urol.* 150:917-921 (1993); Boedecker et al., *American Gastroenterological Assoc.* 999:A-222 (1993)). The number of doses will depend upon the disease, the formulation, and efficacy data from clinical trials. Without intending any limitation as to the course of treatment, the treatment can be administered over 3 to 8 doses for a primary immunization schedule over 1 month (Boedeker, *American Gastroenterological Assoc.* 888:A-222 (1993)).

In a preferred embodiment, a vaccine composition of the invention can be based on a killed whole *E. coli* preparation with an immunogenic fragment of an *H. pylori* protein of the invention expressed on its surface or it can be based on an *E. coli* lysate, wherein the killed *E. coli* acts as a carrier or an adjuvant.

It will be apparent to those skilled in the art that some of the vaccine compositions of the invention are useful only for preventing *H. pylori* infection, some are useful only for treating *H. pylori* infection, and some are useful for both preventing and treating *H. pylori* infection. In a preferred embodiment, the vaccine composition of the invention provides protection against *H. pylori* infection by stimulating humoral and/or cell-mediated immunity against *H. pylori*. It should be understood that amelioration of any of the symptoms of *H. pylori* infection is a desirable clinical goal, including a lessening of the dosage of medication used to treat *H. pylori*-caused disease, or an increase in the production of antibodies in the serum or mucous of patients.

VII. Antibodies Reactive With *H. pylori* Polypeptides

The invention also includes antibodies specifically reactive with the subject *H. pylori* polypeptide. Anti-protein/anti-peptide antisera or monoclonal antibodies can be made by standard protocols (See, for example, *Antibodies: A Laboratory Manual* ed. by Harlow and Lane (Cold Spring Harbor Press: 1988)). A mammal such as a mouse, a hamster or rabbit can be immunized with an immunogenic form of the peptide. Techniques for conferring immunogenicity on a protein or peptide include conjugation to carriers or other techniques well known in the art. An immunogenic portion of the subject *H. pylori* polypeptide can be administered in the presence of adjuvant. The progress of immunization

can be monitored by detection of antibody titers in plasma or serum. Standard ELISA or other immunoassays can be used with the immunogen as antigen to assess the levels of antibodies.

5 In a preferred embodiment, the subject antibodies are immunospecific for antigenic determinants of the *H. pylori* polypeptides of the invention, e.g. antigenic determinants of a polypeptide of the invention contained in the Sequence Listing, or a closely related human or non-human mammalian homolog (e.g., 90% homologous, more preferably at least 95% homologous). In yet a further preferred embodiment of the invention, the anti-*H. pylori* antibodies do not substantially cross react (i.e., react specifically) with a protein which is
10 for example, less than 80% percent homologous to a sequence of the invention contained in the Sequence Listing. By "not substantially cross react", it is meant that the antibody has a binding affinity for a non-homologous protein which is less than 10 percent, more preferably less than 5 percent, and even more preferably less than 1 percent, of the binding affinity for a protein of the invention contained in the Sequence Listing. In a most
15 preferred embodiment, there is no crossreactivity between bacterial and mammalian antigens.

The term antibody as used herein is intended to include fragments thereof which are also specifically reactive with *H. pylori* polypeptides. Antibodies can be fragmented using conventional techniques and the fragments screened for utility in the same manner as
20 described above for whole antibodies. For example, $F(ab')_2$ fragments can be generated by treating antibody with pepsin. The resulting $F(ab')_2$ fragment can be treated to reduce disulfide bridges to produce Fab' fragments. The antibody of the invention is further intended to include bispecific and chimeric molecules having an anti-*H. pylori* portion.

Both monoclonal and polyclonal antibodies (Ab) directed against *H. pylori*
25 polypeptides or *H. pylori* polypeptide variants, and antibody fragments such as Fab' and $F(ab')_2$, can be used to block the action of *H. pylori* polypeptide and allow the study of the role of a particular *H. pylori* polypeptide of the invention in aberrant or unwanted intracellular signaling, as well as the normal cellular function of the *H. pylori* and by microinjection of anti-*H. pylori* polypeptide antibodies of the present invention.

30 Antibodies which specifically bind *H. pylori* epitopes can also be used in immunohistochemical staining of tissue samples in order to evaluate the abundance and pattern of expression of *H. pylori* antigens. Anti *H. pylori* polypeptide antibodies can be used diagnostically in immuno-precipitation and immuno-blotting to detect and evaluate *H. pylori* levels in tissue or bodily fluid as part of a clinical testing procedure. Likewise, the
35 ability to monitor *H. pylori* polypeptide levels in an individual can allow determination of the efficacy of a given treatment regimen for an individual afflicted with such a disorder. The level of an *H. pylori* polypeptide can be measured in cells found in bodily fluid, such as in urine samples or can be measured in tissue, such as produced by gastric biopsy. Diagnostic assays using anti-*H. pylori* antibodies can include, for example, immunoassays

-88-

designed to aid in early diagnosis of *H. pylori* infections. The present invention can also be used as a method of detecting antibodies contained in samples from individuals infected by this bacterium using specific *H. pylori* antigens.

Another application of anti-*H. pylori* polypeptide antibodies of the invention is in the immunological screening of cDNA libraries constructed in expression vectors such as λ gt11, λ gt18-23, λ ZAP, and λ ORF8. Messenger libraries of this type, having coding sequences inserted in the correct reading frame and orientation, can produce fusion proteins. For instance, λ gt11 will produce fusion proteins whose amino termini consist of β -galactosidase amino acid sequences and whose carboxy termini consist of a foreign polypeptide. Antigenic epitopes of a subject *H. pylori* polypeptide can then be detected with antibodies, as, for example, reacting nitrocellulose filters lifted from infected plates with anti-*H. pylori* polypeptide antibodies. Phage, scored by this assay, can then be isolated from the infected plate. Thus, the presence of *H. pylori* gene homologs can be detected and cloned from other species, and alternate isoforms (including splicing variants) can be detected and cloned.

VIII. Kits Containing Nucleic Acids, Polypeptides or Antibodies of the Invention

The nucleic acid, polypeptides and antibodies of the invention can be combined with other reagents and articles to form kits. Kits for diagnostic purposes typically comprise the nucleic acid, polypeptides or antibodies in vials or other suitable vessels. Kits typically comprise other reagents for performing hybridization reactions, polymerase chain reactions (PCR), or for reconstitution of lyophilized components, such as aqueous media, salts, buffers, and the like. Kits may also comprise reagents for sample processing such as detergents, chaotropic salts and the like. Kits may also comprise immobilization means such as particles, supports, wells, dipsticks and the like. Kits may also comprise labeling means such as dyes, developing reagents, radioisotopes, fluorescent agents, luminescent or chemiluminescent agents, enzymes, intercalating agents and the like. With the nucleic acid and amino acid sequence information provided herein, individuals skilled in art can readily assemble kits to serve their particular purpose. Kits further can include instructions for use.

IX. Drug Screening Assays Using *H. pylori* Polypeptides

By making available purified and recombinant *H. pylori* polypeptides, the present invention provides assays which can be used to screen for drugs which are either agonists or antagonists of the normal cellular function, in this case, of the subject *H. pylori* polypeptides, or of their role in intracellular signaling. Such inhibitors or potentiators may be useful as new therapeutic agents to combat *H. pylori* infections in humans. A variety of assay formats will suffice and, in light of the present inventions, will be comprehended by the skilled artisan.

In many drug screening programs which test libraries of compounds and natural extracts, high throughput assays are desirable in order to maximize the number of compounds surveyed in a given period of time. Assays which are performed in cell-free systems, such as may be derived with purified or semi-purified proteins, are often preferred as "primary" screens in that they can be generated to permit rapid development and relatively easy detection of an alteration in a molecular target which is mediated by a test compound. Moreover, the effects of cellular toxicity and/or bioavailability of the test compound can be generally ignored in the *in vitro* system, the assay instead being focused primarily on the effect of the drug on the molecular target as may be manifest in an alteration of binding affinity with other proteins or change in enzymatic properties of the molecular target. Accordingly, in an exemplary screening assay of the present invention, the compound of interest is contacted with an isolated and purified *H. pylori* polypeptide.

Screening assays can be constructed *in vitro* with a purified *H. pylori* polypeptide or fragment thereof, such as an *H. pylori* polypeptide having enzymatic activity, such that the activity of the polypeptide produces a detectable reaction product. The efficacy of the compound can be assessed by generating dose response curves from data obtained using various concentrations of the test compound. Moreover, a control assay can also be performed to provide a baseline for comparison. Suitable products include those with distinctive absorption, fluorescence, or chemi-luminescence properties, for example, because detection may be easily automated. A variety of synthetic or naturally occurring compounds can be tested in the assay to identify those which inhibit or potentiate the activity of the *H. pylori* polypeptide. Some of these active compounds may directly, or with chemical alterations to promote membrane permeability or solubility, also inhibit or potentiate the same activity (e.g., enzymatic activity) in whole, live *H. pylori* cells.

EXEMPLIFICATION

I. Cloning and Sequencing of *H. pylori* DNA

H. pylori chromosomal DNA was isolated according to a basic DNA protocol outlined in Schleif R.F. and Wensink P.C., *Practical Methods in Molecular Biology*, p.98, Springer-Verlag, NY., 1981, with minor modifications. Briefly, cells were pelleted, resuspended in TE (10 mM Tris, 1 mM EDTA, pH 7.6) and GES lysis buffer (5.1 M guanidium thiocyanate, 0.1 M EDTA, pH 8.0, 0.5% N-laurylsarcosine) was added. Suspension was chilled and ammonium acetate (NH₄Ac) was added to final concentration of 2.0 M. DNA was extracted, first with chloroform, then with phenol-chloroform, and reextracted with chloroform. DNA was precipitated with isopropanol, washed twice with 70% EtOH, dried and resuspended in TE.

Following isolation whole genomic *H. pylori* DNA was nebulized (Bodenteich et al., *Automated DNA Sequencing and Analysis* (J.C. Venter, ed.), Academic Press, 1994) to

-90-

a median size of 2000 bp. After nebulization, the DNA was concentrated and separated on a standard 1% agarose gel. Several fractions, corresponding to approximate sizes 900-1300 bp, 1300-1700 bp, 1700-2200 bp, 2200-2700 bp, were excised from the gel and purified by the GeneClean procedure (Bio101, Inc.).

5 The purified DNA fragments were then blunt-ended using T4 DNA polymerase. The healed DNA was then ligated to unique BstXI-linker adapters (5' TCTAGACCACTGC and 5' GTGGTCTAGA in 100-1000 fold molar excess). These linkers are complimentary to the BstXI-cut pMPX vectors, while the overhang is not self-complimentary. Therefore, the linkers will not concatemerize nor will the cut-vector
10 religate itself easily. The linker-adopted inserts were separated from the unincorporated linkers on a 1% agarose gel and purified using GeneClean. The linker-adopted inserts were then ligated to each of the 20 pMPX vectors to construct a series of "shotgun" subclone libraries. The vectors contain an out-of-frame lacZ gene at the cloning site which becomes in-frame in the event that an adapter-dimer is cloned, allowing these to be avoided by their
15 blue-color.

 All subsequent steps were based on the multiplex DNA sequencing protocols outlined in Church G.M. and Kieffer-Higgins S., *Science* 240:185-188, 1988. Only major modifications to the protocols are highlighted. Briefly, each of the 20 vectors was then transformed into DH5 α competent cells (Gibco/BRL, DH5 α transformation protocol). The
20 libraries were assessed by plating onto antibiotic plates containing ampicillin, methicillin and IPTG/Xgal. The plates were incubated overnight at 37°C. Successful transformants were then used for plating of clones and pooling into the multiplex pools. The clones were picked and pooled into 40 ml growth medium cultures. The cultures were grown overnight at 37°C. DNA was purified using the Qiagen Midi-prep kits and Tip-100 columns
25 (Qiagen, Inc.). In this manner, 100 μ g of DNA was obtained per pool. Fifteen 96-well plates of DNA were generated to obtain a 5-10 fold sequence redundancy assuming 250-300 base average read-lengths.

 These purified DNA samples were then sequenced using the multiplex DNA sequencing based on chemical degradation methods (Church G.M. and Kieffer-Higgins S.,
30 *Science* 240:185-188, 1988) or by Sequithrem (Epicenter Technologies) dideoxy sequencing protocols. The sequencing reactions were electrophoresed and transferred onto nylon membranes by direct transfer electrophoresis from 40 cm gels (Richterich P. and Church G.M., *Methods in Enzymology* 218:187-222, 1993) or by electroblotting (Church, *supra*). 24 samples were run per gel. 45 successful membranes were produced by chemical
35 sequencing and 8 were produced by dideoxy sequencing. The DNA was covalently bound to the membranes by exposure to ultraviolet light, and hybridized with labeled oligonucleotides complimentary to tag sequences on the vectors (Church, *supra*). The membranes were washed to rinse off non-specifically bound probe, and exposed to X-ray film to visualize individual sequence ladders. After autoradiography, the hybridized probe

-91-

was removed by incubation at 65° C, and the hybridization cycle repeated with another tag sequence until the membrane had been probed 38 times for chemical sequencing membranes and 10 times for the dideoxy sequencing membranes. Thus, each gel produced a large number of films, each containing new sequencing information. Whenever a new blot was processed, it was initially probed for an internal standard sequence added to each of the pools.

Digital images of the films were generated using a laser-scanning densitometer (Molecular Dynamics, Sunnyvale, CA). The digitized images were processed on computer workstations (VaxStation 4000's) using the program REPLICA™ (Church et al., *Automated DNA Sequencing and Analysis* (J.C. Venter, ed.), Academic Press, 1994). Image processing included lane straightening, contrast adjustment to smooth out intensity differences, and resolution enhancement by iterative gaussian deconvolution. The sequences were then automatically picked in REPLICA™ and displayed for interactive proofreading before being stored in a project database. The proofreading was accomplished by a quick visual scan of the film image followed by mouse clicks on the bands of the displayed image to modify the base calls. Many of the sequence errors could be detected and corrected because multiple sequence reads covering the same portion of the genomic DNA provide adequate sequence redundancy for editing. Each sequence automatically received an identification number (corresponding to microtiter plate, probe information, and lane set number). This number serves as a permanent identifier of the sequence so it is always possible to identify the original of any particular sequence without recourse to a specialized database.

Routine assembly of *H. pylori* sequences was done using the program FALCON (Church, Church et al., *Automated DNA Sequencing and Analysis* (J.C. Venter, ed.), Academic Press, 1994). This program has proven to be fast and reliable for most sequences. The assembled contigs were displayed using a modified version of GelAssemble, developed by the Genetics Computer Group (GCG) (Devereux et al., *Nucleic Acid Res.* 12:387-95, 1984) that interacts with REPLICA™. This provided for an integrated editor that allows multiple sequence gel images to be instantaneously called up from the REPLICA™ database and displayed to allow rapid scanning of contigs and proofreading of gel traces where discrepancies occurred between different sequence reads in the assembly.

II. Identification, cloning and expression of recombinant *H. pylori* DNA sequences

To facilitate the cloning, expression and purification of membrane and secreted proteins from *H. pylori* a powerful gene expression system, the pET System (Novagen), for cloning and expression of recombinant proteins in *E. coli*, was selected. Also, a DNA sequence encoding a peptide tag, the His-Tag, was fused to the 3' end of DNA sequences of interest in order to facilitate purification of the recombinant protein products. The 3' end

-92-

was selected for fusion in order to avoid alteration of any 5' terminal signal sequence. The exception to the above was ppiB, a gene cloned for use as a control in the expression studies. In this study, the sequence for *H. pylori* ppiB contains a DNA sequence encoding a His-Tag fused to the 5' end of the full length gene, because the protein product of this gene does not contain a signal sequence and is expressed as a cytosolic protein.

PCR Amplification and cloning of DNA sequences containing ORF's for membrane and secreted proteins from the J99 Strain of Helicobacter pylori.

Sequences chosen (from the list of the DNA sequences of the invention) for cloning from the J99 strain of *H. pylori* were prepared for amplification cloning by polymerase chain reaction (PCR). Synthetic oligonucleotide primers (Table 4) specific for the 5' and 3' ends of open reading frames (ORFs) were designed and purchased (GibcoBRL Life Technologies, Gaithersburg, MD, USA). All forward primers (specific for the 5' end of the sequence) were designed to include an NcoI cloning site at the extreme 5' terminus, except for HpSeq. 4821082 (SEQ ID NO: 820) where NdeI was used. These primers were designed to permit initiation of protein translation at a methionine residue followed by a valine residue and the coding sequence for the remainder of the native *H. pylori* DNA sequence. An exception is *H. pylori* sequence 4821082 (SEQ ID NO: 820) where the initiator methionine is immediately followed by the remainder of the native *H. pylori* DNA sequence. All reverse primers (specific for the 3' end of any *H. pylori* ORF) included a EcoRI site at the extreme 5' terminus to permit cloning of each *H. pylori* sequence into the reading frame of the pET-28b. The pET-28b vector provides sequence encoding an additional 20 carboxy-terminal amino acids (only 19 amino acids in HpSeq. 26380318 (SEQ ID NO: 658) and HpSeq. 14640637 (SEQ ID NO: 447)) including six histidine residues (at the extreme C-terminus), which comprise the His-Tag. An exception to the above, as noted earlier, is the vector construction for the ppiB gene. A synthetic oligonucleotide primer specific for the 5' end of ppiB gene encoded a BamHI site at its extreme 5' terminus and the primer for the 3' end of the ppiB gene encoded a XhoI site at its extreme 5' terminus.

TABLE 4

Oligonucleotide primers used for PCR amplification of *H. pylori* DNA sequences

Outer membrane Proteins	Forward primer 5' to 3'	Reverse Primer 5' to 3'
16225006 (SEQ ID NO: 465)	5'-TATACCATGGTGGG CGCTAA-3' (SEQ ID NO:1897)	5'-ATGAATTCGAGTAAG GATTTTGTG-3' (SEQ ID NO:1898)
26054702 (SEQ ID NO: 649)	5'-TTAACCATGGTGAAA AGCGATA-3' (SEQ ID NO:1899)	5'-TAGAATTCGCATAAC GATCAATC-3' (SEQ ID NO:1900)
7116626 (SEQ ID NO: 865)	5'-ATATCCATGGTGAGT TTGATGA-3' (SEQ ID NO:1901)	5'-ATGAATTCAATTTTT TATTTTGCCA-3' (SEQ ID NO:1902)
29479681 (SEQ ID NO: 677)	5'-AATTCCATGGTGGGG GCTATG-3' (SEQ ID NO:1903)	5'-ATGAATTCTCGATAG CCAAAATC-3' (SEQ ID NO:1904)
14640637 (SEQ ID NO: 447)	5'-AATTCCATGGTGCAT AACTTCCATT-3' (SEQ ID NO:1905)	5'-AAGAATTCTCTAGCA TCCAAATGGA-3' (SEQ ID NO:1906)
Periplasmic/ Secreted Proteins		
30100332 (SEQ ID NO: 685)	5'-ATTTCCATGGTCATG TCTCATATT-3' (SEQ ID NO:1907)	5'-ATGAATTCATCTTT TATTCCAC-3' (SEQ ID NO:1908)
4721061 (SEQ ID NO: 812)	5'-AACCATGGTGATTT TAAGCATTGAAAG-3' (SEQ ID NO:1909)	5'-AAGAATTCCTCA AAATTTTAAACAG-3' (SEQ ID NO:1910)
Other Surface Proteins		
4821082 (SEQ ID NO: 820)	5'-GATCATCCATATGTT ATCTTCTAAT-3' (SEQ ID NO:1911)	5'-TGAATTCAACCATTT TAACCCTG-3' (SEQ ID NO:1912)
978477 (SEQ ID NO: 880)	5'-TATACCATGGTGAA ATTTTTCTTTTA-3' (SEQ ID NO:1913)	5'-AGAATTCAATTGCG TCTTGTAAG-3' (SEQ ID NO:1914)
Inner Membrane Protein		
26380318 (SEQ ID NO: 658)	5'-TATACCATGGTGAT GGACAACTC-3' (SEQ ID NO:1915)	5'-ATGAATTCCTCACTT GGGGCGATA-3' (SEQ ID NO:1916)
Cytoplasmic Protein		
ppi	5'-TTATGGATCCAAAC CAATTAAACT-3' (SEQ ID NO:1917)	5'-TATCTCGAGTTATA GAGAAGGGC-3' (SEQ ID NO:1918)

-94-

Genomic DNA prepared from the J99 strain of *H. pylori* (ATCC #55679) was used as the source of template DNA for PCR amplification reactions (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). To amplify a DNA sequence containing an *H. pylori* ORF, genomic DNA (50 nanograms) was introduced into a reaction vial containing 2 mM MgCl₂, 1 micromolar synthetic oligonucleotide primers (forward and reverse primers) complementary to and flanking a defined *H. pylori* ORF, 0.2 mM of each deoxynucleotide triphosphate; dATP, dGTP, dCTP, dTTP and 2.5 units of heat stable DNA polymerase (Amplitaq, Roche Molecular Systems, Inc., Branchburg, NJ, USA) in a final volume of 100 microliters. The following thermal cycling conditions were used to obtain amplified DNA products for each ORF using a Perkin Elmer Cetus/ GeneAmp PCR System 9600 thermal cycler:

Sequences 26054702 (SEQ ID NO: 649), 7116626 (SEQ ID NO: 865), 29479681 (SEQ ID NO: 677), 30100332 (SEQ ID NO: 685), 4821082 (SEQ ID NO: 820) and 978477 (SEQ ID NO: 880);

Denaturation at 94°C for 2 min,
2 cycles at 94°C for 15 sec, 30°C for 15 sec and 72°C for 1.5 min
23 cycles at 94°C for 15 sec, 55°C for 15 sec and 72°C for 1.5 min
Reactions were concluded at 72°C for 6 minutes.

Sequence 16225006 (SEQ ID NO: 465);

Denaturation at 94°C for 2 min,
25 cycles at 95°C for 15 sec, 55°C for 15 sec and 72°C for 1.5 min
Reaction was concluded at 72°C for 6 minutes.

Sequence 4721061 (SEQ ID NO: 812);

Denaturation at 94°C for 2 min.
2 cycles at 94°C for 15 sec, 36°C for 15 sec and 72°C for 1.5 min
23 cycles at 94°C for 15 sec, 60°C for 15 sec and 72°C for 1.5 min
Reactions were concluded at 72°C for 6 minutes.

Sequence 26380318 (SEQ ID NO: 658);

Denaturation at 94°C for 2 min.
2 cycles at 94°C for 15 sec, 38°C for 15 sec and 72°C for 1.5 min
23 cycles at 94°C for 15 sec, 62°C for 15 sec and 72°C for 1.5 min
Reactions were concluded at 72°C for 6 minutes.

-95-

Sequence 14640637 (SEQ ID NO: 447);

Denaturation at 94°C for 2 min,

2 cycles at 94°C for 15 sec, 33°C for 15 sec and 72°C for 1.5 min

30 cycles at 94°C for 15 sec, 55°C for 15 sec and 72°C for 1.5 min

- 5 Reactions were concluded at 72°C for 6 minutes.

Conditions for amplification of *H. pylori* ppiB;

Denaturation at 94°C for 2 min,

2 cycles at 94°C for 15 sec, 32°C for 15 sec and 72°C for 1.5 min

- 10 25 cycles at 94°C for 15 sec, 56°C for 15 sec and 72°C for 1.5 min

Reactions were concluded at 72°C for 6 minutes

- Upon completion of thermal cycling reactions, each sample of amplified DNA was washed and purified using the Qiaquick Spin PCR purification kit (Qiagen, Gaithersburg, MD, USA). All amplified DNA samples were subjected to digestion with the restriction endonucleases, NcoI and EcoRI (New England BioLabs, Beverly, MA, USA), or in the case of HpSeq. 4821082 (SEQ ID NO: 820), with NdeI and EcoRI (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). DNA samples were then subjected to electrophoresis on 1.0 % NuSeive (FMC BioProducts, Rockland, ME USA) agarose gels. DNA was visualized by exposure to ethidium bromide and long wave uv irradiation. DNA contained in slices isolated from the agarose gel was purified using the Bio 101 GeneClean Kit protocol (Bio 101 Vista, CA, USA)
- 15
- 20

Cloning of H. pylori DNA sequences into the pET-28b prokaryotic expression vector.

- The pET-28b vector was prepared for cloning by digestion with NcoI and EcoRI, or in the case of *H. pylori* sequence 4821082 (SEQ ID NO: 820) with NdeI and EcoRI (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). In the case of cloning ppiB, the pET-28a vector, which encodes a His-Tag that can be fused to the 5' end of an inserted gene, was used and the cloning site prepared for cloning with the ppiB gene by digestion with BamHI and XhoI restriction endonucleases.
- 25
- 30

- Following digestion, DNA inserts were cloned (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994) into the previously digested pET-28b expression vector, except for the amplified insert for ppiB, which was cloned into the pET-28a expression vector. Products of the ligation reaction were then used to transform the BL21 strain of *E. coli* (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994) as described below.
- 35

Transformation of competent bacteria with recombinant plasmids

Competent bacteria, *E. coli* strain BL21 or *E. coli* strain BL21(DE3), were transformed with recombinant pET expression plasmids carrying the cloned *H. pylori*

-96-

sequences according to standard methods (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). Briefly, 1 microliter of ligation reaction was mixed with 50 microliters of electrocompetent cells and subjected to a high voltage pulse, after which, samples were incubated in 0.45 milliliters SOC medium (0.5% yeast extract, 2.0 % tryptone, 10 mM NaCl, 2.5 mM KCl, 10 mM MgCl₂, 10 mM MgSO₄ and 20, mM glucose) at 37°C with shaking for 1 hour. Samples were then spread on LB agar plates containing 25 microgram/ml kanamycin sulfate for growth overnight. Transformed colonies of BL21 were then picked and analyzed to evaluate cloned inserts as described below.

10

Identification of recombinant pET expression plasmids carrying H. pylori sequences

Individual BL21 clones transformed with recombinant pET-28b-H.pylori ORFs were analyzed by PCR amplification of the cloned inserts using the same forward and reverse primers, specific for each *H. pylori* sequence, that were used in the original PCR amplification cloning reactions. Successful amplification verified the integration of the *H. pylori* sequences in the expression vector (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994).

Isolation and Preparation of plasmid DNA from BL21 transformants

Individual clones of recombinant pET-28b vectors carrying properly cloned *H. pylori* ORFs were picked and incubated in 5 mls of LB broth plus 25 microgram/ml kanamycin sulfate overnight. The following day plasmid DNA was isolated and purified using the Qiagen plasmid purification protocol (Qiagen Inc., Chatsworth, CA, USA).

Expression of recombinant H. pylori sequences in E. coli

The pET vector can be propagated in any *E. coli* K-12 strain e.g. HMS174, HB101, JM109, DH5, etc. for the purpose of cloning or plasmid preparation. Hosts for expression include *E. coli* strains containing a chromosomal copy of the gene for T7 RNA polymerase. These hosts are lysogens of bacteriophage DE3, a lambda derivative that carries the lacI gene, the lacUV5 promoter and the gene for T7 RNA polymerase. T7 RNA polymerase is induced by addition of isopropyl-B-D-thiogalactoside (IPTG), and the T7 RNA polymerase transcribes any target plasmid, such as pET-28b, carrying a T7 promoter and a gene of interest. Strains used include: BL21(DE3) (Studier, F.W., Rosenberg, A.H., Dunn, J.J., and Dubendorff, J.W. (1990) Meth. Enzymol. 185, 60-89).

To express recombinant *H. pylori* sequences, 50 nanograms of plasmid DNA isolated as described above was used to transform competent BL21(DE3) bacteria as described above (provided by Novagen as part of the pET expression system kit). The lacZ gene (beta-galactosidase) was expressed in the pET-System as described for the *H. pylori* recombinant constructions. Transformed cells were cultured in SOC medium for 1 hour,

-97-

and the culture was then plated on LB plates containing 25 micrograms/ml kanamycin sulfate. The following day, bacterial colonies were pooled and grown in LB medium containing kanamycin sulfate (25 micrograms/ml) to an optical density at 600 nm of 0.5 to 1.0 O.D. units, at which point, 1 millimolar IPTG was added to the culture for 3 hours to induce gene expression of the *H. pylori* recombinant DNA constructions .

After induction of gene expression with IPTG, bacteria were pelleted by centrifugation in a Sorvall RC-3B centrifuge at 3500 x g for 15 minutes at 4°C. Pellets were resuspended in 50 milliliters of cold 10 mM Tris-HCl, pH 8.0, 0.1 M NaCl and 0.1 mM EDTA (STE buffer). Cells were then centrifuged at 2000 x g for 20 min at 4°C. Wet pellets were weighed and frozen at -80°C until ready for protein purification.

III. Purification of recombinant proteins from *E. coli*

Analytical Methods

The concentrations of purified protein preparations were quantified spectrophotometrically using absorbance coefficients calculated from amino acid content (Perkins, S.J. 1986 Eur. J. Biochem. 157, 169-180). Protein concentrations were also measured by the method of Bradford, M.M. (1976) Anal. Biochem. 72, 248-254, and Lowry, O.H., Rosebrough, N., Farr, A.L. & Randall, R.J. (1951) J. Biol. Chem. 193, pages 265-275, using bovine serum albumin as a standard.

SDS-polyacrylamide gels (12% or 4.0 to 25 % acrylamide gradient gels) were purchased from BioRad (Hercules, CA, USA), and stained with Coomassie blue. Molecular weight markers included rabbit skeletal muscle myosin (200 kDa), *E. coli* (-galactosidase (116 kDa), rabbit muscle phosphorylase B (97.4 kDa), bovine serum albumin (66.2 kDa), ovalbumin (45 kDa), bovine carbonic anhydrase (31 kDa), soybean trypsin inhibitor (21.5 kDa), egg white lysozyme (14.4 kDa) and bovine aprotinin (6.5 kDa).

1. Purification of soluble proteins

All steps were carried out at 4°C. Frozen cells were thawed, resuspended in 5 volumes of lysis buffer (20 mM Tris, pH 7.9, 0.5 M NaCl, 5 mM imidazole with 10% glycerol, 0.1 % 2-mercaptoethanol, 200 µg/ml lysozyme, 1 mM phenylmethylsulfonyl fluoride (PMSF), and 10 µg/ml each of leupeptin, aprotinin, pepstatin, L-1-chloro-3-[4-tosylamido]-7-amino-2-heptanone (TLCK), L-1-chloro-3-[4-tosylamido]-4-phenyl-2-butanone (TPCK), and soybean trypsin inhibitor, and ruptured by several passages through a small volume microfluidizer (Model M-110S, Microfluidics International Corporation, Newton, MA). The resultant homogenate was made 0.1 % Brij 35, and centrifuged at 100,000 x g for 1 hour to yield a clear supernatant (crude extract).

Following filtration through a 0.8 µm Supor filter (Gelman Sciences, FRG) the crude extract was loaded directly onto a Ni²⁺-nitrilotriacetate-agarose (NTA) with a 5 milliliter bed volume (Hochuli, E., Dbeli, H., and Schacheer, A. (1987) J. Chromatography

411, 177-184) pre-equilibrated in lysis buffer containing 10 % glycerol, 0.1 % Brij 35 and 1 mM PMSF. The column was washed with 250 ml (50 bed volumes) of lysis buffer containing 10 % glycerol, 0.1 % Brij 35, and was eluted with sequential steps of lysis buffer containing 10 % glycerol, 0.05 % Brij 35, 1 mM PMSF, and 20, 100, 200, and 500 mM imidazole in succession. Fractions were monitored by absorbance at OD₂₈₀ nm, and peak fractions were analyzed by SDS-PAGE. Fractions containing the recombinant protein eluted at 100 mM imidazole.

10 *Recombinant protein 14640637 (SEQ ID NO: 447) and proteins, beta-galactosidase (lacZ) and peptidyl-prolyl cis-trans isomerase (ppiB)*

Fractions containing the recombinant proteins from the Ni²⁺-NTA-agarose columns were pooled and then concentrated to approximately 5 ml by centrifugal filtration (Centriprep-10, Amicon, MA), and loaded directly onto a 180-ml column (1.6 X 91 cm) of Sephacryl S-100 HR gel filtration medium equilibrated in Buffer A (10 mM Hepes, pH 7.5, 150 mM NaCl, 0.1 mM EGTA) and run in Buffer A at 18 ml/h. Fractions containing the recombinant protein were identified by absorbance at 280 nm and analyzed by SDS-PAGE. Fractions were pooled and concentrated by centrifugal filtration.

20 *Recombinant protein 7116626 (SEQ ID NO: 865)*

Fractions containing the recombinant protein from the Ni²⁺-NTA-agarose column were pooled and dialyzed overnight against 1 liter of dialysis buffer (10 mM MOPS, pH 6.5, 50 mM NaCl, 0.1 mM EGTA, 0.02% Brij 35 and 1 mM PMSF). In the morning, a fine white precipitate was removed by centrifugation and the resulting supernatant was loaded onto an 8 ml (8 x 75 mm) MonoS high performance liquid chromatography column (Pharmacia Biotechnology, Inc., Piscataway, NJ, USA) equilibrated in buffer B (10 mM MOPS, pH 6.5, 0.1 mM EGTA) containing 50 mM NaCl. The column was washed with 10 bed volumes of buffer B containing 50 mM NaCl, and developed with a 50-ml linear gradient of increasing NaCl (50 to 500 mM). Recombinant protein 7116626 (SEQ ID NO: 865) eluted as a sharp peak at 300 mM NaCl.

30

2. Purification of insoluble proteins from inclusion bodies

The following steps were carried out at 4°C. Cell pellets were resuspended in lysis buffer with 10% glycerol 200 µg/ ml lysozyme, 5 mM EDTA, 1mM PMSF and 0.1 % -mercaptoethanol. After passage through the cell disrupter, the resulting homogenate was made 0.2 % deoxycholate, stirred 10 minutes, then centrifuged at 20,000 x g, for 30 min. The pellets were washed with lysis buffer containing 10 % glycerol, 10 mM EDTA, 1% Triton X-100, 1 mM PMSF and 0.1% -mercaptoethanol, followed by several washes with lysis buffer containing 1 M urea, 1 mM PMSF and 0.1 % 2-mercaptoethanol. The resulting

white pellet was composed primarily of inclusion bodies, free of unbroken cells and membranous materials..

5 *Recombinant proteins 26054702 (SEQ ID NO: 649), 16225006 (SEQ ID NO: 465),
30100332 (SEQ ID NO: 685), 4721061 (SEQ ID NO: 812)*

10 The following steps were carried out at room temperature. Purified inclusion bodies were dissolved in 20 ml 8.0 M urea in lysis buffer with 1 mM PMSF and 0.1 % 2-mercaptoethanol, and incubated at room temperature for 1 hour. Materials that did not dissolve were removed by centrifugation. The clear supernatant was filtered, then loaded
15 onto a Ni^{2+} -NTA agarose column pre-equilibrated in 8.0 M urea in Lysis Buffer. The column was washed with 250 ml (50 bed volumes) of lysis buffer containing 8 M urea, 1.0 mM PMSF and 0.1 % 2-mercaptoethanol, and developed with sequential steps of lysis buffer containing 8M urea, 1 mM PMSF, 0.1 % 2-mercaptoethanol and 20, 100, 200, and 500 mM imidazole in succession. Fractions were monitored by absorbance at OD₂₈₀ nm,
and peak fractions were analyzed by SDS-PAGE. Fractions containing the recombinant protein eluted at 100 mM imidazole.

20 *Recombinant proteins 29479681 (SEQ ID NO: 677), 978477 (SEQ ID NO: 880), 26380318 (SEQ ID NO: 658)*

25 The pellet containing the inclusion bodies was solubilized in buffer B containing 8 M urea, 1 mM PMSF and 0.1 % 2-mercaptoethanol, and incubated for 1 hour at room temperature. Insoluble materials were removed by centrifugation at 20,000 x g for 30 min, and the cleared supernatant was loaded onto a 15 ml (1.6 x 7.5 cm) SP-Sepharose column pre-equilibrated in buffer B, 6 M urea, 1 mM PMSF, 0.1 % 2-mercaptoethanol. After
washing the column with 10 bed volumes, the column was developed with a linear gradient from 0 to 500 mM NaCl.

Dialysis and concentration of protein samples

30 Urea was removed slowly from the protein samples by dialysis against Tris-buffered saline (TBS; 10 mM Tris pH 8.0, 150 mM NaCl) containing 0.5 % deoxycholate (DOC) with sequential reduction in urea concentration as follows; 6M, 4M, 3M, 2M, 1M, 0.5 M and finally TBS without any urea. Each dialysis step was conducted for a minimum of 4 hours at room temperature.

35 After dialysis, samples were concentrated by pressure filtration using Amicon stirred-cells. Protein concentrations were measured using the methods of Perkins (1986 Eur. J. Biochem. 157, 169-180), Bradford ((1976) Anal. Biochem. 72, 248-254) and Lowry ((1951) J. Biol. Chem. 193, pages 265-275).

The recombinant proteins purified by the methods described above are summarized in Table 5 below.

TABLE 5

J99 Sequence Identifier	Homolog Identified by Blast	Gene symbol of Homolog	Bacterial cell fraction used to purify recombinant proteins	Method of purification	Relative MW on SDS-PAGE gel	Final concentration of purified protein	Composition of buffer
Outer Membrane Proteins							
16225006 (SEQ ID NO: 465)	P28635	YEAC	Inclusion bodies	His-Tag	18 kDa	5 mg/ml	B
26054702 (SEQ ID NO: 649)	P15929	ngH	Inclusion bodies	His-Tag	37 kDa	1.18 mg/ml	B
7116626 (SEQ ID NO: 865)	P26093	e(P4)	Soluble fraction	His-Tag	29 kDa	0.8 mg/ml	A
29479681 (SEQ ID NO: 677)	P13036	fecA	Inclusions bodies	SP-Sepharose	23 kDa	2.36 mg/ml	B
14640637 (SEQ ID NO: 447)	P16665	TPF1	Soluble fraction	His-Tag	17 kDa	2.4 mg/ml	as dry pellet A
				gel filtration S100 HR			

TABLE 5 (continued)

Periplasmic/Secreted Protein			Inclusion bodies	His-Tag	11 kDa	2.88 mg/ml	B
3010032 (SEQ ID NO: 685)	P23847	dppA					
4721061 (SEQ ID NO: 812)	P36175	GCP	Inclusion bodies	His-Tag	38 kDa	2.8 mg/ml	B
Other Surface Proteins							
4821082 (SEQ ID NO: 820)	P08089	M protein	Inclusion bodies	His-Tag	20 kDa	1.16 mg/ml	B
978477 (SEQ ID NO: 880)	L28919	FBP54	Inclusion bodies	SP-Sepharose	44 kDa	2.56 mg/ml	B
Inner Membrane Proteins						0.3 mg/ml	B
26380318 (SEQ ID NO: 658)	P15933	flgG	Inclusion bodies	SP-Sepharose	11 kDa	22 mg/ml	B
Control Proteins with His-Tag							
	P00722	lacZ	Soluble fraction	His-Tag gel filtration S200 HR	116 kDa	10 mg/ml	A
		ppiB	Soluble fraction	His-Tag gel filtration S100 HR	21 kDa	4.4 mg/ml	A
Buffer compositions:							
A= 10 mM Hepes pH 7.5, 150 mM NaCl, 0.1 mM EGTA							
B= 10 mM Tris pH 8.0, 150 mM NaCl, 0.5 % DOC							
C= 10 mM MOPS pH 6.5, 300 mM NaCl, 0.1 EGTA							

-102-

IV. Analysis of *H. pylori* proteins as Vaccine candidates

To investigate the immunomodulatory effect of *H. pylori* proteins, a mouse/*H. pylori* model was used. This model mimics the human *H. pylori* infection in many respects. The focus is on the effect of oral immunization in *H. pylori* infected animals in order to test the concept of therapeutic oral immunotherapy.

Animals

Female SPF BALB/c mice were purchased from Bomholt Breeding center (Denmark). They were kept in ordinary makrolon cages with free supply of water and food. The animals were 4-6 weeks old at arrival.

Infection

After a minimum of one week of acclimatization, the animals were infected with a type 2 strain (VacA negative) of *H. pylori* (strain 244, originally isolated from an ulcer patient). In our hands, this strain has earlier proven to be a good colonizer of the mouse stomach. The bacteria were grown overnight in Brucella broth supplemented with 10 % fetal calf serum, at 37°C in a microaerophilic atmosphere (10% CO₂, 5% O₂). The animals were given an oral dose of omeprazole (400 µmol/kg) and 3-5 h after this an oral inoculation of *H. pylori* in broth (approximately 10⁸ cfu/animal). Positive take of the infection was checked in some animals 2-3 weeks after the inoculation.

Antigens

Recombinant *H. pylori* antigens were chosen based on their association with externally exposed *H. pylori* cell membrane. These antigens were selected from the following groups: (1.) Outer Membrane Proteins; (2.) Periplastic/Secreted proteins; (3.) Outer Surface proteins; and (4.) Inner Membrane proteins. All recombinant proteins were constructed with a hexa-HIS tag for purification reasons and the non-*Helicobacter pylori* control protein (β-galactosidase from *E. coli*; LacZ), was constructed in the same way.

All antigens were given in a soluble form, i.e. dissolved in either a HEPES buffer or in a buffer containing 0.5% Deoxycholate (DOC).

The antigens are listed in Table 6 below.

Table 6

Helicobacter pylori proteins

Outer membrane Proteins

SEQ ID NO:447

SEQ ID NO:677

SEQ ID NO:865

SEQ ID NO:812

SEQ ID NO:465

Periplastic/Secreted proteins

SEQ ID NO:685

5 **Other cell envelope proteins**

SEQ ID NO:820

SEQ ID NO:880

10 **Flagella-associated proteins**

SEQ ID NO:658

Control proteins β -galactosidase (LacZ)15 **Immunizations**

Ten animals in each group were immunized 4 times over a 34 day period (day 1, 15, 25 and 35). Purified antigens in solution or suspension were given at a dose of 100 μ g/mouse. As an adjuvant, the animals were also given 10 μ g/mouse of Cholera toxin (CT) with each immunization. Omeprazole (400 μ mol/kg) was given orally to the animals 3-5 h prior to immunization as a way of protecting the antigens from acid degradation. Infected control animals received HEPES buffer + CT or DOC buffer + CT. Animals were sacrificed 2-4 weeks after final immunization. A general outline of the study is shown in Table 7 below.

25 **Table 7****Study outline, therapeutic immunization:**

Mice were all infected with *H. pylori* strain Ah244 at day 30. Proteins are listed by their SeqID #'s.

30	<u>Substance</u>	<u>Mouse strain</u> n=10	<u>Dose/mouse</u>	<u>Dates for dosing</u>
	1. Controls, PBS	Balb/c	0,3 ml	0, 14, 24, 34
	2. Cholera toxin, 10 μ g	Balb/c	0,3 ml	0, 14, 24, 34
35	3. Protein 447, 100 μ g + CT 10 μ g	Balb/c	0,3 ml	0, 14, 24, 34
	4. Protein 465, 100 μ g + CT 10 μ g	Balb/c	0,3 ml	0, 14, 24, 34
	5. Protein 649, 100 μ g + CT 10 μ g	Balb/c	0,3 ml	0, 14, 24, 34
	6. Protein 658, 100 μ g + CT 10 μ g	Balb/c	0,3 ml	0, 14, 24, 34
	7. Protein 677, 100 μ g + CT 10 μ g	Balb/c	0,3 ml	0, 14, 24, 34
40	8. Protein 685, 100 μ g + CT 10 μ g	Balb/c	0,3 ml	0, 14, 24, 34
	9. Protein 812, 100 μ g + CT 10 μ g	Balb/c	0,3 ml	0, 14, 24, 34
	10. Protein 820, 100 μ g + CT 10 μ g	Balb/c	0,3 ml	0, 14, 24, 34
	11. Protein 880, 100 μ g + CT 10 μ g	Balb/c	0,3 ml	0, 14, 24, 34
	12. Protein 865, 100 μ g + CT 10 μ g	Balb/c	0,3 ml	0, 14, 24, 34

Analysis of infection

Mucosal infection: The mice were sacrificed by CO₂ and cervical dislocation. The abdomen was opened and the stomach removed. After cutting the stomach along the greater curvature, it was rinsed in saline. The mucosa from the antrum and corpus of an area of 25mm² was scraped separately with a surgical scalpel. The mucosa scraping was suspended in Brucella broth and plated onto Blood Skirrow selective plates. The plates were incubated under microaerophilic conditions for 3-5 days and the number of colonies was counted. The identity of *H. pylori* was ascertained by urease and catalase test and by direct microscopy or Gram staining.

10 The urease test was performed essentially as follows. The reagent, Urea Agar Base Concentrate, was purchased from DIFCO Laboratories, Detroit, MI (Catalog # 0284-61-3). Urea agar base concentrate was diluted 1:10 with water. 1 ml of if the diluted concentrate was mixed with 100-200 µl of actively growing *H. pylori* cells. Color change to magenta indicated that cells were urease positive.

15 The catalase test was performed essentially as follows. The reagent, N,N,N',N'-Tetramethyl-p-Phenylenediamine, was purchased from Sigma, St. Louis, MO (Catalog # T3134). A solution of the regent (1% w/v in water) was prepared. *H. pylori* cells were swabbed onto Whatman filter paper and overlaid with the 1% solution. Color change to dark blue indicated that the cells were catalase positive.

20 Serum antibodies: From all mice serum was prepared from blood drawn by heart puncture. Serum antibodies were identified by regular ELISA techniques, where the specific antigens of *Helicobacter pylori* were plated.

25 Mucosal antibodies: Gentle scrapings of a defined part of the corpus and of 4 cm of duodenum were performed in 50% of the mice in order to detect the presence of antibodies in the mucous. The antibody titers were determined by regular ELISA technique as for serum antibodies.

30 Statistical analysis: Wilcoxon-Mann-Whitney sign rank test was used for determination of significant effects of the antigens on *Helicobacter pylori* colonization. P<0.05 was considered significant. Because the antrum is the major colonization site for *Helicobacter* most emphasis was put upon changes in the antral colonization.

Results

35 Antibodies in sera: All antigens tested given together with CT gave rise to a measurable specific titer in serum. The highest responses were seen with SEQ ID NOs:865, 812, 658, 447, and 820 (see Figure 1).

Antibodies in mucus: In the mucus scrapings, specific antibodies against all antigens tested were seen. By far the strongest response was seen with SEQ ID NOs:685, followed by 447, 865, and 658 (see Figure 2).

Therapeutic immunization effects:

All control animals (BALB/c mice) were well colonized with *H. pylori* (strain AH244) in both antrum and corpus of the stomach. Of the antigens tested 3 proteins (SEQ ID NOs: 812, 820, and 447) gave a good and significant reduction and/or eradication of the *H. pylori* infection. The degree of colonization of the antrum was lower following immunization with SEQ ID NOs: 880, 658, and 865 compared to control. The effect of SEQ ID NOs: 465, 677, and 685 did not differ from control. The control protein lacZ, i.e. the non-*H. pylori* protein, had no eradication effect and in fact had higher *Helicobacter* colonization compared to the HEPES + CT control. All data are shown in Figures 3 and 4 for proteins dissolved in HEPES and DOC respectively. Data is shown as geometric mean values. n=8-10 Wilcoxon-Mann-Whitney sign rank test * = p<0.05; x/10 = number of mice showing eradication of *H. pylori* over the total number of mice examined.

The data presented indicate that all of the *H. pylori* associated proteins included in this study, when used as oral immunogens in conjunction with the oral adjuvant CT, resulted in stimulation of an immune response as measured by specific serum and mucosal antibodies. A majority of the proteins led to a reduction, and in some cases complete clearance of the colonization of *H. pylori* in this animal model. It should be noted that the reduction or clearance was due to heterologous protection rather than homologous protection (the polypeptides were based on the *H. pylori* J99 strain sequence and used in the therapeutic immunization studies against a different (AH244) challenge strain), indicating the vaccine potential against a wide variety of *H. pylori* strains.

The highest colonization in the antrum was seen in animals treated with the non-*Helicobacter* protein LacZ, indicating that the effects seen with the *Helicobacter pylori* antigens were specific.

Taken together these data strongly support the use of these *H. pylori* proteins in a pharmaceutical formulation for the use in humans to treat and/or prevent *H. pylori* infections.

V. Sequence Variance Analysis of genes in *Helicobacter pylori* strains

Four genes were cloned and sequenced from several strains of *H. pylori* to compare the DNA and deduced amino acid sequences. This information was used to determine the sequence variation between the *H. pylori* strain, J99, and other *H. pylori* strains isolated from human patients.

Preparation of Chromosomal DNA.

Cultures of *H. pylori* strains (as listed in Table 10) were grown in BLBB (1% Tryptone, 1% Peptamin 0.1% Glucose, 0.2% Yeast Extract 0.5% Sodium Chloride, 5% Fetal Bovine Serum) to an OD₆₀₀ of 0.2. Cells were centrifuged in a Sorvall RC-3B at 3500 x g at 4°C for 15 minutes and the pellet resuspended in 0.95 mls of 10 mM Tris-HCl,

-106-

0.1 mM EDTA (TE). Lysozyme was added to a final concentration of 1mg/ml along with, SDS to 1% and RNase A + T1 to 0.5mg/ml and 5 units/ml respectively, and incubated at 37°C for one hour. Proteinase K was then added to a final concentration of 0.4mg/ml and the sample was incubated at 55 C for more than one hour. NaCl was added to the sample to a concentration of 0.65 M, mixed carefully, and 0.15 ml of 10% CTAB in 0.7M NaCl (final is 1% CTAB/70mM NaCl) was added followed by incubation at 65°C for 20 minutes. At this point, the samples were extracted with chloroform:isoamyl alcohol, extracted with phenol, and extracted again with chloroform:isoamyl alcohol. DNA was precipitated with either EtOH (1.5 x volumes) or isopropanol (0.6 x volumes) at -70°C for 10 minutes, washed in 70% EtOH and resuspended in TE.

PCR Amplification and cloning.

Genomic DNA prepared from twelve strains of *Helicobacter pylori* was used as the source of template DNA for PCR amplification reactions (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994). To amplify a DNA sequence containing an *H. pylori* ORF, genomic DNA (10 nanograms) was introduced into a reaction vial containing 2 mM MgCl₂, 1 micromolar synthetic oligonucleotide primers (forward and reverse primers, see Table 8) complementary to and flanking a defined *H. pylori* ORF, 0.2 mM of each deoxynucleotide triphosphate; dATP, dGTP, dCTP, dTTP and 0.5 units of heat stable DNA polymerase (Amplitaq, Roche Molecular Systems, Inc., Branchburg, NJ, USA) in a final volume of 20 microliters in duplicate reactions.

Table 8

Oligonucleotide primers used for PCR amplification of *H. pylori* DNA sequences.

Outer membrane Proteins	Forward primer 5' to 3'	Reverse Primer 5' to 3'
SEQ ID NO:649 (for strains AH4, AH15, AH61, 5294, 5640, AH18, and AH244)	5'-TTAACCATGGTGAAAAGC GATA-3' (SEQ ID NO:1919)	5'-TAGAATTCGCCTCTAAACT TTAG-3' (SEQ ID NO:1920)
SEQ ID NO:649 (for strains AH5, 5155, 7958, AH24, and J99)	5'-TTAACCATGGTGAAAAGC GATA-3' (SEQ ID NO:1921)	5'-TAGAATTCGCATAACGATCA ATC-3' (SEQ ID NO:1922)
SEQ ID NO:865	5'-ATATCCATGGTGAGTTGA TGA-3' (SEQ ID NO:1923)	5'-ATGAATTCAATTTTTTATTTT GCCA-3' (SEQ ID NO:1924)
SEQ ID NO:677	5'-AATTCATGGCTATCCAAA TCCG-3' (SEQ ID NO:1925)	5'-ATGAATTCGCCAAAATCGTA GTATT-3' (SEQ ID NO:1926)
SEQ ID NO:764	5'-GATACCATGGAATTTATGA AAAAG-3' (SEQ ID NO:1927)	5'-TGAATTCGAAAAAGTGTAGT TATAC-3' (SEQ ID NO:1928)

-107-

The following thermal cycling conditions were used to obtain amplified DNA products for each ORF using a Perkin Elmer Cetus/ GeneAmp PCR System 9600 thermal cycler:

- 5 Sequences (by SEQ ID NO:) 865 and 764;
Denaturation at 94°C for 2 min,
2 cycles at 94°C for 15 sec, 30°C for 15 sec and 72°C for 1.5 min
23 cycles at 94°C for 15 sec, 55°C for 15 sec and 72°C for 1.5 min
Reactions were concluded at 72°C for 6 minutes.
- 10 Sequence (by SEQ ID NO:) 649 for strains AH5, 5155, 7958, AH24, and J99;
Denaturation at 94°C for 2 min,
2 cycles at 94°C for 15 sec, 30°C for 15 sec and 72°C for 1.5 min
25 cycles at 94°C for 15 sec, 55°C for 15 sec and 72°C for 1.5 min
- 15 Reaction was concluded at 72°C for 6 minutes.
- Sequences (by SEQ ID NO:) 677 and 649 for strains AH4, AH15, AH61, 5294, 5640,
AH18, and Hp244 ;
Denaturation at 94°C for 2 min,
20 2 cycles at 94°C for 15 sec, 30°C for 20 sec and 72°C for 2 min
25 cycles at 94°C for 15 sec, 55°C for 20 sec and 72°C for 2 min
Reactions were concluded at 72°C for 8 minutes.
- 25 Upon completion of thermal cycling reactions, each pair of samples were combined
and used directly for cloning into the pCR cloning vector as described below.
- Cloning of H. pylori DNA sequences into the pCR TA cloning vector.*
- All amplified inserts were cloned into the pCR 2.1 (pCRII in the case of *H. pylori*
sequence 865) vector by the method described in the Original TA cloning kit (Invitrogen,
30 San Diego, CA). Products of the ligation reaction were then used to transform the
TOP10F' (INVaF' in the case of *H. pylori* sequence 865) strain of *E. coli* as described
below.
- Transformation of competent bacteria with recombinant plasmids*
- 35 Competent bacteria. *E. coli* strain TOP10F' or *E. coli* strain INVaF' were
transformed with recombinant pCR expression plasmids carrying the cloned *H. pylori*
sequences according to standard methods (Current Protocols in Molecular Biology, John
Wiley and Sons, Inc., F. Ausubel et al., editors, 1994). Briefly, 2 microliters of 0.5
micromolar BME was added to each vial of 50 microliters of competent cells.

-108-

- Subsequently, 2 microliters of ligation reaction was mixed with the competent cells and incubated on ice for 30 minutes. The cells and ligation mixture were then subjected to a "heat shock" at 42°C for 30 seconds, and were subsequently placed on ice for an additional 2 minutes, after which, samples were incubated in 0.45 milliliters SOC medium (0.5% yeast extract, 2.0 % tryptone, 10 mM NaCl, 2.5 mM KCl, 10 mM MgCl₂, 10 mM MgSO₄ and 20, mM glucose) at 37°C with shaking for 1 hour. Samples were then spread on LB agar plates containing 25 microgram/ml kanamycin sulfate or 100 micrograms/ml ampicillin for growth overnight. Transformed colonies of TOP10F' or INVaF' were then picked and analyzed to evaluate cloned inserts as described below.
- 10 *Identification of recombinant PCR plasmids carrying H. pylori sequences*
- Individual TOP10F' or INVaF' clones transformed with recombinant pCR-*H. pylori* ORFs were analyzed by PCR amplification of the cloned inserts using the same forward and reverse primers, specific for each *H. pylori* sequence, that were used in the original PCR amplification cloning reactions. Successful amplification verified the integration of
- 15 the *H. pylori* sequences in the cloning vector (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994).
- Individual clones of recombinant pCR vectors carrying properly cloned *H. pylori* ORFs were picked for sequence analysis. Sequence analysis was performed on ABI Sequencers using standard protocols (Perkin Elmer) using vector-specific primers (as found
- 20 in PCRII or pCR2.1, Invitrogen, San Diego, CA) and sequencing primers specific to the ORF as listed in Table 9 below.

Table 9

Oligonucleotide primers used for sequencing of *H. pylori* DNA sequences.

Outer membrane Proteins	Forward primers 5' to 3'	Reverse Primers 5' to 3'
SEQ ID NO:649	5'-CCCTTCATTTTAGAAATCG-3' (SEQ ID NO:1929) 5'-ATTTCAACCAATTCAATGCG-3' (SEQ ID NO:1930) 5'-GCCCCTTTTGATTTGAAGCT-3' (SEQ ID NO:1931) 5'-TCGCTCCAAGATACCAAGAAGT-3' (SEQ ID NO:1932) 5'-CTTGAATTAGGGGCAAAGATCG-3' (SEQ ID NO:1933) 5'-ATGCGTTTTTACCCAAAGAAGT-3' (SEQ ID NO:1934) 5'-ATAACGCCACTTCCTTATTGGT-3' (SEQ ID NO:1935)	5'-CTTTGGGTAAAAACGCATC-3' (SEQ ID NO:1936) 5'-CGATCTTTGATCCTAATTCA-3' (SEQ ID NO:1937) 5'-ATCAAGTTGCCTATGCTGA-3' (SEQ ID NO:1938)
SEQ ID NO:865	5'-TTGAACACTTTTGATTATGCGG-3' (SEQ ID NO:1939) 5'-GGATTATGCGATTGTTTTACAAG-3' (SEQ ID NO:1940)	5'-GTCTTTAGCAAAAATGGCGTC-3' (SEQ ID NO:1941) 5'-AATGAGCGTAAGAGAGCCTTC-3' (SEQ ID NO:1942)
SEQ ID NO:677	5'-CTTATGGGGGTATTGTCA-3' (SEQ ID NO:1943) 5'-AGCATGTGGGTATCCAGC-3' (SEQ ID NO:1944)	5'-AGGTTGTTGCCTAAAGACT-3' (SEQ ID NO:1945) 5'-CTGCCTCCACCTTTGATC-3' (SEQ ID NO:1946)
SEQ ID NO:764	5'-ACCAATATCAATTGGCACT-3' (SEQ ID NO:1947) 5'-ACTTGGAAGCTCTGCA-3' (SEQ ID NO:1948)	5'-CTTGCTTGTCTATCTAGC-3' (SEQ ID NO:1949) 5'-GTTGAAGTGTGGTGCTA-3' (SEQ ID NO:1950)
	5'-CAAGCAAGTGGTTTGGTTTAG-3' (SEQ ID NO:1951) 5'-TGGAAGAGCAAATCATTGAAG-3' (SEQ ID NO:1952)	5'-GCCATAATCAAAAAGCCCAT-3' (SEQ ID NO:1953) 5'-CTAAAACCAACCCTTGTGCTC-3' (SEQ ID NO:1954)
Vector Primers	5'-GTAAAACGACGGCCAG-3' (SEQ ID NO:1955)	5'-CAGGAAACAGCTATGAC-3' (SEQ ID NO:1956)

5 Results

To establish the PCR error rate in these experiments, five individual clones of SEQ ID NO:649, prepared from five separate PCR reaction mixtures from *H. pylori* strain J99, were sequenced over a total length of 897 nucleotides for a cumulative total of 4485 bases of DNA sequence. DNA sequence for the five clones was compared to the DNA sequence of SEQ ID NO:649 obtained previously by a different method, i.e., random shotgun cloning and sequencing. The PCR error rate for the experiments described herein was determined to be 2 base changes out of 4485 bases, which is equivalent to an estimated error rate of less than or equal to 0.04%.

-110-

DNA sequence analysis was performed on four different open reading frames identified as genes and amplified by PCR methods from a dozen different strains of the bacterium *Helicobacter pylori*. The deduced amino acid sequences of three of the four open reading frames that were selected for this study showed statistically significant

5 BLAST homology to defined proteins present in other bacterial species. Those ORFs included: SEQ ID NO:649, homologous to the val A & B genes encoding an ABC transporter in *F. novicida*; SEQ ID NO:865, homologous to lipoprotein e (P4) present in the outer membrane of *H. influenzae*; SEQ ID NO:677, homologous to fecA, an outer

10 membrane receptor in iron (III) dicitrate transport in *E. coli*. SEQ ID NO:764 was identified as an unknown open reading frame, because it showed low homology with sequences in the public databases.

To assess the extent of conservation or variance in the ORFs across various strains of *H. pylori*, changes in DNA sequence and the deduced protein sequence were compared to the DNA and deduced protein sequences found in the J99 strain of *H. pylori* (see Table

15 10 below). Results are presented as percent identity to the J99 strain of *H. pylori* sequenced by random shotgun cloning. To control for any variations in the J99 sequence each of the four open reading frames were cloned and sequenced again from the J99 bacterial strain and that sequence information was compared to the sequence information that had been

20 collected from inserts cloned by random shotgun sequencing of the J99 strain. The data demonstrate that there is variation in the DNA sequence ranging from as little as 0.12 % difference (SEQ ID NO:764, J99 strain) to approximately 7% change (SEQ ID NO:649, strain AH5). The deduced protein sequences show either no variation (SEQ ID NO:764, strains AH18 and AH24) or up to as much as 7.66% amino acid changes (SEQ ID NO:649, Strain AH5).

25

-111-

Table 10Multiple Strain DNA Sequence analysis of *H. pylori* Vaccine Candidates

<u>J99 Seq. ID #:</u>	649	649	865	865	677	677	764	764
<u>Length of Region Sequenced:</u>	248 a.a.	746 nt.	232 a.a.	696 nt.	182 a.a.	548 nt.	273 a.a.	819 nt.
<u>Strain Tested</u>	AA identity	Nuc. identity	AA identity	Nuc. identity	AA identity	Nuc. identity	AA identity	Nuc. identity
J99	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	99.63%	99.88%
AH244	95.16%	95.04%	n.d.	n.d.	99.09%	96.71%	98.90%	96.45%
AH4	95.97%	95.98%	97.84%	95.83%	n.d.	n.d.	97.80%	95.73%
AH5	92.34%	93.03%	98.28%	96.12%	98.91%	96.90%	98.53%	95.73%
AH15	95.16%	94.91%	97.41%	95.98%	99.82%	97.99%	99.63%	96.09%
AH61	n.d.	n.d.	97.84%	95.98%	99.27%	97.44%	n.d.	n.d.
5155	n.d.	n.d.	n.d.	n.d.	99.45%	97.08%	98.53%	95.60%
5294	94.35%	94.37%	98.28%	95.40%	99.64%	97.26%	97.07%	95.48%
7958	94.35%	94.10%	97.84%	95.40%	n.d.	n.d.	99.63%	96.46%
5640	95.16%	94.37%	97.41%	95.69%	99.09%	97.63%	98.53%	95.48%
AH18	n.d.	n.d.	98.71%	95.69%	99.64%	97.44%	100.00%	95.97%
AH24	94.75%	95.04%	97.84%	95.40%	99.27%	96.71%	100.00%	96.46%

n.d. = not done

5 VI. Experimental Knock-Out Protocol for the Determination of Essential *H. pylori* Genes as Potential Therapeutic Targets

Therapeutic targets are chosen from genes whose protein products appear to play key roles in essential cell pathways such as cell envelope synthesis, DNA synthesis, transcription, translation, regulation and colonization/virulence.

- 10 The protocol for the deletion of portions of *H. pylori* genes/ORFs and the insertional mutagenesis of a kanamycin-resistance cassette in order to identify genes which are essential to the cell is modified from previously published methods (Labigne-Roussel et al., 1988, J. Bacteriology 170, pp. 1704-1708; Cover et al., 1994, J. Biological Chemistry 269, pp. 10566-10573; Reytrat et al., 1995, Proc. Natl. Acad. Sci. 92, pp 8768-8772). The
- 15 result is a gene "knock-out."

Identification and Cloning of H. pylori Gene Sequences

- The sequences of the genes or ORFs (open reading frames) selected as knock-out targets are identified from the *H. pylori* genomic sequence and used to design primers to
- 20 specifically amplify the genes/ORFs. All synthetic oligonucleotide primers are designed with the aid of the OLIGO program (National Biosciences, Inc., Plymouth, MN 55447, USA), and can be purchased from Gibco/BRL Life Technologies (Gaithersburg, MD, USA). If the ORF is smaller than 800 to 1000 base pairs, flanking primers are chosen outside of the open reading frame.

Genomic DNA prepared from the *Helicobacter pylori* HpJ99 strain (ATCC 55679) is used as the source of template DNA for amplification of the ORFs by PCR (polymerase chain reaction) (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994). For the preparation of genomic DNA from *H. pylori*, see

5 Example I. PCR amplification is carried out by introducing 10 nanograms of genomic HpJ99 DNA into a reaction vial containing 10 mM Tris pH 8.3, 50 mM KCl, 2 mM MgCl₂, 2 microMolar synthetic oligonucleotide primers (forward=F1 and reverse=R1), 0.2 mM of each deoxynucleotide triphosphate (dATP, dGTP, dCTP, dTTP), and 1.25 units of heat stable DNA polymerase (Amplitaq, Roche Molecular Systems, Inc., Branchburg, NJ, USA)

10 in a final volume of 40 microliters. The PCR is carried out with Perkin Elmer Cetus/GeneAmp PCR System 9600 thermal cyclers.

Upon completion of thermal cycling reactions, each sample of amplified DNA is visualized on a 2% TAE agarose gel stained with Ethidium Bromide (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994) to

15 determine that a single product of the expected size had resulted from the reaction. Amplified DNA is then washed and purified using the Qiaquick Spin PCR purification kit (Qiagen, Gaithersburg, MD, USA).

PCR products are cloned into the pT7Blue T-Vector (catalog#69820-1, Novagen, Inc., Madison, WI, USA) using the TA cloning strategy (Current Protocols in Molecular

20 Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994). The ligation of the PCR product into the vector is accomplished by mixing a 6 fold molar excess of the PCR product, 10 ng of pT7Blue-T vector (Novagen), 1 microliter of T4 DNA Ligase Buffer (New England Biolabs, Beverly, MA, USA), and 200 units of T4 DNA Ligase (New England Biolabs) into a final reaction volume of 10 microliters. Ligation is allowed to

25 proceed for 16 hours at 16°C.

Ligation products are electroporated (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994) into electroporation-competent XL-1 Blue or DH5- α *E. coli* cells (Clontech Lab., Inc. Palo Alto, CA, USA). Briefly, 1 microliter of ligation reaction is mixed with 40 microliters of electrocompetent cells and subjected to

30 a high voltage pulse (25 microFarads, 2.5 kV, 200 ohms) after which the samples are incubated in 0.45 ml SOC medium (0.5% yeast extract, 2% tryptone, 10 mM NaCl, 2.5 mM KCl, 10 mM MgCl₂, 10 mM MgSO₄ and 20 mM glucose) at 37°C with shaking for 1 hour. Samples are then spread onto LB (10 g/l bacto tryptone, 5 g/l bacto yeast extract, 10 g/l sodium chloride) plates containing 100 microgram/ml of Ampicillin, 0.3% X-gal, and 100

35 microgram/ml IPTG. These plates are incubated overnight at 37°C. Ampicillin-resistant colonies with white color are selected, grown in 5 ml of liquid LB containing 100 microgram/ml of Ampicillin, and plasmid DNA is isolated using the Qiagen miniprep protocol (Qiagen, Gaithersburg, MD, USA).

-113-

To verify that the correct *H. pylori* DNA inserts had been cloned, these pT7Blue plasmid DNAs are used as templates for PCR amplification of the cloned inserts, using the same forward and reverse primers used for the initial amplification of the J99 *H. pylori* sequence. Recognition of the primers and a PCR product of the correct size as visualized on a 2% TAE, ethidium bromide stained agarose gel are confirmation that the correct inserts had been cloned. Two to six such verified clones are obtained for each knock-out target, and frozen at -70°C for storage. To minimize errors due to PCR, plasmid DNA from these verified clones are pooled, and used in subsequent cloning steps.

The sequences of the genes/ORFs are again used to design a second pair of primers which flank the region of *H. pylori* DNA to be either interrupted or deleted (up to 250 basepairs) within the ORFs but are oriented away from each other. The pool of circular plasmid DNAs of the previously isolated clones are used as templates for this round of PCR. Since the orientation of amplification of this pair of deletion primers is away from each other, the portion of the ORF between the primers is not included in the resultant PCR product. The PCR product is a linear piece of DNA with *H. pylori* DNA at each end and the pT7Blue vector backbone between them which, in essence, results in the deletion of a portion of the ORFs. The PCR product is visualized on a 1% TAE, ethidium bromide stained agarose gel to confirm that only a single product of the correct size has been amplified.

A Kanamycin-resistance cassette (Labigne-Roussel et al., 1988 J. Bacteriology 170, 1704-1708) is ligated to this PCR product by the TA cloning method used previously (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994). The Kanamycin cassette containing a *Campylobacter* kanamycin resistance gene is obtained by carrying out an EcoRI digestion of the recombinant plasmid pCTB8:kan (Cover et al., 1994, J. Biological Chemistry 269, pp. 10566-10573). The proper fragment (1.4 kb) is isolated on a 1% TAE gel, and isolated using the QIAquick gel extraction kit (Qiagen, Gaithersburg, MD, USA). The fragment is end repaired using the Klenow fill-in protocol, which involved mixing 4ug of the DNA fragment, 1 microliter of dATP, dGTP, dCTP, dTTP at 0.5 mM, 2 microliter of Klenow Buffer (New England Biolabs) and 5 units of Klenow DNA Polymerase I Large (Klenow) Fragment (New England Biolabs) into a 20 microliter reaction, incubating at 30°C for 15 min, and inactivating the enzyme by heating to 75°C for 10 minutes. This blunt-ended Kanamycin cassette is then purified through a QIAquick column (Qiagen, Gaithersburg, MD, USA) to eliminate nucleotides. The "T" overhang is then generated by mixing 5 micrograms of the blunt-ended kanamycin cassette, 10 mM Tris pH 8.3, 50 mM KCl, 2 mM MgCl₂, 5 units of DNA Polymerase (Amplitaq, Roche Molecular Systems, Inc., Branchburg, NJ, USA), 20 microliters of 5 mM dTTP, in a 100 microliter reaction and incubating the reaction for 2 hours at 37°C. The "Kan-T" cassette is purified using a QIAquick column (Qiagen, Gaithersburg, MD, USA). The PCR product of the deletion primers (F2 and R2) is ligated

-114-

to the Kan-T cassette by mixing 10 to 25 ng of deletion primer PCR product, 50 - 75 ng Kan-T cassette DNA, 1 microliter 10x T4 DNA Ligase reaction mixture, 0.5 microliter T4 DNA Ligase (New England Biolabs, Beverly, MA, USA) in a 10 microliter reaction and incubating for 16 hours at 16°C.

- 5 The ligation products are transformed into XL-1 Blue or DH5- α *E.coli* cells by electroporation as described previously. After recovery in SOC, cells are plated onto LB plates containing 100 microgram/ml Ampicillin and grown overnight at 37°C. These plates are then replica plated onto plates containing 25 microgram/ml Kanamycin and allowed to grow overnight. Resultant colonies have both the Ampicillin resistance gene present in the
- 10 pT7Blue vector, and the newly introduced Kanamycin resistance gene. Colonies are picked into LB containing 25 microgram/ml Kanamycin and plasmid DNA is isolated from the cultured cells using the Qiagen miniprep protocol (Qiagen, Gaithersburg, MD, USA).

- Several tests by PCR amplification are conducted on these plasmids to verify that the Kanamycin is inserted in the *H. pylori* gene/ORF, and to determine the orientation of
- 15 the insertion of the Kanamycin-resistance gene relative to the *H. pylori* gene/ORF. To verify that the Kanamycin cassette is inserted into the *H. pylori* sequence, the plasmid DNAs are used as templates for PCR amplification with the set of primers originally used to clone the *H. pylori* gene/ORFs. The correct PCR product is the size of the deleted gene/ORF but increased in size by the addition of a 1.4 kilobase Kanamycin cassette. To
- 20 avoid potential polar effects of the kanamycin resistance cassette on *H. pylori* gene expression, the orientation of the Kanamycin resistance gene with respect to the knock-out gene/ORF is determined and both orientations are eventually used in *H. pylori* transformations (see below). To determine the orientation of insertion of the kanamycin resistance gene, primers are designed from the ends of the kanamycin resistance gene
- 25 ("Kan-1" 5'-ATCTTACCTATCACCTCAAAT-3', and "Kan-2" 5'-AGACAGCAACATCTTTGTGAA-3'). By using each of the cloning primers in conjunction with each of the Kan primers (4 combinations of primers), the orientation of the Kanamycin cassette relative to the *H.pylori* sequence is determined. Positive clones are classified as either in the "A" orientation (the same direction of transcription is present
- 30 for both the *H. pylori* gene and the Kanamycin resistance gene), or in the "B" orientation (the direction of transcription for the *H.pylori* gene is opposite to that of the Kanamycin resistance gene). Clones which share the same orientation (A or B) are pooled for subsequent experiments and independently transformed into *H. pylori*.

35 *Transformation of Plasmid DNA into H. pylori cells*

 Two strains of *H. pylori* are used for transformation: ATCC 55679, the clinical isolate which provided the DNA from which the *H. pylori* sequence database is obtained, and AH244, an isolate which had been passaged in, and has the ability to colonize the mouse stomach. Cells for transformation are grown at 37°C, 10% CO₂, 100% humidity,

-115-

either on Sheep-Blood agar plates or in Brucella Broth liquid. Cells are grown to exponential phase, and examined microscopically to determine that the cells are "healthy" (actively moving cells) and not contaminated. If grown on plates, cells are harvested by scraping cells from the plate with a sterile loop, suspended in 1 ml of Brucella Broth, spun down (1 minute, top speed in eppendorf microfuge) and resuspended in 200 microliters Brucella Broth. If grown in Brucella Broth liquid, cells are centrifuged (15 minutes at 3000 rpm in a Beckman TJ6 centrifuge) and the cell pellet resuspended in 200 microliters of Brucella broth. An aliquot of cells is taken to determine the optical density at 600 nm, in order to calculate the concentration of cells. An aliquot (1 to 5 OD₆₀₀ units/25 microliter) of the resuspended cells is placed onto a prewarmed Sheep-Blood agar plate, and the plate is further incubated at 37°C, 6% CO₂, 100% humidity for 4 hours. After this incubation, 10 microliters of plasmid DNA (100 micrograms per microliter) is spotted onto these cells. A positive control (plasmid DNA with the ribonuclease H gene disrupted by kanamycin resistance gene) and a negative control (no plasmid DNA) are done in parallel. The plates are returned to 37°C, 6% CO₂ for an additional 4 hours of incubation. Cells are then spread onto that plate using a swab wetted in Brucella broth, and grown for 20 hours at 37°C, 6% CO₂. Cells are then transferred to a Sheep-Blood agar plate containing 25 micrograms/ml Kanamycin, and allowed to grow for 3 to 5 days at 37°C, 6% CO₂, 100% humidity. If colonies appear, they are picked and regrown as patches on a fresh Sheep-Blood agar plate containing 25 micrograms/ml Kanamycin.

Three sets of PCR tests are done to verify that the colonies of transformants have arisen from homologous recombination at the proper chromosomal location. The template for PCR (DNA from the colony) is obtained by a rapid boiling DNA preparation method as follows. An aliquot of the colony (stab of the colony with a toothpick) is introduced into 100 microliters of 1% Triton X-100, 20 mM Tris, pH 8.5, and boiled for 6 minutes. An equal volume of phenol : chloroform (1:1) is added and vortexed. The mixture is microfuged for 5 minutes and the supernatant is used as DNA template for PCR with combinations of the following primers to verify homologous recombination at the proper chromosomal location.

TEST 1. PCR with cloning primers originally used to amplify the gene/ORF. A positive result of homologous recombination at the correct chromosomal location should show a single PCR product whose size is expected to be the size of the deleted gene/ORF but increased in size by the addition of a 1.4 kilobase Kanamycin cassette. A PCR product of just the size of the gene/ORF is proof that the gene had not been knocked out and that the transformant is not the result of homologous recombination at the correct chromosome location.

TEST 2. PCR with F3 (primer designed from sequences upstream of the gene/ORF and not present on the plasmid), and either primer Kan-1 or Kan-2 (primers designed from the ends of the kanamycin resistance gene), depending on whether the plasmid DNA used

-116-

was of "A" or "B" orientation. Homologous recombination at the correct chromosomal location will result in a single PCR product of the expected size (i.e., from the location of F3 to the insertion site of kanamycin resistance gene). No PCR product or PCR product(s) of incorrect size(s) will prove that the plasmid had not integrated at the correct site and that the gene had not been knocked out.

TEST 3. PCR with R3 (primer designed from sequences downstream of the gene/ORF and not present on the plasmid) and either primer Kan-1 or Kan-2, depending on whether the plasmid DNA used was of "A" or "B" orientation. Homologous recombination at the correct chromosomal location will result in a single PCR product of the expected size (i.e., from the insertion site of kanamycin resistance gene to the downstream location of R3). Again, no PCR product or PCR product(s) of incorrect size(s) will prove that the plasmid had not integrated at the correct site and that the gene had not been knocked out.

Transformants showing positive results for all three tests above indicate that the gene is not essential for survival *in vitro*.

A negative result in any of the three above tests for each transformant indicates that the gene had not been disrupted, and that the gene is essential for survival *in vitro*.

In the event that no colonies result from two independent transformations while the positive control with the disrupted ribonuclease H plasmid DNA produces transformants, the plasmid DNA is further analyzed by PCR on DNA from transformant populations prior to plating for colony formation. This will verify that the plasmid can enter the cells and undergo homologous recombination at the correct site. Briefly, plasmid DNA is incubated according to the transformation protocol described above. DNA is extracted from the *H. pylori* cells immediately after incubation with the plasmid DNAs and the DNA is used as template for the above TEST 2 and TEST 3. Positive results in TEST 2 and TEST 3 would verify that the plasmid DNA could enter the cells and undergo homologous recombination at the correct chromosomal location. If TEST 2 and TEST 3 are positive, then failure to obtain viable transformants indicates that the gene is essential, and cells suffering a disruption in that gene are incapable of colony formation.

VII. High-throughput drug screen assay

Cloning, expression and protein purification

Cloning, transformation, expression and purification of the *H. pylori* target gene and its protein product, e.g., an *H. pylori* enzyme, to be used in a high-throughput drug screen assay, is carried out essentially as described in Examples II and III above. Development and application of a screening assay for a particular *H. pylori* gene product, peptidyl-propyl *cis-trans* isomerase, is described below as a specific example.

-117-

Enzymatic Assay

The assay is essentially as described by Fisher (Fischer, G., et.al. (1984) *Biomed. Biochim. Acta* 43:1101-1111). The assay measures the *cis-trans* isomerization of the Ala-Pro bond in the test peptide N-succinyl-Ala-Ala-Pro-Phe-p-nitroanilide (Sigma # S-7388, lot # 84H5805). The assay is coupled with α -chymotrypsin, where the ability of the protease to cleave the test peptide occurs only when the Ala-Pro bond is in *trans*. The conversion of the test peptide to the trans isomer in the assay is followed at 390 nm on a Beckman Model DU-650 spectrophotometer. The data are collected every second with an average scanning of time of 0.5 second. Assays are carried out in 35 mM Hepes, pH 8.0, in a final volume of 400 μ l, with 10 μ M α -chymotrypsin (type 1-5 from bovine Pancreas, Sigma # C-7762, lot 23H7020) and 10 nM PPIase. To initiate the reaction, 10 μ l of the substrate (2 mM N-Succinyl-Ala-Ala-Pro-Phe-p-nitroanilide in DMSO) is added to 390 μ l of reaction mixture at room temperature.

15 *Enzymatic assay in crude bacterial extract.*

A 50 ml culture of *Helicobacter pylori* (strain J99) in Brucella broth is harvested at mid-log phase ($OD_{600\text{ nm}} \sim 1$) and resuspended in lysis buffer with the following protease inhibitors: 1 mM PMSF, and 10 μ g/ml of each of aprotinin, leupeptin, pepstatine, TLCK, TPCK, and soybean trypsin inhibitor. The suspension is subjected to 3 cycles of freeze-thaw (15 minutes at -70°C , then 30 minutes at room temperature), followed by sonication (three 20 second bursts). The lysate is centrifuged (12,000 g x 30 minutes) and the supernatant is assayed for enzymatic activity as described above.

Many *H. pylori* enzymes can be expressed at high levels and in an active form in *E. coli*. Such high yields of purified proteins provide for the design of various high throughput drug screening assays.

EQUIVALENTS

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments and methods described herein. Such equivalents are intended to be encompassed by the scope of the following claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Astra Aktiebolag
- (B) STREET: S-151 85
- (C) CITY: Sodertalje
- (D) STATE:
- (E) COUNTRY: Sweden
- (F) POSTAL CODE (ZIP):

- (ii) TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS

- (iii) NUMBER OF SEQUENCES: 1956

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: 8-mm cartridge tape
- (B) COMPUTER: SPARC station LX
- (C) OPERATING SYSTEM: SunOS Release 4.1.3
- (D) SOFTWARE: tar

(v) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: PCT/US96/09122
- (B) FILING DATE: June 6, 1996

(vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/630,405
- (B) FILING DATE: 01-APR-1996

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/561,469
- (B) FILING DATE: 17-NOV-1995

(viii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/487,032
- (B) FILING DATE: 07-JUNE-1995

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- (A) NAME: Mandragouras, Amy E.
- (B) REGISTRATION NUMBER: 36,207
- (C) REFERENCE/DOCKET NUMBER: GTN-001C5PC

(xi) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (617)227-7400
- (B) TELEFAX: (617)227-5941

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1

ATGTGTTCTC	AGGAAATTTT	ATCAAGCTTG	CAAACCATTA	TTGCCGAACA	ATTTTCTATA	60
AATATCATCA	CTCAGCTTGC	TAATAAACTC	ACACAAGTTA	AAAATCTAAA	TTTTTTTGAG	120
AATAAGACC	ATACTATCAA	GCTTAACACT	ATCCATAACG	GACTGCACAT	CCGCCCCCTA	180
AATTATGTCA	GTAATCTTTT	TTTCAATCTA	CAACGCATTA	TAGGGCTTAT	CAGTCTGTTT	240
GGGATATTAT	TTTCCATTAG	TATTATCTA	CCCTTTATAA	TGATTTTTCG	AACAGTGCCT	300
TGTATTCTCA	TTTCCAACCA	TATAGCAAAA	AAACATAGTG	CTTCCATAGA	TAAACTTCAA	360
GACCAAAAAG	AAAGCATGCA	AAATTACTTA	TACTCTGGAC	TAGATAACCA	AAAGAACAAG	420
GACAACCTAT	TATTTAACTT	CATGCTAAAT	TTTCACCATA	AATTTATTGA	AACAAAAGAA	480
TTGTATCTCA	ATAATTTTGT	GAAAGTAGCC	CAAAAAAAGT	TAATATTTAC	CATATATGCT	540
GATGTTTTAA	TCACCACTCT	AAGTATTGCA	CTATTTTTC	TAATGGTTTT	TATTATCCTT	600
TCAAAATTAA	TTGGTGTGGG	AGCAATTGCT	GGGTATATCC	AAGCATTTAG	CTCTACCCAA	660
CAACAACCTAC	AAGATTTATC	ATTTTATGGA	AAGTGGTTTT	TTGCTATCAA	TAAATACTTT	720
GAAAATTATT	TCTGTATTTT	AGATTACAAA	ATACCGAAAC	CAGAAACACA	AATCAAATTA	780
GAAGAAAAAA	TCCATAGCAT	TACATTTGAA	AATATTAGTT	TCTCTTATCC	TAATTCAAAA	840
CTTATTTTTG	AAAACTTTAA	TCTCTCTTTA	CACTCTAATA	AAATTTATGC	ATTAGTCGGC	900
AAGAATGCTA	GCGGAAAAAG	CACGCTGATT	AATTTATTAT	TAGGTTTTTTA	TACCCCAAAT	960
TCAGGTCAAA	TTATCATTAA	TAACAAATAC	CCATTACAAG	ACTTGGAAGT	AAATAGCTAC	1020
CATCAACAAA	TGAGTGCCAT	ATTTCAAGAT	TTTTCTCTTT	ATGCTGGGTA	TAGCATTGAT	1080
GATAATCTTT	TTATGCAAAA	CAATATCACT	AAAGAGCAAT	TGAAGCAAAA	AAGAGAAATA	1140
CTAAAATCTT	TTGATGAGAA	TTTTCAAAAT	TGTCTTAATG	ATTGCAACAA	CACACTATTT	1200
GGAGCGCAAT	ATAATGGGGT	AGATTTTCT	TTAGGTCAAA	AGCAACGCAT	AGCTACCATG	1260
AGAGCCTTTT	TAAAACCAAG	TAATTGCATT	GTTTTAGATG	AGCCAAGCAG	CGCCATCGAT	1320
CCCATTATGG	AAAAAGAGTT	TTTAGATTTT	ATTTTAAAAA	AATCGCAATC	TAAGATGGCT	1380
TTAATTATTA	CACACCGCAT	GAATAGTGTC	AAGCAAGCTA	ATGAAATTAT	CGTGTTAGAT	1440
CAAGGCAAAAC	TAATAGAACA	GGGCAACTTT	GAAACCCTTA	TGAAAAACA	GGGATTATTT	1500
TGCGAATTGT	TTTTGAAACA	ACAATAC				1527

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

120

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2

ATGGAGCGCA	AGACGCTCCA	GAGCATTTTA	TGTTTAATAA	AAAAAGAAAT	GATGAGACCA	60
AAAGGTATTC	TAATGAATTG	TTGCAGGSCT	TGGAAACACC	AGGTTCTTAA	GCAAAGCACG	120
ACAGGTTTAG	TGGTGTGAG	CATTATCTCT	TCTACAGCCC	CCTTTATTGG	TTTGTGTTGGG	180
ACGGTAGTTG	AAATTTTAGA	AGCGTTTAAC	AATTTGGGCG	CGTTAGGTCA	AGCTTCTTTT	240
GGAGTGATCG	CACCCATTAT	TTCTAAGGCG	CTTATCGCCA	CCGCTGCAGG	GATTTTAGCA	300
GCCATTCAG	CTATTCTTT	TTACTTGATC	TTAAAGCGCA	AGGTGTATGA	TTTATCGGTT	360
TATGTGCAGA	TGCAAGTGA	TATTTGTCT	TCTAAAAA			399

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 474 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3

ATGCATGAAC	GCATTGAAAG	AGGTATTGGA	AATAATGAAT	GTAAAGAAAT	TTTTGGCAAT	60
GAACCTAAAC	AAAGAAAGAC	AAAATTGATT	GAAGACATAG	AACGGCGGTT	CAAAGAATGC	120
GAGGAACAAT	TCCGTGGAAG	TGTAGGAAAA	AATATTGAAC	AACCTGAAGA	AAGAGTTAAA	180
GATTCTCTAG	CGATTATAAA	ACGCATCAAT	AACCTTGGTC	TTAATCCTAA	TTCTAATTTT	240
AATATGGATA	GCGGCATTGA	TACAATAGGC	TTATTAGTT	CAATAGGAGG	TTTGGTGTG	300
CTTCTATTGA	CGCCTGTAGT	AGGTGAGTTT	GCGTTAATTG	CAGGAGTGGG	TTTAGCATT	360
GTGGGGGTAG	GTAAATCAAT	ATGGAGTTTT	TTTGATTGAG	ATTATAAAAA	ATCCCAACAA	420
AGAAAAGAAG	TGATAAGAA	TTTACATCAA	ATTTGCGAAA	AATTGTGCAG	GATG	474

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 336 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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121

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4

ATGCCTGGCG TGTATCAAAT GAGTATAGAG CCTCTTTTAA AAGAATGCCA AGAATTAGTG	60
GGTTTAGGCA TAAAGCCGT TTTATTGTTT GGCATTCCCTA AACATAAGGA CGCTACAGGA	120
AGCCATGCGT TAAATAAGGA TCACATTGTC GCAAAGCTA CGAGAGAAAT TAAAAACGA	180
TTTAAGGATT TGATCGTTAT AGCGGATTG TGTTTTTCG AATACACCGA CCATGGGCAT	240
TGCGGGATT TAGAAAACGC TTCTGTGTCT AACGATAAAA CGCTAAAGAT TTTAAATCTT	300
CAAGGGCTTA TTTGCTGAA AGCGGTGTGG ATATTC	336

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5

GTGGAAACA ACAAGAGTTT AAAGCATGCG AATGAGTTAA GGGATAAGCG AGATGAATTA	60
GAGTTTCATT TGCGAGAGCT TTTCGGGGG AATGTTTTTA AAAGCAGCAT TAAACCCAT	120
TCGCTCACAG ATAAAGACTC AGCGGACTTT GATGAGAGCT ATAACCTTAA TATCGGGCAT	180
GGYTCAATA TSATA	195

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1857 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

SUBSTITUTE SHEET (RULE 26)

122

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1857

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6

GTGTTTGTGG	CAAGCAAACA	AGCTGACGAA	CAAAAAAGC	TAGTTATAGA	GCAAGAGGTT	60
CAAAAGCGGC	AGTTTCAAAA	AATAGAAGAA	CTTAAAGCAG	ACATGCAAAA	GGGTGTCAAT	120
CCCTTTTITA	AAGTCTTGTT	TGATGGGGGG	AATAGGTTGT	TTGGTTTCCC	TGAAACTTTT	180
ATTTATTCTT	CTATATTTAT	ATTGTTTGTA	ACAATTGTAT	TATCTGTTAT	TCTTTTTCAA	240
GCCTATGAAC	CTGTTTTGAT	TGTAGCGATT	GTTATTGTGC	TTGTAGCTCT	TGGATTCAAG	300
AAAGATTACA	GGCTTTATCA	AAGAATGGAG	CGAGCGATGA	AATTTAAAAA	ACCTTTTTTG	360
TTTAAGGGCG	TGAAAAACAA	AGCGTTCATG	AGCATTTTTT	CCATGAAGCC	TAGTAAAGAA	420
ATGGCTAATG	ACATCCACTT	AAATCCAAAC	AGAGAAGACA	GGCTTGTGAG	CGCTGCAAAC	480
TCCTATCTAG	CGAATAACTA	TGAATGTTTT	TTAGATGATG	GGGTGATCCT	TACTAACCAAC	540
TATTCCTCTT	TAGGCACAAT	CAATTGGGG	GGCATTGATT	TTTTAACCAC	TTCCAAAAAA	600
GATCTCATAG	AGTTACACGC	TTCTATTTAT	AGCGTTTTTA	GGAATTTTTGT	TACCCCTGAA	660
TTCAAATTTT	ATTTTCACAC	TGTTAAAAAG	AAAATCGTTA	TTGATGAAAC	CAATAGGGAT	720
TATGGTCTTA	TTTTTCTAA	TGATTTTCATG	CGAGCCTATA	ATGAGAAGCA	AAAGAGAGAA	780
AGTTTTTATG	ATATTAGTTT	TTATCTCACC	ATAGAGCAAG	ATTTATTAGA	CACCTCTCAAT	840
GAACCCGTTA	TGAATAAAAA	GCATTTTGCA	GACAATAATT	TTGAAGAGTT	TCAAAGGATT	900
ATTAGAGCCA	AGCTTGAAAA	CTTCAAAGAT	AGGATAGAGC	TCATAGAAGA	GCTACTGAGT	960
AAATACCACC	CCACTAGATT	AAAAGAATAC	ACTAAAGATG	GCATTATTTA	CTCCAAACAA	1020
TGCGAATTTT	ACAATTTTCT	TGTGGGAATG	AATGAAGCCC	CTTTTATTTG	CAACAGAAAA	1080
GACTTGTATC	TCAAGGAAAA	AATGCATGGT	GGGGTGAAAG	AAGTTTATTT	TGCCAATAAG	1140
CATGGAAAAA	TCTTAAATGA	CGATTTGAGT	GAAAAATATT	TTAGCGCTAT	TGAGATCAGT	1200
GAATACGCC	CTAAATCACA	GAGCGATTGT	TTTGATAAAA	TCAACGCTCT	AGACAGCGAA	1260
TTTATCTTTA	TGCATGCTTA	TTGCGCTAAA	AACTCACAAG	TTTTAAAGGA	CAAACTAGCT	1320
TTACCTCTA	GAAGGATTAT	TATTAGTGGA	GGCTCCAAAG	AGCAAGGCAT	GACTTTGGGT	1380
TGCTTGAGCG	AATTAGTGGG	TAATGGTGAT	ATTACGCTAG	GCAGTTATGG	TAATTCTTTA	1440
GTGCTGTTTG	CTGATAGCTT	TGAAAAAATG	AAACAAAGCG	TTAAGGAATG	CGTCTCTAGT	1500
CTTAACGCTA	AAGGTTTTTT	AGCCAACGCA	GCGACTTTCT	CTATGGAAAA	TTACTTTTTT	1560
GCCAAACATT	GCTCTTTTAT	CACGCTTCCT	TTTATTTTTG	ATGTAACCTC	TAACAATTTT	1620
GCTGATTTCA	TAGCGATGAG	AGCGATGAGT	TTTGATGGCA	AAGAAGACAA	TAACGCTTGG	1680
GGCAATAGCG	TGATGACGTT	AAAAAGCGAG	ATCAATTTCG	CTTTTTATTT	GAACCTCCAC	1740
ATGCCCACTG	ATTTTGTTTC	AGCTTCAGCA	GGACACACTT	TGATACTTGG	CTCAACCGGT	1800
TCAGGTAAGA	ACAGTGTTTA	TGTCCATGAC	TCTAAACGCT	ATGGGGCAAT	TTGCCTA	1857

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7

GTGAAAACAT	CGTCTTTGGT	TACAAATAGGG	AGGATCCGGG	GCGTTTTTAT	CATTAAGGCG	60
CAGTTGTTGC	TTGCTGAGGG	AGGTTTTATG	AATTTTACCG	CTTATAACAC	GAAGACGCCA	120
GGGCATTTGC	ATTTGTATGT	GCATAAGGGG	CATACGGAAT	TAGGCGAGGG	TGAAAGGCTG	180
ATTAAAACCT	TATCCATGAA	ATTAGCGCAA	GGGTTCCTA	AAGAATGGAG	GTTTTTCCTT	240

123

AGCAATGAAT GGCCTAAGGA ATTTAATATT TTAGCTTTAC CTTATGAAGT GTTTGCAAAA 300
 GAGCGCGGGA GCTCTTGGGC GAAGCATTTA 330

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8

GTGGCTAAAG ACATCATCAG CGAGTCTCAA AACCTTTGCG CAAGAAAATT CCGCCGTTTG 60
 TATGCGTTAT TGAAAGAAAA TGAAATGCTC ATTCGCATCG GATCTTATCA AATGGGGAAC 120
 GATAAAGAGC TTGATGAAGC GATTAAGAAA AAGGCTCTAA TGGAGCAATT TTTAGTGCAA 180
 GATGAAAACG CTTTACYAGC CTTT 204

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9

ATGAAATCAC GCCCAATCCT CGCACAAGCT TACGCGCTCC AAATGATGGT CAAACAGATC 60
 GCTTTTTTAG AAACCATTTT AGTGGAAGAC GAGCAAGACG CTTTGATT TT GGAAAATTCT 120
 TTGATCAAGC AGCTCAAGCC TAAATACAAC ATTCTTTTAA GAGACGATAA AACTTACCCT 180
 TATATTTTACA TGGATTTTTC TATTGATTTC CCTATCCCTT TAATCACACG AAAAATCTTA 240
 AAACAGCCTG GCGTTAAATA TTTTGGCCCT TTTACGAGCG GGGCTAAGGA TATTTTGGAC 300
 AGCTTGATG AATTGCTCCC TTTGGTTCAA AAGAAAATT GCATCAAGGA TAAAAAGGCA 360
 TGCATGTTTT ATCAAATAGA GCGTTGTAAA GCGCCATGCG AGGATAAAAT CACTAAAGAA 420
 GAATATTTAA AAATCGCTAA AGAATGTTA GAAATGATTG AAAATAAAGA CAGGCTCATC 480
 AAAGAGCTTG AATTGAAAT GGAGCGCCTT TCTAGTAACT TCGGTTTTGA AGAAGCCTTA 540

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124

ATTTATAGGG	ATAGGATTGC	AAAAATCCAA	AAAATCGCCC	CTTTCCTTG	CATGGATTTA	600
GCCAAACTCT	ACGATTTGGA	TATTTTGGCT	TTTTATGGTG	GGAACAACAA	GGCGGTGTTA	660
GTGAAATGT	TCATGCGTGG	GGGTAAAATC	ATTTCTTCAG	CGTTTGAAAA	AATCCACTCT	720
CTCAACGGGT	TTGACACTGA	TGAAGCGATG	AAACAAGCCA	TTATCAATCA	TTACCAATCG	780
CATTTGCCTT	TGATGCCTGA	ACAAATCTTA	TTGAGCGCTT	GTTCTAATGA	AACGCTTAAA	840
GAATTGCAAG	AGTTTATCTC	TCACCAATAT	TCTAAAAAAA	TCGCTCTTAG	CATTCTTAAA	900
AAGGGTGATA	AGCTCGCTTT	AATAGAAATC	GCTATGAAAA	ACGCTCAAGA	GATTTTTAGC	960
CAAGAAAAAA	CCTCTAATGA	AGATCGGATC	TTAGAAGAAG	CGCGATCGCT	CTTCAATTTA	1020
GAGTGCCTG	CTTATAGGGT	AGAAATCTTT	GACACAAGCC	ACCATTCAAA	CAGCCAATGC	1080
GTGGGGGAA	TGGTCGTGTA	TGAAAACAAT	GCATTTCAAA	AAGACTCTTA	TCGGCGCTAC	1140
CATCTAAAAG	GCTCTAACGA	ATATGATCAA	ATGAGCGAAT	TGCTCACCAG	AAGGGCTTTA	1200
GACTTTGCTA	AAGAGCCACC	GCCTAATTTG	TGGGTGATAG	ATGGAGGGAG	GGCGCAATTA	1260
AACATCGCTT	TAGAAATTTT	AAAAAGCAGC	GGGAGTTTGT	TAGAAGTGAT	CGCTATTTCT	1320
AAAGAAAAAA	GGGGATTTC					1338

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10

GTGAGTTTGG	GGGCGTTTCA	GGGGTATTAT	GGAGGGCTAG	TGGATTTAGT	GGGGCAAAGG	60
TTGAGCGAAA	TTTGGAGCGC	GATCCCCATG	CTTTTTTTAC	TCATTGTGAT	TTCTAGCGCG	120
TTCAATTCTA	ATTTTGGGAT	CATCTTGTTT	TTAGTCTTGC	TCTTTAGCTG	GATGGGGCTT	180
TCTCAAGTCG	TGCGCACGGA	GTTTTTAAAA	GCAAGGAATA	TGGACTACAC	CAAAGCCGCT	240
AGAGCGTTGG	GG					252

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

125

(B) LOCATION 1...120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11

ATGAGTGAAG CCTATTTTTT ACACCATAAA AACGCTTCTC AAGTGTCTCT TAATGAACAA	60
GTTTTAAACG TTATGAAACA AGTTCAATTG GATGAAAATT TTTGGAATGT TTCTCTTATG	120

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12

GTGATCCTGA TATTTATCAT CGTGGTGGAA GATCAGAAAG GCATTTTCCC TATCGCAGCG	60
TCAAAAAGAA AAAGCCAAAG CTCTGTGATC ATTGAAGACG TGTGCTTCAG CAAAGAGGAT	120
TTTGTAGAAG GGGCAAAAGC GATTGAGGGG CTTTTAAAAA AACATGGCTT TAAGGATAAT	180
GGCATTATTT TTGGGCATGC GTTAAGCGGG AATTGCACT TTGTCGTTAC GCCGATTCTA	240
GAAAATGAAG CTGAAAGAAA AGCGTTTGAA AATTTAGTTT CTGAGATGTT TTTAATGGTG	300
AGCAAAAGCT CTGGCTCTAT TAAAGCCGAA CATGGCACAG GCAGGATGGT AGCCCCTTTT	360
GTGGAATGG AGTGGGGAGA AAAAGCTTAT AAGATCCACA AACAAATCAA GGAATGTTT	420
GATCCTAATG GCCTTTTAAA CCTGATGTG ATCATCACA ACGATAAAGA AATCCACACT	480
AAAAATTTAA AGAGCATTTA CCTATTGAA GAGCATTGG ACATGTGCAT GGAATGTGGG	540
TTTGTGAAA GGATCGCCC CAGTAAAGAT TTATCCTTAA CGCCACGACA ACGCATCGTC	600
ATCCACAGAG AGGTAGAGCG TTGAAAGAA AGGGTAAGTC ATGGTCATGA TGAAGATCAG	660
GTTTACTAG ATGAGCTTTT AAAAGAGTCT GAATACTTAG CGCATGCCAC TTGCGCGGTG	720
TGCCATATGT GTTCCACTTT ATGCCCTTTA GGGATTGATA CCGGGAGYAT CGCTTTAAAT	780
CATTATCAAA AAAACCTTAA AGGCGAAAAG ATCGCTTCAA AGATTCTTAA ATCACATGCA	840
AACGACCACA AGCGTGGCTC GTTTTCTTT AAAARGCGCT TTCGTGGTTT CAAAACTCA	900

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori***SUBSTITUTE SHEET (RULE 26)**

126

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13

ATGAAAGAAA	AAACTTTTG	GCCTTTAGGA	ATCATGAGCG	TGCTTATTTT	TGGGCTTGGG	60
ATCGTGGTGT	TTTAGTGGT	GTTTGCCCTA	AAAAATCGC	CTAAAAATGA	TTTAGTGAT	120
TTCAAGGGTC	ATAACGAAGT	GGATTAAAC	TTTAACGCCA	TGCTTAAAC	TTATGAAAAC	180
TTTAAATCCA	ATTATCGTTT	TTCAGTGGGT	TTAAAGCCTC	TTACCGAAAG	CCCTAAAACC	240
CCCATTTTGC	CCTATTTTTC	TAAAGGCACG	CATGGGGATA	AAAAAATCCA	AGAAAACCTT	300
TTAAACAACG	CTTTGATTTT	AGAAAAGTCC	AACACGCTTT	ATGCACAATT	GCAACCGCTC	360
AAACCCGCTT	TAGATTGCGC	AAATATTCAA	GTGTATTTAG	CGTTCATCC	CAGCCAATCC	420
CAGCCAGAT	TATTAGGAAC	GCTTGATTGT	AAAAACGCAT	GCGAACCTTT	AAAATTTGAT	480
TTGTTAGAGG	GCGATAAAGT	GGGCGCTAT	AAGATCCTTT	TTAAATTTGT	TTTTAAAAAT	540
AAAGAAGAAT	TGATTTTGA	GCAACTGCTT	TTTTTAAGTA	GCATGGCTTG	TATGGGTATA	600
TCAATTTTAA	AAAACGCTAA	AGCATTTTTT	AAATACAAAA	TA		642

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14

ATGCCCCATTA	AAGGCTCTTT	TTTAGCCAGA	AACCGCCTGG	TGATCGCTTT	AACCGATGCG	60
GTGATTATCC	CCCAAGCGGA	TTTAAAAAGC	GGCTCTATGA	GCAAGTGCAG	ATTAGCCAG	120
AAATACCAA	AACCCTTGTT	TGTTTACCC	CAACGCCTGA	ATGAGAGCGA	CGGCACTAAT	180
GAGCTTTTAG	AAAAGGGCA	GGCTCAAGGG	ATATTTAATA	TTCAAAATTT	TATAAACACC	240
CTTTTAAAG	ATTACCATTT	AAAAGAAATG	CCTGAAATGA	AAGATGAATT	TTTAGAATAT	300
TGCGCGAAAA	ACCCTAGCTA	TGAAGAAGCG	TATCTCAAAT	TTGGGGATAA	GCTTTTAGAA	360
TACGAGCTGT	TGGTAAGAT	TAAGCGCATC	AATCATCTCG	TGGTGTTAGC	A	411

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

127

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15

ATGCTAGTAG	AATTAAAAA	CATTGAAAAG	ATTTATGAAA	ACGGGTTTCA	TGCTCTAAAA	60
GGCGTGAATT	TGGAATTGAA	AAAAGGCGAT	ATTTTGGGCG	TGATAGGCTA	TTCAGGGGCG	120
GGGAAATCCA	CGCTCATTCT	CTTGATCAAT	TGTTTAGAGC	GCCCCAGTTC	TGGCGAAGTT	180
TTAGTCAATG	GGGTCAATCT	GTTAACTTA	AAGCCTAAAG	AATTGCAAAA	AGCGCGCCAA	240
AAAATAGGCA	TGATTTTCCA	GCATTTCAAT	TTATTGAGCG	CTAAAAACGT	GTTTGAAAAC	300
GTGCTTTTCG	CTCTAGAAAT	CGCCCGATGG	GAAAAAATA	AGATTAAATC	AAGGGTGCAT	360
GAATTGTTGG	AATTAGTGGG	GTTAGAAGAT	AAAGTGCATT	TTATCCTAA	ACAGCTCAGC	420
GGCGGGCAAA	AACAACGAGT	GGCGATCGCT	AGGAGTTTAG	CGAATTGCCC	TAATTGTTG	480
CTTTGCGATG	AAGCCACATC	CGCTTTGGAT	TCTAAAACCA	CGCATTCTAT	TTTAACGCTT	540
CTAAGCGGCA	TTCAAAAAA	GTTTGATTG	AGCATCGTTT	TCATCACACA	CCAGATTGAA	600
GTGGTTAAAG	AATTGTGCAA	TCAAATGTGT	GTGATCAGCA	GCGGCGAAAT	CGTAGAAAGA	660
GGCTCGGTGG	AAGAAATTTT	TGCTAACCTT	AAACATGCTG	TTACTAAAGA	ATTGCTTGCC	720
ATCAAAAACG	AACATGCGGA	TCAAAAATCG	CAAGACATTT	ATCGCATCGT	GTTTTTAGGG	780
GAGCATTTAG	ACGAGCCGAT	CATTTCTAAW	TTTTGW			816

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 318 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16

ATGGGGGCTT	TGATAGCCAT	GTTTTTTTTA	ATGCTCATT	AAAAGACTAT	CGCTTATAAA	60
GAAGATAAAA	AGAGCGCGGC	TTTAAAGGTC	GTGCCTTATT	TGGTGGCGTT	GATGAGCTTA	120
GCCTTTAGCT	GGTATTGAT	CGTGAAGGTT	TTAAAACGCC	TCTATGCGGT	GAGTTTGA	180
ATCCAGCTCG	CTTGCGGTTG	TGTCCTTGCG	CTTTTGATTT	TTATCCTTTT	TAAAAGATTT	240
GTGTTAAAAA	AAGCCCCGCA	ATTAGAAAAT	AGCCACGAAA	GCGTCAATGA	GCTTTTAAAT	300
GTCCCTTTGA	TTTTTGCC					318

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 471 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

128

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...471
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17

ATGATTAAAA	GAATTGCTTG	TATTTTAAAGC	TTGAGCGCGA	GTTTAGCGTT	AGCTGGCGAA	60
GTGAATGGGT	TTTTCATGGG	TGCGGGTTAT	CAACAAGGTC	GTTATGGCCC	TTATAACAGC	120
AATTACTCTG	ATTGGCGTCA	TGGCAATGAC	CTTATGGTT	TGAATTTCAA	ATTAGGTTT	180
GTAGGCTTTG	CCAATAAATG	GTTTGGGGCT	AGGGTGTATG	GCTTTTITAGA	TTGGTTTAAAC	240
ACTTCAGGGA	CTGAACACAC	CAAAACCAAT	TTGCTCACCT	ATGGCGGCGG	TGGCGATTG	300
ATTGTCAATC	TCATTCTTTT	GGATAAATTC	GCTCTAGGTC	TCATTGGTGG	CGTTCAATTA	360
GCCGGAACA	CTTGATGTT	CCCTTATGAT	GTCAATCAA	CCAGATTCCA	GTTCTTATGG	420
AATTTAGGCG	GAAGAATGCG	TGTTGGGGAT	RCAGTGCCTT	TGAAGCGGGC	G	471

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 834 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...834
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18

ATGTATCGCC	ATGTGTTGAA	AGATTTCTCC	CTAGATTTTA	GCAAAGAAAG	CGTTCAAGAG	60
CTGTTTAAAC	AGCTGGCTAA	AGACACTTTT	TTATTGCTTT	TGCTGTTTT	AATCATTTTA	120
ATGGTGGTGG	CGTTTTTGTC	TAATGTCTTG	CAATTTGGCT	GGCTCTTTC	CCCTAAAGTC	180
ATTGAGCCTA	AATTTTCTAA	AATCAACCCT	ATCAATGGCG	TCAAAAACCT	TTTTTCTTTA	240
AAAAAGATCC	TTGATGGGAG	TTTGATCACT	TTAAAAGTTT	TTTTAGCTTT	TTTTCTGGGG	300
TTTTTCATCT	TTTCTTATT	TTTAGGGGAA	TTAAACCATG	CGGCTCTTTT	GAATTGCAA	360
GGCCAGTTGT	TGTGGTTTAA	AAGCAAGGCG	TTATGGCTCA	TTTCTTCGCT	TTTATTTTAA	420
TTTTTTGTCT	TGGCTTTTGT	GGATTTAATC	ATCAAACGCC	GCCAATACAC	TAACTCTTTA	480
AAAATGACTA	AACAAGAAGT	TAAGGACGAA	TACAAACAGC	AAGAAGGAAA	CCCAGAAATC	540
AAAGCCAAAA	TCGCCAGAT	GATGGTAAAA	AACGCCACGA	ATAAAATGAT	GCAAGAAATC	600
CCCAATCCA	ATGTCGTGGT	GACTAACCCCT	ACCCATTATG	CCGTCGCTCT	CAAATTTGAT	660
GAAGAACACC	CTGTGCCTGT	GGTAGTGGCT	AAAGGCACGG	ATTATTTAGC	CATTAGGATT	720
AAGGGTATCG	CCAGAGAGCA	TGACATAGAA	ATTATAGAAA	ATAAAACGCT	CGCTAGAGAG	780
CTTTATAGAG	ACGTGAAATT	GAACGCCACC	ATACCAGAAG	AATTGTTTGA	GCGG	834

(2) INFORMATION FOR SEQ ID NO:19:

SUBSTITUTE SHEET (RULE 26)

129

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 360 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...360
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19

ATGAATACAA	GSCCCTTAAT	CGCTACGCTT	TTGCAAGCGC	CTTTGCATGT	TTTAGGGATT	60
AGAGAGCCAG	TTTCTTTTCA	GCCTTTTTTAC	CCCCAAACAG	AAAAGCCTAA	TCGCCCTCAA	120
AAGTTCGCGC	ATGTTTCTAG	CATGCCCAGT	TTGGAATTTT	TAGAAAAATT	GGTGATCCGC	180
TACCTTTTAG	AAGACAGAAG	CCTATTGGAT	TTAGCGGTGG	GTTATATCCA	TAGTGGGGTA	240
TTCTTGCATA	AAAAACAAGA	ATTTGACGCT	TTATGTCAAG	AAAAATTGGA	CGACCCTAAA	300
TTAGTTGCGT	TATTATTAGA	TGCGAATTTA	CCCCTAAAAA	AAGGGGGTTT	TGAAAAGGAA	360

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 678 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...678
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20

ATGGGGCAGG	CATTTTTTAA	AAAAATTGTT	GGCTGTTTCT	GTCTTGTTTA	TTTATTTTAA	60
TCTAGCGCAA	TAGAAGCAGT	AGCACTTGAC	ATTAAGAATT	TTAATCGTGG	TAGGGTGAAA	120
GTGGTGAATA	AGAAGATTGC	TTATTTGGGA	GATGAAAAAC	CTATTACGAT	TTGGACTTCA	180
TTAGACAATG	TTACCGTGAT	CCAACCTGAA	AAAGATGAAA	CTATTTCCTA	CATCACAAACA	240
GGTTTCAATA	AAGGTTGGAG	TATTGTGCCT	AATTCTAATC	ATATATTCAT	TCAACCTAAA	300
TCGGTAAAAA	GTAATCTCAT	GTTTGAAAAA	GAAGCAGTGA	ATTTTGCCCT	AATGACAAGA	360
GATTACCAAG	AATTTTTTAA	GACAAAAAAA	CTTATCGTAG	ATGCGCCTGA	CCCTAAAGAA	420
TTAGAAGAAC	AAAAAAAAGC	TCTAGAAAAA	GAAAAAGAAG	CTAAAGAACA	GGCGCAAAAG	480
GCACAAAAAG	ATAAAGAGA	AAAAAGAAAG	GAGGAGCGTG	CAAAAAATAG	AGCCAATTTA	540
GAAAAATCTCA	CTAACGCTAT	GAGTAACCCA	CAAAATTGGA	GCAATAACAA	AAATCTTAGC	600
GAATTGATCA	AGCAACAGAG	AGAAAAATGAA	TTAGACCAAA	TGGAACGAAC	TAGAGGACAT	660
GCAAGAGCAG	GCTCAAGC					678

SUBSTITUTE SHEET (RULE 26)

130

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21

ATGAATACAG AAATTTTAAC CATCATGTTA GTTGTCTCCG TGCTTATGGG ATTGGTAGGC	60
TTAATAGCGT TTTTATGGGG GGTTAAAAGC GGTCAGTTTG ACGATGAAAA ACGCATGCTT	120
GAAAGCGTGT TGTATGACGC GCGAGCGACT	150

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22

ATGTTTGTAG CGGCCGGGCT TGGGGCTTAT GCGATCGCGC TTTCCACCT CTTTACGCAT	60
GCGTTCTTCA AATCCCTCCT TTTCTTAGGC TCAGGCAATG TCATGCATGC GATGGAAGAC	120
AATCTGGATA TTACTAAAAT GGGCCCTTTA TACAAGCCTA TGAGGATCAC AGCTGTCTTT	180
ATGATTATAG GTTCAGTGGC TTTGTGTGGG ATCTACCCCT TTGCGGGCTA TTTCTCCAAA	240
GACAAGATTT TAGAGGTCGC CTTTGGGATG CACCACCACA TTTTATGGTT TGTTCCTTTG	300
ATTGGGGCGA TCTTTACCGC TTTTATAGC TTCAGACTCA TCATGCTGGT GTTTTTTGCA	360
CCCAACAAC ATGAAATCAA CCACCCCCCA	390

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs

SUBSTITUTE SHEET (RULE 26)

131

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23

ATGTTTATAT	CTTCTTCTTA	CACGCTGAGT	TTTGATGCGC	TTTTTTTAAT	TTTCTTTTTT	60
TTCAAAAATA	AGCCATTGGG	TTTGAGGTTT	TCGCTCTCTT	TGATAAGCGT	GATTTTAAGC	120
AATATCGCTT	TGAAAGACTC	CCTATCGCTC	AATGAATTTT	TAAGCAGTTT	TACAGCCCCC	180
TTAAGCCCCC	TTAGCTGTCT	TTTGATCCTT	GCTTATGCAA	GCTTTTCTTG	CCATATACTC	240
AAAAAGCCCC	CTTTAGAAAC	CTTGCAATCT	TATAGCGTCA	TGCTGTTTTT	CAATCTGTTG	300
CTTTTGACAG	ATATTTTAGG	GTTTTGCCT	TTTTCAATCT	ACCATCATTT	CATGGCTTCT	360
CTGATTTTTA	GCGCGCTTTT	TTGCAGCAGT	TTGTTTTTGA	GTAGCCCCCT	ATTAGGCGTG	420
ATCGCTTTAG	TGGCTTTATC	CAGTTCGCTT	TTGATGCGTT	CTAATTTTCA	AATCTTAGAT	480
TCTTTATTGG	ATTTCCCAT	ATTTCTTTT	GTCTTTTTTA	AGACTTTATA	TCTTGCTAAA	540
AAAAGGTTA						549

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24

ATGCGCCTAG	ATTACGCCCT	ATTCAACCAG	CATTTAGCAA	ATAGCAGAGA	AAAAGCTAAA	60
GCGTTGGTTT	TAAAAAACA	GGTTTAGTC	AATAAAATGG	TGGTTTCTAA	ACCCTCTTTT	120
ATCGTTAAAG	AGGGCGATCA	AATTGAACCT	ATCGCTCCCA	ATCTATTCTG	TAGCAGGGCT	180
GGGGAATAAT	TAGGGGCTTT	TTTAGAAGAT	CATTTTATAG	ATTTTAAAGA	AAAGGTTGTT	240
TTAGATGTGG	GAGCGAGTAA	GGGAGGCTTT	AGTCAAGTGG	CTCTTTTAAA	AGGGGCTAAA	300
AAGGTGCTTT	GCGTGGATGT	GGGAAAAATG	CAATTAGATG	AAAGTTTGAA	AAACGACCAA	360
CGCATAGAAT	GTTACGAAGA	ATGCGATATT	AGAGGGTTTA	AAACGCCAGA	AAAAATTGAT	420
TTAGCACTTT	GTGATGTGAG	CTTTATTTCT	TTATATTGTA	TTTTAGAAGC	GATTTTGCCT	480
TTAAGCGGTG	AATTTTAAAC	GCTTTTCAAA	CCGCAATTG	AAGTGGGCAG	AACAATAAAA	540
CGCAATAAAA	AGGGGGTGGT	GATGGATAAA	GAAGCCATTT	TGAACGCTTT	AGAAAACCTT	600
AAAAACCATT	TAAAAACAAA	GGATTTTCAA	ATCTTAACGA	TCCAAGAAAG	CTTAGTGAAA	660

SUBSTITUTE SHEET (RULE 26)

132

GGGAAAAACG GGAATGTTGA ATTTTTTATC CATTTCAGC GAGCC

705

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25

ATGAGCCTAC CACCGGTTTG CATTTTGAAA GATGTGAATC ACCTTTTACA AGTCTTRCAT	60
TCCTTGGTGG CGTTAGGCAA TTCCATGCTA GTGATTGAGC ATAATTTAGA CATCATCAAA	120
AACGCTGACT ACATTATAGA CATGGGGCCT GATGGGGGGG ATAAGGGCGG GAAAGTCATT	180
GCGAGCGGCA CGCCTTTAGA AGTGCGGCAA AATTGCGAAA AAACCCAAAG CTATACGGGA	240
AAATTTTITAG CTTTGGAATT GAAA	264

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26

ATGCAAAATC GATCGCATGA AATACAAGGC GTATCACACA TTAAGAATAA TTATAAATTT	60
TTCACCAAAG AGCTTGACAA TTATATCAGC AAAGGGTATC GCATTGAAGA GATTTATGGC	120
GCGTTTTTGT GGCTCAAAAT CGTAGCCATA GGTTTAGAGT TGGGCGAAGA CGATCCGCAA	180
GTGGTGTTTG AGAGCATCAA CGCTACAGGC GTGCAATTAA AAGGGCTGGA TCTCATCCGC	240
AACTATTTGA TGATGGGGGA AAATYCTGAC AACCAGAATC GTCTTTATAA TACTTATTTG	300
GTGCCTTTAG AAAATTGGCT TGGTGAAAAG GATTTGAATG ATTTCATCAA AACCTATTTG	360
AGAATCTATT TTGAGGATAG AGTTACAAGA GGGAGAGCGC GAAGTGATT ACGCGCTAAA	420
AGCCCACCAC AGAGACAATT TCCC	444

SUBSTITUTE SHEET (RULE 26)

133

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27

ATGGATACCA TAAAAAGCAT TCCCATAGA ACTTTTATTT TACTCTATAA AAGCTCACCA	60
AAATGTGTTG TGTTGGCATC AATTACAGTG CTATTTGTCG GCATTCTTYC ATCTCTGAAT	120
ATTCTTGTTA TGATAAAATT GATTGATATT GTGGTGAATC TATTACAAAA GCATACGCAT	180
TTTGAATACA GCTTGCTGTT ACCAACTTTA CTACTATGGG GAGCCTTGCT GTTTTAAACG	240
CATGTGTTCT CAGGAAATTT TATCAAGCTT GCAAACCATT ATTGCCGAAC AATTTTCTAT	300
AAATATCATC ACTCAGCTTG C	321

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28

ATGATCTTTT ACACCACCAT TAAAGAGCCT TAAAAAACC TCCAATACCG CTATGCGCAA	60
TTTTTTGGCA AGATCAAGCC TTGTTCTTC TTAGAGTCTC TAAAATCATG CTTTTTTCAA	120
ACCTATTCTT TTTCTTTAAC GCGAAAACAA GATTTCAAAT CGCATTGCG CCATTTCATT	180
GACAGCGCCC ATTCCAACGC CTTAGTGGGT AATTGTATC GAGCGTTATT CATAGGGGAT	240
AGCTTGAATA AAGACTTAAG AGACAGGGCT AACGCGCTAG GGATCAACCA CTTACTGGCC	300
ATTAGCGGGT TTCATTAGG GATTTTGAGC GCGAGCGTGT ATTTTCTTTT CTCTCTTTTT	360
TATACCCCTT TACAAAACG CTATTTCCCT TACAGGAACG CTTTTTWA	408

(2) INFORMATION FOR SEQ ID NO:29:

SUBSTITUTE SHEET (RULE 26)

134

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29

ATGAATAAAC CATTTTTAAT CTTACTCATA GCCCTAATTG CCTTTAGCGG CTGTAACATG	60
AGAAAATACT TCAAACCCGC TAAACACCAA ATTAAAGCGA AGCGTATTTC CCTAACCATT	120
TGCAAGAAAG CATCGTTTCG TCTAATCGTT ATGGAGCCAT TT	162

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30

ATGGCGGCTT GGAACACTTT AGTAGAAAAA ATCATCGCTC CTAAACACAA GGTCAAAATT	60
GGTTTTGTGG GCAAGTATTT AAGCTTAAAA GAATCTTATA AATCCTTGAT TGAAGCCCTA	120
ATCCATGCCG GGGCGCATCT GGATACGCAA GTCAATATTG AATGGCTGGA TAGCGAGAAT	180
TTTAATGAAA AGACTGATTT AGAGGGCGTT GATGCGATTT TAGTGCCGGG GGGCTTTGGA	240
GAAAGGGGGA TTGAGGGCAA AATTTGCGCC ATTCAAAGGG CTAGGTAGA AAAACTCCCC	300
TTTTTAGGGA TTTGTTTGGG CATGCAATTA GCGATCGTTG AATTTTGTCT CAAATGTTTT	360
AGGCTTGAAA GGGGC	375

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

SUBSTITUTE SHEET (RULE 26)

135

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...747

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31

ATGACTAAAG	CGTTTGTGCC	TTTAAGTTTG	TTAGTGAGCG	CGATTTTATT	AGCGTTTTTCG	60
CTCATCTTAA	TCCCCACTTC	TAAGAGCGCT	TATTACGGGT	TTTTGCGTCA	AAAAAAGAC	120
AAGATTGACA	TTAACATCAG	AGCGGGTGAA	TTGCGGCAAA	AATTAGGCGA	TTGGCTCGTG	180
TATGTGGATA	AGACTGAAAA	CAATTCCTAT	GATAATTGG	TGCTTTTTTC	TAATAAAAGT	240
CTCTCTCAAG	AAAGCTTTAT	TTTGGCTCAA	AAAGGCAATA	TCAACAATCA	AAACGGCGTG	300
TTTGAATTGA	ATTTGTATAA	CGGGCATGCG	TATTTCACTC	AAGGCGATAA	AATGCGTAAG	360
GTTGATTTTG	AAGAATTGCA	TTTGGCAAC	AAGCTCAAGT	CTTTC AATTC	TAATGATGCG	420
GCTTATTTCG	AAGGCACGGA	TTATTGGGT	TATTGGAAAA	AAGCCTTTGG	TAAAAACGCT	480
AATAAAAATC	AAAAACGCCG	TTTTTCTCAA	GCGATCTTAG	TTTCCTTGTT	CCCTTTAGCG	540
AGCGTGTTTT	TAATCCCTT	ATTGGGCATC	GCCAACCCGC	GATTCAAAAC	GAATTGGAGT	600
TATTTTCYAWG	TCCTTGGAGC	GGTTGGGGTW	TATTTTTTAA	TGGTGCATGT	GATTCTACG	660
GATTTGTTTT	TGATGACCTT	TTCTTCCCC	TTTATTGGG	CGTTTATTTC	TTATTTATTG	720
TTTAGAAAAT	TCATTTTAAA	GCCTTAT				747

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32

ATGAGTAAGA	GCGCGATTTT	TGTTCTTTCT	GGCTTTTTAG	CGTTCTTGCT	CTATGCTTTG	60
TTATTATATG	GTTTGTGTT	AGAAAGGCAT	AATAAAGAAG	CAGAGAAAAT	CCTTTTAGAT	120
TTAAATAAAA	AGGACGAACA	AGCCATTGAC	TTGAATTTAG	AAGATCTGCC	AAGCGAGAAA	180
AAGAATGAAA	AAATTAAAA	AGTAACGGAA	AAACAGGACG	ATTTTTTTAGA	GCCTAAAAGA	240
AGAACCCCAA	GAGGAGCC					258

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

136

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33

GTGATGGCTC AATCCTTGCT TGTTCATGCC TTTTGTGCCG CCTTGCTCGC CCTAGCCTTT	60
ATGATCAATC TTTACACCTT TTTTAAAGAA AAGAATTTCA TCCAATTGAA CCGGAAAATC	120
TATCTTGTC TGCCAGCGAT TTATATTCTT TTAAGCATCG CTCTTTTGAG TGGGGTTTTT	180
ATTGGGGCGA TGCAACAATT TGAATTTTCT TTTAGCGCTG TTGTCATGCT TTTGGGGTTG	240
TTGTTGATGC TCATTGCAGA AATCAAACGC CATAAAAGCG TGAAATTCGC TATCACTAAA	300
AAAGAAAGGA TGAAAGCCTA TATCAAAAAA GCTAAAATCC TGTATTTTTT AGAAACGATT	360
CTTATCATCG TGTTAATGGG CATT	384

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34

GTGCGTAATG TGGTTTTATT CATTTTAACA GCGATCTTTT TAGCGTTCAT GCTTTTAGTG	60
AGTTATTGCA TGCCCCATTA TAGCGTGGCT GTCATTAGCG GGGTGGAAGT CAAAAGAATG	120
AATGAAAATG AAAACACGCC CAATAATAAG GAAGTAAAAA CCCTTGCTAG AGATGTCTAT	180
TTTGTGCAAA CTTACGACCC TAAGGATCAA AAAAGCGTGA CCGTCTATCG TAACGAAGAC	240
ACGCGCTTTG GCTTCCCTTT TTATTTTAAG TTTAATTCGG CTGATATTTC AGCTCTCGCC	300
AAAGTT	306

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid

SUBSTITUTE SHEET (RULE 26)

137

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35

ATGTTTAAAA AAATCATTTT TTTGTGCGTT TTTTGATAG GGGGATTGTG CATTCCACCC	60
CTTGAAGCCA TGCCTATTTT GCGCAATAAA ACCCCCCAAA AAAATTACCA AGAAGCCCAT	120
GAAAAGCTCT ATAGAAGCAT CATTAAACCGC CAAAASSTCA CGCGTAAAAA AAGCGGGTGG	180
TATTTTITAG GGGGGGTGG CGCTGTAGAA GCCATTAAGG ACTATCAAGG CAAGGAAATG	240
AAAGATTGGA TGCCACGCTC AATT	264

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 384 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36

GTGCATTTTA CGTGATCTT TCTAACCTTA TTAAATGGA TTTTGCCAGC CAAAAACAAG	60
CAGGCGTGCA AAAAGGCCAC CAACCAGATC CATTCAAGGY YTGCAAAACA TCCAGCAAAA	120
TATCCCCCCT CAAGTATTAA CCCCTCAATC CAAGCGGGTA TACAAGGGGT GATGCAAGGT	180
TTTGGGGCTT TGAGCAGCAY YTTAGAAGYC CCCYTATTG TTTTYAAGC AAAATGTGGG	240
TGGATTGGGG GCTTTGAGCA TTATTTATCC CTTTATATG GGTGGGGCAA GATTACGAT	300
GGTGCGCATT GCGATTTGAT GCAAAAAGAC GCCAATGGAA GGGGTATCGG CTTGGAAAAA	360
GGTCTTCCAC CTTTCAAGGG GCTG	384

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 324 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

138

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...324
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37

ATGCAGAAGT	TTTTCTCTCG	TTTGTAGAAGG	TGGGCGTTGC	CCTTTTATTT	TGTGAGCGCT	60
TTAGCAGCGA	TTGATATTGA	TGAAGTAACA	GAAGCTCAAG	CTAATAGCAT	TAAATTAAGC	120
GATCAGTTAG	TGAGCCTGAG	CGATAAGCTT	TTAGAAAAAG	CGGTGGATAG	GGGGCGCAAT	180
ACCGATCACT	TAAAAGATCT	TAACGATTTC	CATGAAAAAA	TCAAACATTT	GCGCTTGATT	240
TTAGAGCCTA	AGCCTAAGGG	CAAAGAAGAT	AGTCCTAACT	TGGGAGGTAA	TAAGGATATG	300
AAAACGGTTG	AAATCGGAAG	CGGT				324

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...354
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38

GTGATTTTAG	CGTTCGCCTT	TGGCATGAGT	CTTCTTGGAT	TAGCGGGCAT	GTTTCATTGAT	60
ATTCCTTTT	TATCCACAGG	CGTTCATATC	CCTAGAAAAG	AGGATATTTT	ATGGATTTCT	120
TTAATAGGGA	TTAGCGGGAC	TTTAGGGCAG	TATTTCTTAA	CCTATGCTTA	CATGAACGCT	180
CCTGCTGGGA	TCATCGCCCC	CATTGAATAC	ACCCGCATTG	TTTGGGGGCT	ATTGTTTGGG	240
CTGTATTTAG	GCGATACATT	TTTGGATCTT	AAAAGCTCTT	TAGGGGTGGC	TTTGATCTTA	300
TGTTCAGGCT	TGCTCATTGC	CTTGCCCGCT	CTTTTAAAAG	AATTAAAAAA	AATT	354

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 162 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

SUBSTITUTE SHEET (RULE 26)

139

- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...162
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39

ATGATCTATT TAGGGAAGAA AAATTTTAAC GCCCTTTTGA AAGGGGCGTA TTTAATGGAT	60
GAGCATTTTA GAAACGCCCC TTTTGAAAGC AATTACCCG TTTTAATGGG ATTAATCTGG	120
CGTGTGGTAT ATCTAACTTT TTTTCCAATC CAAAAGCCA CT	162

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 864 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...864
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40

ATGGCCGCCA AATCCAAAGC GYAAACGCTT AAAGTCTTTT CAAAATTTTT CAGCAATTTT	60
AAAATCACTA AACTCAAAGA CAACCACGAA GAAGCCCACA AACTTTTTTG AGAAAATAGC	120
CGTAAAGCCC ATGACACTGA GATCATTTAC TCCACTTTGC AAGTGGTCCC CAGGTATTCA	180
ATAGAAACCG TGGGCTTTAG TTTGTTGATT TTAGCGGTCG CTTACATCTT ATTCAAATAC	240
GGCGAAGCTA GAATGGTACT CCCTACCATT TCTATGTATG CCCTAGCGCT TTATCGCATA	300
CTCCCTTCTG TAACTGGAGT GATCAGCTAT TATAATGAAA TCGCTTACAA CCAGCTTGCA	360
ACCAATGTTG TTTTAAAAG CCTTCTAAG ACCATCGTTG AAGAGGATTT AGTCCCTTTA	420
GACTTTAATG AAAAAATCAC TCTCCAAAAC ATTTCAATCG CTTATAAGTC AAAACACCCG	480
GTTTTAAAAA ATTTCAACCT CACCATTCAA AAAGGTCAAA AAATCGCTCT CATAGGCCAT	540
AGCGGGTGCG GAAAATCCAC GCTGGCGGAT ATTATTATGG GGCTTACCTA CCCTAAAAGT	600
GGGGAAATTT TTATTGATAA CACCCTTTTA ACCAGCGAAA ACAGGCGCTC ATGGCGTAAA	660
AAAATAGGCT ATATCCCCCA AAATATTTAC CTTTTTGATG GCACTGTGGG GGATAATATC	720
GCTTTTGGGA GTGCTATAGA TGAAAAACGC TTGATTAAGG TGTGCAAAAT GGCTCATATC	780
TATGATTTTT TATGCGAGCA TGAGGCGCTT AAAACCCAAG TGGGCGAAGG GCGCGTAAGC	840
TTAGCGGCGG TCAAAAACAG CGCA	864

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

SUBSTITUTE SHEET (RULE 26)

140

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...576
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41

ATGCTTGATA	TATGGATAGA	TATGATAATC	TGTATTTTTT	ATTTGCTCTT	TTTTACGACT	60
CCTTACATTG	TAGGCGATAT	TTTGCAATTG	AAATTTATCC	GTCAAAAAC	CTGCCGAGAAG	120
CCTGTTTTAC	TCCCACAAAA	GGATTATGAA	GAAGCGGGAA	ATTATGCTAT	TAGGAAAATG	180
CAATTATCCA	TTATTCTCA	AATTTTAGAT	GGGGTGATCT	TTGCTGGTTG	GGTCTTTTTT	240
GGTTTGACGC	ATTTAGAAGA	TCTCACGCAT	TATTTAAACC	TTCTGAAAC	GCTAGGTTAC	300
TTGGTGTGTT	CCTTGTTGTT	TTTAGCGATT	CAAAGCGTTT	TAGCTTTACC	CATTAGCTAC	360
TATACTACCA	TGCATTTGGA	TAAGGAATTT	GGCTTTTCTA	AGGTGAGTTT	ATCGTTGTTT	420
TTTAAGGATT	TTTTCAAAGG	ATTATTGCTC	ACTTTAGGCG	TGGGGTTGTT	GTTGATTTAC	480
ACTCTCATAA	TGATCATTGA	ACATGTGGAG	CATTGGGAGA	TCAGCTCGTT	TTTTGTCTGT	540
TTTGTTTTCA	TGATTTTGGC	TAATCTTTTT	TTACCC			576

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 504 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...504
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42

ATGCTAAAAA	AAATATTTTT	AACCAACAGC	TTAGGGATTT	TATGCTCTAG	GATTTTTGGC	60
TTTTTACGGG	ATTTAATGAT	GGCCAATATC	CTAGGGGCTG	GGGTGTATAG	CGATATTTTC	120
TTTGTGCGTT	TCAAATTGCC	TAATCTATTG	AGGCGTATTT	TTGCCGAGGG	CTCTTTTCT	180
CAAAGCTTTT	TACCGAGCTT	CATACGAGT	TCCATTAAGG	GGGGTTTTGC	GAGTTTGGTG	240
GGGCTTATTT	TTTGTGGCGT	TTTATTCATG	TGGTGCTTAT	TAGTAGCGCT	CAATCCCTTA	300
TGGCTAACCA	AACTCCTAGC	TTACGGCTTT	GATGAAGAAA	CGCTCAAAC	ATGCACCCCT	360
ATTGTAGCGA	TCAATTTTGG	GTATCTTTTA	TTGGTGTMTA	TCACCACTTT	TTTAGGCGCG	420
CTTTTACAAT	ACAAACACAG	CTTTTGTGCC	GCGCTTATGC	GCAAGCTTAC	TCAATTTATG	480
CATGATTTTA	GCCCTTTTGA	TTTC				504

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 459 base pairs

SUBSTITUTE SHEET (RULE 26)

141

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43

ATGAATTTAG AAGTGGCTCT AAAGGCGTTT GAAACGCTAT TGCCATGCAA TAAACAAGAA	60
GTTTTAAAAA ACCTAAAGCC CCTAGATTTA ATCGGCCGTT GCGAGCTTTT AAGCCCTAAC	120
ATTTTAATAG ATGTGGGGCA TAACCCCAT AGCGCTAAAG CCTTAAAAGA AGAAATCAAA	180
CGCATCTTTA ACGCTCCAAT CGTTTGATT TATAATTGCT ATCAAGATAA AGACGCTTTT	240
TTGGTGCTAG AAATTTTAAA GTCTGTGGTT AAAAAGGTTT TGATTTTAGA ATTGCATAAT	300
GAAAGAATTA TCCAATTAGA AAAACTTAAA GGGATTTTAG AAACCTTAGG GTTAGAACAC	360
GCCTTGTTTG AAGAACTGAA AGAAAAATGAA AATTATTTGG TGTATGGCTC ATTTCTGGTA	420
GCCAACGCTT TTTATGAACG CTATCCAAAG AAGAGGGAT	459

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44

ATGGCTATCG GGTTCGTT AGTGTGTTGGG ATTTTACTCA CCCTTTTATAG CCGTTCTTAT	60
TGGCGTGAGT TTGGGGGCGT TTCAGGGGTA TTATGGAGGG CTAGTGGATT TAGTGGGGCA	120
AAGGTTGAGC GAAATTGGA GCGCGATCCC CATGCTTTT TTACTCATTG TGATTTC	177

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

142

- (ii) MOLECULE TYPE: DNA (genomic).
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...666
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45

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ATGAAGAAAA AAGCAAAAGT CTTTGGTGT TGTTTTAAAA TGATTCGTTG GTTGTATTTG      60
GCGGTCTTTT TTTTGTGAG CGTATCAGAC GCTAAAGAAA TCGCTATGCA ACGATTTGAC      120
AAACAAAACC ATAAGATTTT TGAAATCCTT GCGGATAAAG TGAGCGCCAA AGACAATGTG      180
ATAACCGCCT CAGGGAATGC GATCCTATTG AATTATGACG TGTATATTCT AGCGGRTAAG      240
GTGCGTTATG ACACCAAGAC TAAAGAAGCG TTATTAGAAG GCAATATTAA GGTTTATAGG      300
GGCGAGGGCT TGCTCGTTAA AACCGATTAT GTGAAATTGA GTTTGAACGA AAAATATGAG      360
ATCATTTTCC CTTTTTATGT CCAAGACAGC GTGAGCGGGA TTTGGGTGAG CGCGGATATT      420
GCTAGCGGGA AGGATCAAAA ATATAAGATT AAAAACATGA GCGCTTCAGG GTGCAGCATT      480
GACAACCCCA TTTGGCATGT CAATGCGACT TCAGGCTCAT TTAACATGCA AAAATCGCAT      540
TTGTCAATGT GGAATCCTAA GATTTATGTC GCGGATATTC CTGTATTGTA TTGCCCTAT      600
ATTTTCATGT CCACGAGCAA TAAAGAAGT ACCGGGTTTT TATACCCTGA GTTTGGCACT      660
TCCMAC

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(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 159 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...159
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46

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ATGCTGGATT TTGATTTGGT TCTTTTGGC GCGACTGGG ATTTAGCCAT GCGAAAGCTC      60
TTTGTTCGC TTTATGAAAT TTATATTCA TTTATGGTTT TAAAAACGAT TCTAGGATTA      120
TCGCATCGGG GCGTAAGGAG CTATCCAATG AAGAGTTTT

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(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

143

- (ii) MOLECULE TYPE: DNA (genomic).
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...327
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47

ATGCAAGATT TACCCCCATG CCCTAAACGC AACGACGCCT ACACCTACCA TGATGGCACG	60
CAGTTCGTTT GCTCTAGCTG TTTGTATGAA TGGAATGGAA ATGAAATTAG TAATGAAGAA	120
TTGATCGTTA AAGATTGCCA TAATAATCTT TTACAAAATG GGGACTCGGT CATTCTCATT	180
AAAGATTTAA AGGTTAAAGG CTCATCTTTG GTGCTTAAAA AAGGCACTAA AATCAAAAAT	240
ATCAAGCTTG TCAATAGCGA TCACAATGTG GATTGTAAAG TGGAAGGGCA GAGCTTGTCT	300
TTAAATCTG AATTCCTTAA AAAAGCT	327

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 219 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...219
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48

GTGGATGGGG CTATCATAAC AGGGAATTAT GCCTTGCAAG CAAAACCTCAC CGGAGCCTTA	60
TTTTCAGAAG ATAAGGACTC GCCTTATGCT AATCTTGTA GCTCTCGTGA GGATAATGCG	120
CAAGATGAAG CGATAAAAGC GTTGATTGAA GCCTTACAGA GCGAAAAGAC CAGGAAATTC	180
ATTTTGGATA CCTATAAGGG GCGGATTATC CCGGCTTTT	219

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 711 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

144

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49

GTGTTTTYCCA	TGCTGGTGT	GGTGTGAGC	GATAATTTT	TAGGGCTTTT	CATTGGCTGG	60
GAAGGGGTGG	GGCTATGCTC	TTACTTGCTC	ATTGGCTTTT	GGTATCATAA	AAAAAGCGCG	120
AATAACGCTT	CTATTGAAGC	CTTTGTGATG	AATCGAATCA	CGGATTTAGG	CATGCTCATG	180
GGGATTATTT	TGATCTTTTG	GAATTTTGGC	ACCCTCCAGT	ATAAAGAAGT	CTTTAGCATG	240
CTCAATAACG	CCGATTATTC	CATGCTCTTT	TACATTAGCG	TGTTTCTTTT	TATTGGCGCT	300
ATGGGGAAGA	GTGCTCAATT	CCCTATGCAC	ACATGGTTAG	CCAACGCTAT	GGAGGGGCCT	360
ACCCCTGTAT	CCGCTCTCAT	CCATGCARCG	ACGATGGTAA	CCGCTGGGGT	GTATCTAATC	420
ATCAGAGCCA	ATCCTTTGTA	TAGTGCGGTG	TTTGAAGTGG	GTTATTTTAT	CGCATGCTTA	480
GGAGCGTTTG	TGGCTCTTTT	TGGAGCGAGC	ATGGCTTTAG	TCAATAAGGA	TTTAAAACGC	540
ATCGTGGSYT	ATTCCACGCT	TTCTCAATTA	GGGCTATATG	TTTGTAGCGG	CCGGGCTTGG	600
GGCTTATGCG	ATCGCGCTTT	TCCACCTCTT	TACGCATGCG	TTCTTCAAAT	CCCTCCTTTT	660
CTTAGGCTCA	GGCAATGTCA	TGCATGCCAT	GGAAGACAAT	CTGGATATTA	C	711

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 291 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50

ATGATGATAA	CCAAACAATC	GTATCAAAGA	TTGCTTTTAA	TGCGGGTTTT	TGTGTTTTTCG	60
CTTTTCGGCGT	TTATTTTTTAA	CACCACGGAG	TTTGTCCCTG	TTGCACTTCT	GTGAGACATT	120
GCGAAAAGCT	TTGAAATGGA	GAGCGCAACA	GTGGGGCTTA	TGATCACTGC	TTATGTCATGG	180
GTGGTGTCTC	TTGGCTCAAT	GCCCTTGATG	CTGCTTAGCG	CTAAAATTGA	AAGGAAACGC	240
TTATTGCTTT	TTCTTTTCGC	TCTTTTATT	TTAGCCATA	TCCTTTCGCG	T	291

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 840 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...840
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51

ATGAACTGA	GAGCAAGTGT	TTTAATCGGT	GTGGCAATTC	TGTGCTTAAT	TTTAAGTGCG	60
TGCAGTAAC	ATGCGAAAAA	AGTGGTGAAA	CAAAAGAACC	ATGTTTATAC	GCCTGTGTAT	120
AATGAAC	TGAAGTA	TAGTGAGATC	CCCTTAAATG	ACAAACTCAA	AGACACACCA	180
TTCATGGTGC	AAGTGAAGTT	GCCAAATTAC	AAGGACTATT	TGTTGGATAA	TAAACAAGTT	240
GTACTAACTT	TCAAACCTTGT	TCACCATTCT	AAAAAGATTA	CGCTCATAGG	CGATGCCAAT	300
AAGATCCTCC	AATACAAGAA	TTACTTCCAA	GCTAACGGGG	CAAGATCTGA	CATTGATTTT	360
TACTTGCAAC	CCACTTTGAA	TCAAAAGGGT	GTGGTGATGA	TAGCGAGTAA	CTACAATGAT	420
AATCCCAACA	ACAAAGAAAA	ACCACAGACC	TTTGATGTGT	TGCAAGGAAG	TCAGCCAATG	480
CTAGGAGCTA	ACACAAAAAA	CTTGCAATGGC	TATGATGTGA	GTGGAGCAAA	CAACAAGCAA	540
GTGATCAATG	AAGTGCCAAG	AGAAAAAGCT	CAGCTAGAAA	AAATCAATCA	GTATTACAAG	600
ACTCTCTTGC	AGACAAGGA	ACAAGAATAT	ACCACTAGGA	AAAATAACCA	ACGAGAAATT	660
TTAGAAACAT	TGAGTAATCG	TGCAGGTTAT	CAAATGAGGC	AGAATGTGAT	TAGTTCTGAG	720
ATTTTAAAGA	ATGGCAACTT	GAACATGCAA	GCCAAAGAAG	AAGAAGTTAG	GGAGAAGCTA	780
CAAGAAGAAA	GAGAGAATGA	ATACTTGCGC	AATCAAATCA	GAAGTTTGCT	CAGTGGTAA	840

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 174 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52

ATGTGGTTAG	ATCACATCGC	TAAAGAGATC	AGAAGTTTAG	TGGAAAACGA	TATTGAAGTG	60
GGTATTGTGA	TTGGTGAGG	CAATATCATT	AGGGGGGTTA	GCGCGGCTCT	AGGGGGGATC	120
ATTAGGCGCA	CCAGTGCGGA	TTATATGGGC	ATGTTAGCCA	CCGTGATTAW	GCGG	174

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 372 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

146

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...372
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53

GTGCATAACT TCCATTGGAA TGTGAAAGGC ACCGATTTTT TCAATGTGCA TAAAGCCACT	60
GAAGAAATTT ATGAAGGTT TCGGACATG TTTGATGATC TCGCTGAAAG GATCGTTCAA	120
TTAGGACACC ACCCCCTAGT CACTTTATCC GAAGCGATCA AACTCACTCG TGTAAAGAA	180
GAAACTAAAA CGAGCTTCCA CTCTAAAGAC ATCTTTAAAG AAATTCTAGA GGACTACAAA	240
CACCTAGAAA AAGAAATTAA AGAGCTCTCT AACACCGCCG AAAAGAAGG CGATAAAGTT	300
ACCGTAAC TTATGCGGACGA TCAATTAGCC AAGTTGCAAA AATCCATTG GATGCTAGAA	360
GCCCATTAG CT	372

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54

ATGAATAAAA CCATAAAGC CGCCGCCCTA GCCTATAACA TGGGGCAAGA TCATGCCCCA	60
AAAGTGATCG CAAGCGGGGT GGGCGAAGTG GCTAAAAGGA TCATTCAAAA AGCTAAGGAA	120
TACGATATAG CGCTCTTTTC TAACCCCATG CTGGTGGATT CGCTCTTAAA GGTGGAATTA	180
GACTGCCGCA TACCTGAAGA ATTGTATGAA AGCGTGGTGC AAGTGTTTT ATGGCTCAAC	240
AGCGTGGAATAAACGCGCA AATGTCCAAG	270

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 633 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

SUBSTITUTE SHEET (RULE 26)

147

- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...633
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55

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ATGGGGAAAA TTTAGCGCA TTTAGCCCAT GAAATCAGAA ACCCCGTAGG CTCTATCTCT 60
CTTTTAGCTT CGGTGTTATT AAAGCATGCG AACGAAAAAA CTAAACCCAT TGTGTAGAA 120
TTGCAAAAAG CTTTATGGCG CGTAGAAAGG ATCATTAAAG CCACCTTGCT TTTTCTTAA 180
GGCATTCAAG CCAACCGCAC CAAGCAAAGT TTGAAAACGC TAGAGAGCGA TCTCAAAGAA 240
GCCCTAAACT GCTACACTTA CTCTAAAGAC ATTGATTTTC TTTTAAATTT TAGCGATGAA 300
GAAGGGTTT TTGACTTTGA TTTAATGGGG ATTGTGTTAC AAAATTTCCT GTATAACGCC 360
ATTGATGCGA TTGAAGCCTT AGAAGAGAGC GAACAAGGTC AGGTCAAAT TGAAGCGTTC 420
ATTCAAAATG AATTTATTGT CTTCAACCAT ATTGATAATG GCAAGGAAGT GGAAAATAAA 480
AGCGCTTTAT TTGAGCCTTT TGAACCACT AAATTAAAGG GGAATGGCTT AGGGTTAGCC 540
CTGTCTTTGC AAGTCGTTAA AGCCCATGAA GGGAGCATTG CGCTATTAGA AAATCAAGAA 600
AAAACCTTTG AAATTAAGAT TCTTAACGCT TCT

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(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 636 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56

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GTGTCAGAAT TTCATCAAGT TTATGACCCT TTGGGTAATA TTTGGCTGAG CGCTCTTGTG 60
GCCTTATGTC CGATTTTGTT ATTTTCTTAA TCTTTAATGG TTTTAAACT CAAAGGTTAT 120
ACAGCGGCCT TTTGAGCGT GGCCTTATCA GCCATTATG CGGTTTTAGT GTATAAAATG 180
CCTGTTAGCA TGGTGGGTC AAGCTTCCTT TATGGCTTTC TTTATGGCCT ATGGCTATTC 240
GCTTGGATCA TTATTGCCGC GATTTTFTA TACAACTCA GCGTTAAATC CGGCTATTTT 300
GAAATCTTAA AAGAAAGCGT TCAGTCCATC ACTTTAGATC ACCGCATTTT AGTGATTTG 360
ATTGGCTTTT GTTTGGCTC ATTTTAGAA GGGGCGATCG GCTTTGGAGG GCCTATTGCC 420
ATCACAGCGG CGATTTTAGT GGGGTTGGGG TTAAGCCCTT TGATTCTGC TGGGTTATGT 480
TTGATCGCTA ACACCGCTCC TGTGCCCTT GCGCGGTGG GTATCCCTAT AAGCGCGATG 540
GCGAGCGCGG TAGGGGTGCC AGCGATCTTA ATTTCAAGCA TGACGGGTAA AATCCTCTTT 600
TTTGTGAGCT TGTTAGTGCC GTTTTATTATT GTGTKT

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(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 546 base pairs
(B) TYPE: nucleic acid

SUBSTITUTE SHEET (RULE 26)

148

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57

ATGGAAATTA	AAATGGCTAA	GGATTATGGT	TTTTGTTTTG	GCGTCAAAAG	AGCGATACAA	60
ATCGCTGAAA	AAAATCAAAA	CAGCTTGATT	TTTGCTCGC	TCATTCATAA	CGCTAAAGAA	120
ATCAATCGTT	TGGAAAAAAA	TTCAATGTG	AAAATTGAAG	AAGATCCTAA	AAAAATCCCT	180
AAAAATAAGA	GCGTGATCAT	AAGAACCCAT	GGCATTCCCTA	AACAGGATTT	AGAATACTTG	240
AAAAATAAGG	GGGTAAAT	CACTGACGCG	ACTTGCCCGT	ATGTGATCAA	ACCTCAGCAA	300
ATTGTGGAAT	CCATGAGTAA	AGAAGGGTAT	CAAATCGTGC	TTTTTGGGGA	CATTAACCAC	360
CCTGAAGTCA	AGGGCGTGAT	CAGCTATGCC	ACTAACCAGG	CTTTAGTCGG	CAATTCGTTA	420
GAAGAATTGC	AAGAAAAAAA	ATTGCAACGG	AAAGTGGCTT	TAGTCTCTCA	AACCACCCAA	480
GCAAACCCCA	AAACTCTTGC	AAATCGCTTC	TTATTGGTG	GARGRTGCAC	TGAAGTGCCT	540
ATTTTT						546

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 672 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58

ATGGATCATG	AGTTTTTGAT	TACCATGCGT	TTGAGCTTTT	CTTTAGCTTT	GATTACCACC	60
CTTATTTTAC	TCCCTATAGG	GATTTTTTTA	GGCTATTTTT	TAAGCCTTAA	ACGCAATCTT	120
TTAACGAGCT	TAACAGAAAC	GCTTGTGTAT	ATGCCCTTAG	TTTTACCCCG	AAGCGTGCTA	180
GGGTTTTATC	TTCTTTTAAT	CTTTTCGCCT	TCTTCTTTTT	TGGGAGCGTT	TTTACAAGAT	240
GTGTTAAATG	TGAAACTCGT	TTTTAGTTTC	CAAGGGCTTA	TCTTAGGGAG	CGTGATTTTT	300
TCCTTGCCCT	TTATGTAAAG	CCCTATTAAA	AGCGCGTTAA	TTTCCTTGCC	CACCTCTTTA	360
AAAGAAGCCA	GTTATAGCTT	GGGTAAAGGG	GAATACTACA	CCCTTTTTTT	TGTCCTACTC	420
CCTAACATCA	AACCCAGTGT	GTTGATGGCT	ATCATTACAA	CTTTTATGCA	CACATAGGT	480
GAATTTGGCG	TGGTGATGAT	GCTTGGGGGT	GATATATTAG	GGGAAACAAG	AGTGGCTAGC	540
ATTACGATCT	TTAACGAAGC	TGAAGCACTC	AATATTCTA	AAGCCCATCA	ATACGCCTTA	600
ACGCTCACGC	TTATTAGTTT	TAGCCTCTTG	TTTGTTACCC	TATTTTAAA	TAAAAACAA	660
AGCTCGTTTT	TA					672

SUBSTITUTE SHEET (RULE 26)

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59

ATGCATCCTA TAATGTTTGC CTATATCGCT AACGCGCTCG CTCAAGCTAG AAAGATCAAC	60
GGAACACTTT GCATGGCGTT TCAAAAAATA TCTCAAGTCA AAGAATTAGG CATTGATAAA	120
GCAAAGAGTT TGATAGGCAA CCTTTCTCAA GTGATTATCT ACCCCACAAA AGATACTGAT	180
GAATTAATAG AATGTGGCGT CCCATTAAGC GATAGTGAAA TCAATTTCTT ACACAACACG	240
GACATGAGAG CCAGACAAGT GCTAGTAAAA AATATCGTTA CAAACGCTTC AGCTTTTATT	300
GAAATGATT TAAAAAAGAT TTGCAAGAAC TACTTTATAT TCTTGATAGC AATGCTGGTA	360
ATAGAAAAAT CCTCAATGAT CTTAAAAAAG CAAACCAAGA AACTTATAAG GAAGAGTATT	420

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60

ATGTGCCTGA CAGGCGGCTT GATGCGTTGG CTCAAATCGG TAAAGCCTGA ACGAATCTTG	60
CATTCTGTGG TGAATTTTGT GGATATTGCC GGATTGATTA AGGGGCGGAG CAAGGGGGAG	120
GGTTTAGGCA ATCAGTTTTT AGCCAATATC AAGGAATGCG AAGTGATCTT GCAAGTGGTG	180
CGCTGTTTTG AAGATGACAA TYATACGCA TGTGAACGA	219

(2) INFORMATION FOR SEQ ID NO:61:

150

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...276
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61

ATGCATGTTG	CTTGTCCTTTT	GGCTTTTAGGG	GATAACCTCA	TCACGCTTAG	CCTTTTAAAA	60
GAAATCGCTT	CCAAACAGCA	ACAGTCCCTT	AAAATCCTAG	GCACTCATTT	GACTTTAAAA	120
ATCGCCAAGC	TTTTAGAATG	CGAAAAACAT	TTTGAAATCA	TTCTCTGTTT	TGAAAATATC	180
CCTGCTTTTT	ATGACCTTAA	AAAACAAGGC	GTTTTTTGGG	CGATGAAGGA	TTTTTTATGG	240
TTATTAAAGC	AATTAAAAAA	CATCAAATCA	AACGTT			276

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 615 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...615
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62

ATGAAAAAGA	AGCCATTGAT	GTGGCGTATC	TGTGCGTTAA	GGAGACTTCT	TCTAGGGTTC	60
AAGAGAGAGA	GAGAGTTATT	AAGCTTCGCT	AAACATTGGA	ATATCCCAAC	GATTGTCGTT	120
TTACACACAC	CTCAAGCCGA	AGCCGGCGAT	GCGTTTGTC	AAGAACTAA	AGGGATCATA	180
GACGAAGAAT	GGGGGTTTAA	AGGTTTTGTC	AGAGCCTATG	TGAGGGTCAA	TTCCGTTGCC	240
TTTTTCATTTA	GGGGGTGAA	AGTCCCTGTT	GAAGGTTTAG	AAGAATTGGT	AGATGAAACG	300
AAAAAATGCC	TTTCAGACGC	TGAAAAAAT	AAGAAAAGGC	ATTTCTTGAG	TATTCAAAGA	360
GTTAAGATTG	AAGAAAGAAA	ACAGGCTATG	ATAGAGGAAT	GTAAACCAT	TATCCATGTT	420
GCATCAGGCG	CTGCAGGAGT	TGCTGGGCTT	ATCCCCATAC	CTTTTAGCGA	TGCGCTCGCT	480
ATCGCACCCA	TTCAAGCAGG	GATGATCTAT	AAAAATGAATG	ACGCTTTTGG	AATGGATTGG	540
GATAAATCTG	TGGGCGCGAG	TTGGTTCGCA	GGATTGTTAG	GCGTAAACTG	TCGCGCAAGT	600
GGGGAGGACT	CTCGT					615

(2) INFORMATION FOR SEQ ID NO:63:

SUBSTITUTE SHEET (RULE 26)

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...123
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63

GTGCTTGGCG TGTTAAATTT AAGGGGCAAT GTCTTCCCTT TGATCAGTTT GCGTTTAAAG	60
TTTGGCTTGA AAGCCGAAAA ACAAACAAA GACACTCGTT ATTTGGTGGT ACGCCATAAC	120
GAT	123

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 657 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...657
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64

GTGAAAAGCG TTTTATAGCGA AGAAAAAGAA ACGCCTGTTA CTAAAGAAAA CGGCTCTTAT	60
TTGATCGCTT ATGACCCCCT AGATGGGAGT TCAGTGATGG AGGCGAATTT CTTAGTAGGC	120
ACGATTATAG GGGTTTATGA AAAGGATTAT AAGGCGCAAA ATTTAGTTGC AAGCCTTTAT	180
GTGGTTTTTG GGCATAAAAT AGAATTGGTG GTGGCTTTAG AAGAAGTTTA TCGTTACGCT	240
TTTTATCAAA ACAAGTTTCA TTTTATAGAA ACCATCGTTT TAGAAAAATA GGGTAAAATC	300
ATCGCTAGCG GAGGCAATCA AAAGGATTTT TCYTTGGGCT TAAAAAAGGC TTTAGAAGGG	360
TTTTTTGCAG AAAATTACCG CTTGCGATAC TCAGGATCTA TGGTGGCTGA TGTCCATCAT	420
GTGTTGGTTA AAAAGGGCGG AATGTTTTCC TACCCGCAAA AGAAATTGCG AAAGCTTTT	480
GAAGTCTTTC CTTTAGCCTT GATGGTTGAA AAAGCTAAAG GGGAAGCGTT TTATTTTGAT	540
AAGGGGGTTA AAAAGCGTTT GCTAGATCAA AGCGTAGAAA GCTACCATGA AAAAAGCGAA	600
TGCTATTTAG CCAGCCCGCA TGAAGCTCAG ATTTTAGAAA AACATTTAAA GGGAGAA	657

(2) INFORMATION FOR SEQ ID NO:65:

152

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65

ATGAAAGCA TTGGAGAAGT GATGGCGATA GGGGGCAATT TCCTAGAAGC CTTACAAAAA	60
GCGTTATGCT CTTTGGAAAA CAATTGGCTA GGGTTTGAAT CGTTAAGCAA AGATTTAGAG	120
GCGATAAAAA AGGAAATCCG CCGGGCCAAT CCCAAACGCT TGCTCTATAT TGCTGATGCG	180
TTCAGGTTCG GCGTTTCTGT GGATGAAGTG TTTGAATTAT GCCAGATTGA CAGGTGGTTT	240
TTATCTCAA TTCAAAAAC AGTCAAAGCA GAAGAGGGCA TCAATTCTAG CGTTTTAACG	300
GACGCCAAAA AATTGAGAGG GCTTAAAAAT TTAGGCTTTA GCGATGCCAG GATTGCCACT	360
AAAATCAAAG AAAATGAAAA TTTAGAGGTC AGCCCTTTTG AAGTGAATT AGCTAGATCT	420
AATTTACAAA TCGCGCCCCA TTTTGAAGAA GTGGACACTT GCGCGGCGGA GTTTTATCG	480
CTCAGGCTTA TTTGTATTCC ACCTATGCCC CTAACCCCTT GCCCCCTATT GGAACAAAC	540
AAGAAAAACA AGAAAAGAAA ATCC	564

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66

ATGTTTGGGA ATAAGCAGTT ACAGCTTCAA ATCAGTCAAA AAGATTCTGA GATTGCGGAG	60
TTAAAAAAG AAGTCAATCT CTATCAAAGC CTTTAAATT TGTGCTTGCA TGAGGGTTTT	120
GTAGGTATTA AAACAATAA AGTCGTTTTT AAAAGCGGGA ATCTTGCAAG CTTAAACAAT	180
TTAGAAGAAC AAAGCGTTCA TTTTAAAGAA AACGCAGAAA GCGTTAATT ACAAGGGGTT	240
TCTTATTCTT TGAAAAGCCA AAATATTGAC GGCGTGCAGT ATTTTTCATT GGCTAAAAAA	300
ACAGGGGGTG TGGGGGAATA CCATAAAAT GATTGTGTTA AGACTTTTTG CACGAGCTTA	360
AAAGAGGGCT TAGAGAAGC GCAAGAAAGC ATGCAGTATT TCCATCAAGA AACAGGCTTG	420
CTCTTGAATG CGGCTAAAAA TGGCGAAGAG CATTCTAATG AAGGATTAAT AACCGTTAAT	480
AAAACGGGTC AAGACATTGA ATCGCTTTAT GAAAAGATGC AAAACGCCAC TTCGTTAGCG	540

SUBSTITUTE SHEET (RULE 26)

153

GACTCCCTCA ACCAACGGAG CAATGAAATC ACTCAAGTCA TTTCTTTGAT TGATGATATT 600
 GCAGAGCAAA CCAATCTCTT AGCCCTAAAC GCCGCTATTG AGGCCGCACG AGCGGTGAAC 660
 ATGGCAGAGG GTTTGCGGTG GTGGCTGATG AGG 693

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67

ATGTGGATTA TGTCTTCACT TTCTAGTTCA TTCTTTCATT CGCTCTTCTT CATCAAATCA 60
 AACCCCTGGCC AACTCTTAAA AGGTTGGGGT TCAAAAATCT TTTTCATAAA TAGAAAGTTT 120
 GTTTTAGCAC AGTATAATCC TAGCGTTTCA ATTTTATTTT TACTCAATAG GGTGTTTGGT 180
 GTTGGCGTT 189

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68

GTGGGCGCTA ACCCTGTGCC GCATGCGCAA ATCTTGCAAT CAGTTGTGGA TGATTTGAAA 60
 GAGAAAGGGA TCAAATTAGT GATCGTGTCT TTTACGGATT ATGTGTTGCC TAATTAGCG 120
 CTCAATGACG GCTCTTTAGA CGCGAATTAC TTCCAGCACC GCCCTTATT GGATCGGTTT 180
 AATTGACACA GAAAAATGCA CCTTGTTGGT TTGGCCAATA TCCATGTGGA GCCTTTAAGA 240
 TTTTATTCTC AAAAAATCAC AGACATTAAA AACCTTAAAA AAGGCTCAGT GATTGCTGTG 300
 CCAATGATC CGGCCAATCA AGGCAGGGCG TTGATTTTAC TCCATAAACA AGGCCTTATC 360
 GCTCTCAAAG ACCCAAGCAA TCTATACGCT ACGGAGTTTG ATATTGTCAA AAATCCTTAC 420
 AACATCAAAA TCAAACCCCT AGAAGCTGCG GTTATTGCC 459

SUBSTITUTE SHEET (RULE 26)

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69

ATGGGGCTTG	TTGCCAGCGG	CATTAACGAT	GAAGAGCTTT	TAAATGGCT	TCAGGCTTTT	60
GGGTTAAAAA	TGGGTCITTG	TTTTCAAGTG	CTAGATGATA	TTATAGACGT	TACACAAGAT	120
GAAAAAGAAA	GCGGTAAAC	CACGCATTTA	GACAGCGCTA	AAAACAGCTT	TGTGAATTTA	180
TTGGGGCTAA	AAAAGGCAGC	GGTTACGCC	AAACTT			216

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70

ATGGGGTTTA	ACCGCTTGGT	GGATAGAGAC	ATTGATAAGG	ATAACCCAAG	GACGAAAAAC	60
CGCCCCAGCG	TGGATGGTAG	GATCAGCGTT	AAAGGCATGG	TCATTITTAG	CGTTTCAAAC	120
GCTCTTTTGT	TCGTGGGAGT	GAGTTATTTT	ATCAACCCTT	TAGCTTTCAA	GCTTTCGTTA	180
CCTTTTTTAA	TCATTTTAGG	GGGTTATTCG	TATTTCAAGC	GCTTTTCTTC	TTGGCGCAT	240
TTTGTCGTGG	GTTTGGCTTT	GGGTTTAGCC	CCCATTGCAG	GAAGCGTGGC	GGTTTTAGGG	300
GATATTCCTT	TATGGAATGT	CTTTTGGCY	TTAGGGGTGA	TGTTGTGGGT	GGCTGGGTTT	360
GATTTGCTCT	ATTCTTTACA	GGATATGGAG	TTTGATAAAG	AAAGGGGCTT	GTTTCCATT	420
CCTAGCCAAT	TAGGGGAAAA	ATGGTGCTTG	AATCTTTCAA	GGCTCTCGCA	CCTTGTGGCA	480
CTGATCTGCT	GGCTTTGTTT	TGTGAAATGC	TATCATGGGG	GGCTTTTTCG	GTATTTGGGC	540
TTAGGGGTTT	CAGCCTTGAT	CTTACTCTAT	GAGCAGATTT	TAGTGGCCAG	AGATTATAAA	600
AACATTCCTA	AAAGCCTTTT	TTGTGAG				627

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71

GTGGAGCAAA ATAAATCAT TAACTCTTC ACTGTGGCGA CTATGGCGAT GATGCCCCC	60
ACATTGATTG GCACGATTWA TGGCATGAAT TTAAATTCA TGCCGGAGTT AGAATGGCAA	120
TACGGGTATC TTTTGGCGCT GATTGTCTAT GCGATTCTA CGATTTTGCC GGTGATTAT	180
TTCAAAAAGA AAGGGTTGGT TGTAGCCTTT CATGGAATTT TTATCCTCAC TCTTAGACGC	240
TCTTTCTACA CCGCATGGCA TAGTCTCCTT GGCTACGCCA CGCTT	285

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72

ATGTTGCGATT CAATCGTTTA TTTTTCAAT AAGAGCGGGT TTGTTACCAC GCTTGTTTTA	60
GTTTGGATTG CGCTTTATTT GGTGATGACT TTATGGGTCT TTTTGTATAA AAGCATTGTA	120
TTAAAGATTG AACTCAGGCG CGAGATGCAA TCTTTGTCTA ACATTCTTAA TGGAGCGCAA	180
GACGCTCCAG AGCATTATTT GTTTAATAAA AAAAGAAATG ATGAGACCAA AAGGTATTCT	240
AATGAATTGT TGCAGGSCTT GGAACACCA GGTCT	276

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

156

(A) LENGTH: 375 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73

ATGGCGATGC	TYTATTGCAT	CGGGTTATTG	ATGCCGATTT	TAGGAGCGAT	TAAAGGGGGG	60
GATATTGGCG	AATGGTTCCC	TGATAATGAC	CCCAAATACA	AAAACGCCTC	TTCTAAAGAG	120
CTTTTAAAAA	TCGTGTTGGA	TTTTTCTCAA	AGCATTGGGT	TTGAATTGCT	TGAAATGGGA	180
GCGACCATCT	TTAGCGAAAT	CCCTAAAATC	ACTCCTTACA	AACCGGCGAT	TTTAGAGAAT	240
TTGAGCCAAC	TTTTGGGTTT	AGAAAAATCT	CAAAATCAGCT	TGAAAGCCAC	TACAATGGAA	300
AAAATGGGGT	TCATTGGCAA	ACAAGAAGGG	CTGTTAGTCC	AAGCGCATGT	GAGCATGCGT	360
TATAAACAAA	AAC TT					375

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3534 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...3534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74

ATGATACCAA	ATTTAGATAT	AGAAGGAGAA	ACAATGACTA	ACGAAGCCAT	TAACCAACAA	60
CCACAAACCG	AAGCGGCTTT	TAACCCGCAG	CAATTTATCA	ATAATCTTCA	AGTGGCTTTT	120
ATTAAAGTTG	ATAATGTTGT	CGCTTCATTT	GATCCTAATC	AAAAACCAAT	CGTTGATAAG	180
AATGATAGGG	ATAATAGGCA	AGCTTTTGAG	AAAATCTCGC	AGCTAAGGGA	GGAATTCGCT	240
AATAAAGCGA	TCAAAAATCC	TACCAAAAAG	AATCAGTATT	TTTCAAGCTT	TATCAGTAAG	300
AGCAATGATT	TAATCGACAA	AGACAATCTC	ATTGATACAG	GTTCTTCCAT	AAAGAGCTTT	360
CAGAAATTTG	GGACTCAGCG	TTACCAAATT	TTTATGAATT	GGGTGTCCCA	TCAAAAACGAT	420
CCGTCTAAAA	TCAACACCCA	AAAAATCCGA	GGTTTTATGG	AAAATATCAT	ACAACCCCTT	480
ATCTCTGATG	ATAAAGAGAA	AGCGGAGTTT	TTGAGGTCTG	CCAAACAAGC	TTTGCAGGA	540
ATTATCATAG	GAAACCAAAT	CCGATCGGAT	CAAAAATTCA	TGGGCGTGTT	TGATGAATCT	600
TTGAAAGAGA	GGCAAGAAGC	AGAAAAAAT	GGAGAGCCTA	ATGGAGATCC	TACTGGTGGG	660
GATTGGCTTG	ATATTTTTTT	ATCATTTGTG	TTTAACAAAA	AACAATCTTC	CGATCTCAAA	720
GAAACGCTCA	ATCAAGAACC	AGTTCCTCAT	GTCCAACCAG	ATGTAGCCAC	TACCACCACT	780

SUBSTITUTE SHEET (RULE 26)

157

GACATACAAA	GCTTACCGCC	TGAAGCTAGG	GATTTGCTTG	ATGAAAGGGG	TAATTTTCT	840
AAATTCACCT	TTGGCGATAT	GAACATGTTA	GATGTTGAGG	GAGTCGCTGA	CATTGATCCT	900
AATTACAAGT	TCAACCAATT	ATTGATCCAC	AATAACGCTC	TGTCTTCTGT	GTTAATGGGG	960
AGTCATAATG	GCATAGAACC	TGAAAAAGTT	TCATTGTTGT	ATGGAAACAA	TGGTGGTCCT	1020
GAAGCTAGGC	ATGATTGGAA	CGCCACCGTT	GGTTATAAAA	ACCAACGAGG	CGACAATGTG	1080
GCTACACTCA	TTAATGTGCA	TATGAAAAAT	GGCAGTGGGT	TAGTCATAGC	AGGTGGTGAG	1140
AAAGGGATTA	ACAACCCTAG	TTTTTATCTC	TACAAAGAAG	ACCAACTCAC	AGGCTCACAA	1200
CGAGCATTGA	GTCAGAAGA	GATCCAAAAC	AAAGTGGATT	TCATGGAATT	TCTTGCACAA	1260
AATAATGCTA	AATTAGACAA	CTTGAGCAAG	AAAGAGAAAG	AAAAATTCCA	AAATGAGATT	1320
GAAGATTTTC	AAAAAGACTC	TAAGGCTTAT	TTAGACGCCC	TAGGGAATGA	TCACATTGCT	1380
TTTGTCTTCTA	AAAAAGACAA	AAAACATTTA	GCTTTAGTTG	CTGAGTTTGG	TAATGGGGAA	1440
TTGAGCTACA	CTCTCAAAGA	TTATGGGAAA	AAAGCAGATA	AAGCTTTAGA	TAGGGAGGCA	1500
AAAACCACTC	TTCAAGGTAG	CCTAAAACAT	GATGGCGTGA	TGTTTGTGTA	TTATTCTAAT	1560
TTCAATACAC	CCAACGCCTC	CAAGAGTCCT	GATAAGGGTG	TGGGTGCTAC	GAATGGCGTT	1620
TCCCATTTAG	AAGCAGGCTT	TAGCAAGGTA	GCTGTCTTTA	ATTGTCCTAA	TTTAAATAAT	1680
CTCGCTATCA	CTAGTGTCTG	AAGGCAGGAT	TTAGAGGATA	AACTAATCGC	TAAAGGATTG	1740
TCCCCACAAG	AAGCTAATAA	GCTTGTCAAA	GATTTTGTGA	GCAGCAACAA	AGAATTGGTT	1800
GGAAAAGCTT	TAAACTTCAA	TAAAGCTGTA	GCTGAAGCTA	AAAACACAGG	CAACTATGAC	1860
GAGGTGAAAC	AAGCTCAGAA	AGATCTTGAA	AAATCTCTAA	AGAAACGAGA	GCGTTTGGAG	1920
AAAGATGTAG	CGAAAAATTT	GGAGAGCAAA	AGCGGCAACA	AAAATAAAAT	GGAAGCAAAA	1980
TCCTCAAGCTA	ACAGCCAAAA	AGATGAGATT	TTTGCGTTGA	TCAATAAAGA	GGCTAATAGG	2040
GATGCAAGAG	CAATCGCTTA	CGCTCAGAAT	CCTTAAAGGCA	TCAAAAGGGA	ATTGTCTGAT	2100
AAACTTGAAA	ATATCAACAA	GGATTTGAAA	GACTTTAGTA	AATCTTTTGA	TGAATTCAAA	2160
AATGGCAAAA	ATAAGGATTT	CAGCAAGGCA	GAAGAAACAC	TAAAAGCCCT	TAAAGGCTCG	2220
GTGAAAGATT	TAGGTATCAA	TCCAGAATGG	ATTTCAAAG	TTGAAAACCT	TAATGCAGCT	2280
TTGAATGAAT	TCAAAAATGG	CAAAAATAAG	GATTTTCAGCA	AGGTAACGCA	AGCAAAAAGC	2340
GACCTTGAAA	ATTCCATTAA	AGATGTGATC	ATCAATCAAA	AGATAACGGA	TAAAGTTGAT	2400
AATCTCAATC	AAGCGGTATC	AGTGGCTAAA	GCAACGGGTG	ATTTTCAGTGG	GGTAGAGCAA	2460
GCGTTAGCCG	ATCTCAAAAA	TTTCTCAAAG	GAGCAATTGG	CTCAACAAGC	TCAAAAAAT	2520
GAAGATTTCA	ATACTGGAAA	AAATTCTGCA	CTATACCAAT	CCGTTAAGAA	TGGTGTAAC	2580
GGAACCCCTAG	TCGGTAATGG	GTTATCTAAA	GCAGAAGCCA	CAACTCTTTC	TAAAAACTTT	2640
TCGGACATCA	AGAAAGAGTT	GAATGCAAAA	CTTGGAATTT	TCAATAACAA	TAACAATAAT	2700
GGACTCGAAA	ACAGCACAGA	ACCCATTAT	ACTCAAGTTG	CTAAAAAGGT	AAAAGCAAAA	2760
ATTGACCGAC	TCGATCAAAT	AGCAAGTGGT	TTGGGTGATG	TAGGGCAAGC	AGCGAGCTTC	2820
CTTTTGAAAA	GGCATGATAA	AGTTGATGAT	CTCAGTAAGG	TAGGGCTTTC	AGCTAACCAT	2880
GAACCCATTT	ACGCTACGAT	TGATGATCTC	GGCGGACCTT	TCCCTTTGAA	AAGGCATGAT	2940
AAAGTTGATG	ATCTCAGTAA	GGTAGGGCTT	TCAGGGGAGC	AAAAATTGAC	TCAGAAAATT	3000
GACAATCTCA	ACCAGGCGGT	ATCAGAAGCT	AAAGCAAGTC	ATTTTGACAA	CCTAGATCAA	3060
ATGATAGACA	AGCTCAAAGA	TTCTACAAA	AAGAATGTTG	TGAATCTATA	TGTTGAAAGT	3120
GCAAAAAAAG	TGCCTACTAG	TTTGTACGCG	AAATTGGACA	ATTACGCTAC	TAACAGCCAC	3180
ACACGCATTA	ATAGCAATGT	CAAAAATGGA	ACAATCAATG	AAAAAGCGAC	CGGCATGCTA	3240
ACGCAAAAAA	ATTCTGAGTG	GCTCAAGCTC	GTGAATGATA	AGATAGTTGC	GCATAATGTG	3300
GGAAGTGCTC	CTTTGTGACG	GTATGATAAA	ATTGGATTCA	ACCAAAAGAA	TATGAAAGAT	3360
TATTCTGATT	CGTTCAAGTT	TTCCACCAGG	TTGAGCAATG	CCGTAAAAGA	CATTAAGTCT	3420
GGCTTTGTGC	AATTTTAAAC	CAATATATTT	TCTATGGGAT	CTTACAGCTT	GATGAAAGCA	3480
AGTGTGGAAC	ATGGAGTCAA	AAATACTAAT	ACAAAAGGTG	GTTTCCAAA	ATCT	3534

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

158

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75

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ATGAAAGCGT TGAAGACTTT TTTAAAAAAA TCCCTTATTC TGTTACTAGC AATTGCCTTA      60
AACCACCTTAA ACGCTGTGGC TATGATTGTG GATAATCCTA CGCAGAACGC TTGGAATGGT      120
GCTAAAAGAG CATGGGATGA AAGCAAGTGG GCTAAACATT TAGCCACTAT TACTGAAAGG      180
ATCAAGCTCG CTCAAGACAC ATTAGATAGG GCTAATCAGA CGCTTAATTC CATCAACAAA      240
GTGAATGATG TTTTGAACAA AACCAATCAA TTTCTAACAG GCAGTATTTT AAGCATCCCC      300
AATCCCATGC AGTATGTAGA AAAAATCCAA AGTTTGGCCA AGCAAGTTCA AGCCAATACT      360
GAAAGGATCA AAGAAAAATGC ACAAAACTAT GATATACGCA ATCAAATTGC AGCCAAACGC      420
ATCTCTGAAA AATGCCCTGA ACTCAATTGG GATGTCAGTC AAGACGCGAG CCCTACAGAG      480
AAAAACTTAC ACCAATTTTT CACGAGCAAG GGGAAAGAAA GCGCTAACAC AAAGGCTCTA      540
AAGGATTTTG CTAACGCCAT AGGTAACACT CAAATCAGCA CGGCGAACGA TTTAGGAGCT      600
GGACTTAGAG GCAGAGCCTT ATTAGAATAC ATTTGCATTG AAAAAGGCAA TTTAGAAGCG      660
GCTAAAAAAA GCAATTATT AGACAGCCAA ATGACTTTAG CTCTACTCAA TAACGACTAT      720
ACGGCTTATG AAAAAGCTAG AGCTGAAAAA GAAGAATTAA AAAGACAAAT CGCTTCAAAT      780
GTGTATGCGA AAGTCAAACA GCTTGTGTGA GCTTCCCAAG ATAGAGCGTT TAGTCAAATG      840
GATAATGAGT TGGGCGTTAA AACTTTTGGG TTCAACGATG AGAATGTTAA AAAAGGTTAT      900
TGCAAGAAAG AAAACAGAAA TGGCAAAAGC GAGTGCAATC CTAACATGCT CAATGTTAAT      960
CGCTTAAAG CGCAATTTGA TGAGCTTAAT TTAGATTATA GTAGGGATAT TGCTGGTAAA     1020
AAAGGTGAAG CAGCCGCTAA AGTGTTCAAT GACTACAAAC ACCGATTCCA ACAATTAAGC     1080
GTAGAACTG CTTTAGAAAT CGCTCAAAT TTAAGTTTGA TGAATAAGAC GCTAGGTTTA     1140
ATGGGTGCAA TGCAAAAGCTA TGCAATTCAG CAACAAATGG GCTATTTTGA AGATATTATT     1200
CCTGCTGACG CCTTAAAGA TGACAAAGAG CATCAAGAAA ATCTTGAACA AAAACAACAA     1260
GAAATAGAGA AAGTCTATAG GGCTAAATTA GACGCTTATG GTTCCCTTAA TGGTAGTGTA     1320
GGAAAGGCAA GTGGCGTGAA TTCAAATAGT AATAATGAAG CCCCAGCTC TGATAATATC     1380
CAGTCGTTTA ATCCGTAT

```

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76

```

GTGATGGATG CAGAAAATGG GGAATTGCTC GTTGCAGGAA GTTACCCTGA ATACAATTTG      60
AACGATTTTG TAGGCGGGAT CAGTCAAGAC AAATGGCAAA AACTCCAAGA TGATATTTAT      120
AACCCTTTAT TAAACCGCTT CGCAATGCCT TGTATCCGCC GGGATCTGTG GTTAAATGG      180
GCGTGGGGT

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(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1263 base pairs

SUBSTITUTE SHEET (RULE 26)

159

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77

ATGAATTTTT	TTGACACCCT	TATGGGTATG	TTTGTGAGC	CATCTCAAAA	AGTAGCCAAA	60
AGTCTTGCTG	AACATGTGGG	TAGCTTTTTT	CATGCACAAC	TCATTTTAAA	CACAATTATT	120
ACTATTTTAT	TTATGATATG	GGCGTATAAG	CGTGTGAAAG	AGGGCGATAT	GTTTGAGTTT	180
AAAACCGCTA	TGGGTGTGGT	TGTATTTATA	GCGTTGTAG	GATTTATCAA	TTGGGGGATT	240
AAAAATCCTA	ATGATTTTAA	CACCTATTTT	ATCAATACGA	TATTCTACCC	ATCTGAAAAA	300
CTAGCCATAC	TTATCGCTCA	AAGCCTAAAT	GATGGCTTAG	AAATCCCCAC	TAACACTAAT	360
TTAAGTCCTA	GTGAAATTTT	TAGCATAGGA	AATTTAGCCT	CAAGTGCCTA	TGCAATGATA	420
GTTAATCTGT	GGGATAATGC	TTTGTATGGT	ATTAACATGT	TTAATTGGCT	CACAATGATA	480
CCTAAAATAA	TTATGTTTTT	TTTAGTGATT	TTAGGGGAAT	TATTGTTTTT	AGGCTTATTG	540
CTTATTATTG	TGTTATTAGT	TACAGCAGAA	ATTTTATGT	GGTCAGCATT	AGGTTTAATT	600
GTATTGCGCT	TAGGTTTAAT	CCCCCAAACC	AAAGGCATGT	TATTTAGCTA	TCTTAAAAAG	660
CTCATTTCCT	TTACTCTTTA	TAAACCTTGT	ATGATGTTAG	TAGCTTTTTT	TAATTATGGA	720
ATAATCTATA	AAGTCAATAC	TTAATCCCC	ACTAAACACG	AAGTCACACA	AGGCTTTTAT	780
GGCAATGCGG	ATAAAATGGC	AAATGAGGGA	AAAATTATTG	ATGTCTTTGG	CAATGTCTTA	840
GAAGGAGATT	GGAACCTCTA	TATAGCCCAT	AGTTCTATTG	TAGGCTTTTT	AACCATTATT	900
GTTTTAGGTT	CTGTGATTTC	TTTCTTTCTA	GTCAAACGAG	TGCCTGATTT	TATCAATAAT	960
ATCTTTGGCA	CAAGTGGAGG	CGTGGGGGCA	GTAACAGAAA	TGATGCAAAA	AATTGGCATG	1020
ACAATAGGCG	GAGCTGTATT	TGGGGGTAGT	GCAGTTATGG	TTGCTAATCA	AGTTAAGCAA	1080
GCCTATCAGA	GTGCTGGGGG	CGGACTAGCA	GGACTTCAAG	CTGGAGCTAA	AGCTTTTGGG	1140
CTTGGAGCAA	TCAGTGGAGG	GGCAAGTGCT	ATGGCAAACC	ACAGGAGTGT	TAAAGCTGGG	1200
GTGAAACACT	TTGTAGCAAG	TGTTAAAAGT	GGCTTTGGAT	TTGATAATGA	TAAAAATAAT	1260
AAA						1263

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78

160

ATGGATGAAC	CAGAAACCAG	TTTAGAGCAA	AACGCTCTTA	TAAGACTATC	AAATCTCATA	60
AGCTTGCACA	ACACCCAACA	ACTTACAAGT	ATCATCGCCA	CTCATGATCC	TATTGTCTTA	120
GATAGTTGCG	AATGGGTATT	GCTCCTTAAG	AATGGCAACA	TTGCTCAATA	CAAACCTTTA	180
AATTCTATAT	TAAAATCTGT	AGCTAAACT	TTTAACTTTA	AAGAAAAACC	AACCACAAAA	240
GACTTATTAG	CGTTACTAAA	GGATATT				267

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79

GTGAAAACCT	TAGGATTGTC	TCGCTTGGT	GGGACTTTAG	AATTTACGA	TTTTATCATC	60
TTTGTAATTT	TTACAAGTAT	CATTGCCAAA	CACTTTTTCC	CAAACACGCT	TAGCCCTATC	120
TGGTCTGAAA	TCAACACTTA	TGGGATCTTT	GCTGCAGGTT	ATCTGGCGCG	CCCGCTTGGT	180
GGCATAAGTGA	TGGCCCACTT	TGGGGATAAA	TTCGGTCGTA	AAAACATGTT	CATGCTCTCT	240
ATTTTATTAA	TGGTAATCCC	AACCTTTGCG	CTAGCTTTGA	TGCCAACTTT	TAATGATTTG	300
GTGGGTTTTG	GCGTGGATAG	CATGGGGCTT	ACCCCTAAAA	ACGCTCATT	TCCTGGTTAC	360
ATAGCTCCTG	TTTTTTTTRGT	RCTTGTTAGG	ATTTGTCAAG	GCGTCGCTGT	GGGTGGTGAA	420
TTGCCTGGCG	CTTGGGTTTT	TGTCCATGAA	CATGCCCCAC	AAGGACAAAA	AAACACTTAT	480
ATCGGTTTTT	TAACCGCTTC	CGTAGTTTCT	GGGATTTTGC	TTGGGAGTTT	GGTTTATATC	540
GGGATTTACA	TGGTTTTTGA	CAAGCCTGTT	GTTGAAGATT	GGGCTTGGCG	GGTTGCCTTT	600
GGCCTTGGAG	GAATTTTTGG	TATCATTTCT	GTGTATTTGA	GGCGCTTTTT	AGAAGAAACT	660
CCCGTTTTTC	AGCAAATGAA	GCAGGGACGA	TGCCTTAGTC	AAATCCCCGC	T	711

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1413

SUBSTITUTE SHEET (RULE 26)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80

ATGCGCAAAT	TTTTGGATGG	GGCAAAAAGT	GAGGTTTTTA	AATACGATGT	GATTTCTTTT	60
GATATTTTGG	ATACCTCCT	TCTAAGACCT	TTCATTAAAC	CCACAGATT	ATTTTGTAT	120
ATTGAGACTA	AATACAATAT	TAAAGGTTTT	CATCAAGCAA	GGATCCTGGC	AGAAATGCAA	180
TCCAGAAAAT	TAAGTAAAAG	ACAAGACATT	ACTCTAGATG	AAATTATCA	TCAAATCCCA	240
AAAGAGTTTC	ATTCATATAA	GGGAGTAGAA	ATCGCTACTG	AAAAAGAGGT	GCTTGTCCA	300
AACCTGGAGA	TGTTAGAACT	CTATCGTTTC	GCTAAAGAGA	ACAATAAGAG	AGTGATTATT	360
GTATCAGATA	TGTATTTACC	TTTAGAGGTT	CTTGAAGATA	TTTTAATTTT	TAAGGGTTTT	420
GATGGTTATA	CAAATTTCTA	TCTTAGTAAC	CATATAATGC	TCACTAAACA	TTCAAAGGAT	480
TTGTTTAAGC	ATGTTTTTAA	ACAAGAAAAT	ATTACTAATA	CGCAGATATT	GCATATCGGT	540
GATAATCTTT	GGGCAGATGA	CGCTATGCCT	AAAAGTTTAG	GCATAGCAAC	GCTATTTAGA	600
AAAAGCGTGT	TGAAACAATT	AGAAGAAGTT	TTTCCTAAAT	ACAAAACATT	TAATCCAACC	660
AGTGTGCGC	AAAGTTTTAT	TTTAGGATCT	TTATGCGTTT	TTTATAAAAA	TTATATTCAA	720
AAACATGAAA	AATTTGATTA	TTGGTTTCTT	TTAGGAGCGA	TGCAGGCAGG	AATTGCAGCC	780
GTTGCTTATT	GCCAGTTTAT	CTATAAGGAG	ATTACAAAA	GAAATATTGA	TACTTTAGTG	840
TTTGTGCGC	GAGATGGTTA	TTTATTGCAA	AAAATTTTTA	ATATTTTATA	TCCAAATTCA	900
TATAAACTA	CTTATGCTA	TGCTCCCGA	ATTTTAAAA	AAGCGGTATT	TTTAGAAGTC	960
GTAGAGGGCG	AGAGTTTGA	AATTTTGCCT	ATTTTAGAAG	GCGAAGAAGA	AGTTAAAAAG	1020
AAGCAAATCA	CCACCAACCA	ACAGGCGTAT	GTATATCTCT	ATAGCAATTT	TGAACATTGC	1080
CGCCATTTAG	CGTTAAATG	TTTAGATAAT	TACAGAAAAT	ACTTGTTTTC	ATCAAATTTA	1140
GAAGGAAATA	TCGCTATTGT	AGATACGATT	ACTTTAGGCT	ATTCTTCGCA	AGGGTTAATC	1200
CAAAAAGCTT	TAAATAAAGA	AGTTTTTGGG	TGCTATGTGG	ATCTCCTAAG	AATTTTAAAT	1260
TATGATTGCG	TCAGTTTCTT	ACCTTTTTC	CACCCTAAAC	CCGTTTATTT	TCATAATTGG	1320
GATTTTATGG	AGTTTTTGCT	AACAAGCCCT	GAATACCCTA	TTTTAAATGT	AGAAAATGGC	1380
GTTCCAATCT	TATCAAAAAG	ACGTTTCATC	TTG			1413

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 369 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81

GTGTTGAAAT	TCTTTGAAGA	TTCCAAACAG	CTTAGCACGC	CTATGGGAAA	GAGCGCGGTG	60
GGGATTTTGA	TTTTCCAAGA	TATTGCAGCC	ATTCCCATGC	TTTAAATTTT	GACGATTCTA	120
GGCAGTAAGG	ATTCTCATGT	CAATTTGCTC	ATTCTTAAAA	CCCTTATTTT	AGCGGGGATT	180
ATTTTAATTC	TTTATTATT	GCCTGGAAAA	AAAGGGGCTA	ATCTCATCTT	AGAGCAAGCG	240
AAAGACACGC	GCTTGCTGA	AATCTTTATA	GGCAGGATT	TTAGTGATTG	TTTGACGCGC	300
GGCGGGGTTG	AGCCATTTTT	TTGGGTTTTC	TATGTCCTTG	GGGGCGTTCA	TTGTGGGCAT	360
GGCGATTTT						369

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 777 base pairs

162

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82

ATGATTTTAG	CCCTTTTGAT	TTCTAAAGAA	AAAACGCATT	TAGAAGCGTT	GTATTATTTG	60
AGCTATGGCG	TGCTTTTAGG	GGGCGTGGCT	CAAATCTTAT	TACACTTTTA	TCCTTTAGTA	120
AAATTAGGCT	TATGGGATTT	ATTATTTAA	GGGTTGTTGG	GTTTAAAGAC	TAAAAATACA	180
AACAAAAAAG	AATATCGTTT	GAATAGGGCT	AAAAAGGATC	TAAAAGCGTT	TTTCAAGCAA	240
TTCTTCCCCA	GCGTCTTAGG	CAATTCTAGC	GCTCAGATCG	CTTCTTTTTT	AGACACCACA	300
ATCGCTTCTT	TTCTGGCGAG	CGGGAGCGTG	TCTTATTTGT	ATTACGCCAA	TAGAGTCTTC	360
CAGCTCCCTT	TAGCCTTATT	CGCTATCGCT	ATCTCCACAG	CTCTTTTCCC	TAGCATTGCG	420
ATCGCGCTTA	AAAACAACCA	GCAGGATTTA	ATCTTACAAC	GCTTGCAAAA	GGCGTGGTTT	480
TTTTTGGTGG	GGGTTTTGCT	TCTTTGCAGC	ATTGGGGGGA	TAATGTTAAG	CAAAGAAATC	540
ACCGAACTTT	TATTTGAAAG	GGGGCAATTT	AGCCCTAAAG	ACACCCCTAAT	CAC TTCGCAA	600
GTCTTTTCGC	TCTATCTTTT	AGGCTTGCTC	CCTTTTGGGC	TAACCAAAC	CTTTTCTTTA	660
TGGCTTTTATG	CGAAATTAGA	GCAAAAAAAA	GCGGCTAAAA	TCTCTTTAAT	TTTCGCTTTT	720
TTAGGTTTAG	CGGCTTCTTT	GAGTTTAATG	CCTTTGTTAG	GGGTTTTGGG	TTTGCCT	777

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83

GTGCTAAAT	ACCCTACRRT	GTTTCATGTG	GCGGATGCGG	TCATTATCAG	TAAGGCGGAC	60
ATGATTGAAG	TGTTTAATTT	TAGGGTTTCT	CAAGTCAAAG	AAGACATGCA	AAAATTAAAG	120
CCTGAAGCGC	CCATTTTTTT	AATGAGCTCC	AAAGACCCCTA	AAAGCTTGGA	AGATTTTAAA	180
AATTTCTTTT	TAGAAAAAAA	GCGTGAAAAT	TACCAATCCA	CGCATTCGTT	T	231

(2) INFORMATION FOR SEQ ID NO:84:

SUBSTITUTE SHEET (RULE 26)

163

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 540 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...540
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84

ATGCTGCTTT	GCGCGGAAG	GAATGAGACT	TTAAAAAAG	CGGTGCCTAT	TGGTGTGGGC	60
TTGATAGAGA	GCGCGATCAA	TTTAACGAGA	ATGTGCCTTA	AAAACCCTGA	TACAGAAAGC	120
CTTATTTTTA	TAGGGAGCGC	GGGGAGTTAT	AGCCCAGAAA	CGGAGATTTT	GAGCGTGTTC	180
GAAAGCATTG	AAGGCTATCA	AATTGAAGAG	AGTTTTCAGC	ATTTAAACAG	CTACACGCCT	240
TTGGATAATT	TCATTACAT	AGAACTAAA	GAGCAGGCTC	TTTTTGAAAG	GGTGCCTGTG	300
AATAGCAGTA	ACTACATCCA	CACCAGCGAA	ATGTTTGCTA	AAAAAATGGT	TCAAAAGGGC	360
GTTTTATTAG	AAAACATGGA	GTTTTTTAGC	GTCTTAAGCG	TGGCTAAAAT	TTTTTCTTTA	420
AAGGCTAAAG	GGATTTTTTG	CGTGAGCAAT	CATGTAGGGC	TTAACGCGCA	TAAGGAATTT	480
AAAGAAAACC	ACGCCAAAGT	CAAACAGATT	CTAGAAAACA	TCATTGATAG	TTTGATAGTT	540

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 639 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...639
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85

GTGTATGAAG	AAAGGATCAC	TCTGGCTTCT	CAAGGGATCC	CTAAAACGAG	TAAAGTGGGC	60
TTTGAAATCT	TTGACACTAA	AGACTTTGGG	GCGACTGATT	TTGATCAAAA	CATCAAATC	120
ATTCGCGCCA	TTGAGGGGGA	ATTGTCGCGC	ACGATTGAAA	GTTTAAACCC	CATTCTTAA	180
GCCAATGTGC	ATATTGCAAT	CCCTAAAGAC	AGCGTGTTCG	TGGCTAAAGA	AGTCCCTCCT	240
AGCGCTTCAG	TGATGCTCAA	GCTTAAGCCT	GACATGAAGC	TTTCACCCAC	TCAAATTTTA	300
GGGATTAAAA	ATTTAATCGC	TGCAGCTGTG	CCTAAACTCA	CGATAGAAAA	CGTGAAAATC	360
GTGAATGAAA	ATGGCGAATC	AATAGGCGAG	GGCGATATAC	TAGAAAACCTC	CAAAGAATTA	420
GCCTTAGAGC	AATTGCGCTA	CAAACAAAAT	TTTGAAAACA	TTTTAGAAAA	TAAGATCGTC	480
AATATCTTAG	CCCCTATTGT	GGGGRGTAAA	AACAARGTRG	TCRCAARRGT	CAATRCGGAG	540
TTTRATTCA	RCCAAAAGAA	AAGCACCAAA	GAGACTTTTG	ATCCCAATAA	TGTCGGTAAG	600

SUBSTITUTE SHEET (RULE 26)

164

GAGCGAGCAA AATTTAGAAG AAAAAAAGA AGGCGCTCC

639

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86

GTGATAARGA AAGGCTATAT AAGAGGAGAT CTTATGCGTA TAGTTAGAAA TTTATTTCTT	60
GTATCGTTTG TGGCGTATAG TAGTGCGTTC GCAGCGGATT TAGAAACCGG AACCAAAAAC	120
GACAAAAAGA GCGGTAAAAA ATTTTACAAA CTCCATAAAA ACCATGGCTC AGAAACCGAG	180
ACTAAAAACG ATAAAAAGCT TTATGATTTC ACTAAAAATA GCGGATTAGA AGGCGTGGAT	240
TTAGAAAAAA GCCCTAACCT TAAAAGCCAT AAAAAAGCG ATAAAAAGTT TTATAACAA	300
CTCGCTAAAA ACAATATCGC TGAAGGGGTG AGCATGCCGA TTGTGAATTT CAATAAGCC	360
CTATCTTTTG GGCCTTATTT TGAAAGGACT AAAAGCAAAA AAACCAATA CATGGACGGC	420
GGGTTGATGA TGCACATCCG TTTT	444

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87

GTGATGATCG ATCCCAAAAT GGTGGAATTT AGCATTTATG CGGACATCCC TCATTTACTC	60
ACGCCCATTA TCACTGACCC TAAAAAAGCT ATCGGGGCTT TGCAAAGCGT GGCTAAAGAA	120
ATGGAGCGCC GATACTCTTT AATGAGCGAA TACAAGGTTA AAACCATGA TTCTTATAAT	180
GAACAAGCCC AAAGTAACGR CGTTGAAGCG TTCCCTATT TGATTCTGGT GATTGATGAA	240
TTAGCGGATT TGATGATGAC AGGGGGCAAA GAAGCGGAGT TTCCTATCGC TAGAATCGCT	300
CAATGGGGC GAGCGAGCGG CTTGCACCTC ATTGTGGCGA CCCAACGCCC GAGCGTGGAT	360

SUBSTITUTE SHEET (RULE 26)

165

GTCGTAACCG	GCTTGATTAA	AACCAACTTG	CCTTCAAGGG	TGAGTTTTAG	GGTAGGCACT	420
AAGATTGATT	CTAAAGTGAT	TTTAGACACC	GATGGGGCGC	AAAGCTTACT	AGGAAGGGGC	480
GATATGCTCT	TTACCCCCC	AGGAACAAAC	GGGTTAGTGC	GCTTGCATGC	CCCCTTTGCC	540
ACTGAAGATG	AAATCAAAAA	AATCGTGGAT	TTTATTAAAG	CCCAAAAAGA	GGTGGAATAC	600
GATAAAGATT	TCTTGCTAGA	AGAATCGCGC	ATGCCTTTAG	ACACCCCTAA	CTATCAAGGC	660
GATGACATTC	TAGAAAGGGC	TAAAGCGGTG	ATTTTAGAAA	AAAAGATCAC	TTCTACGAGC	720
TTTTTACAAC	GCCAATTAAA	AATCGGCTAC	AACCAAGCCG	CCACCATTAC	TGACGAATTA	780
GAAGCTCAAG	GCTTCTATC	CCCAAGAAAC	GCCAAAGGCA	ACAGAGAGAT	TTTGCAAAAT	840
TTT						843

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88

ATGAATTTTT	TTAAATCCT	TTAATGGAG	TTAAGAGCCA	TTGTTTCTCA	TAAGGGCGTT	60
TTATTGATCC	TTATAGGCGC	TCCTTTAATC	TATGGCTTGT	TATACCCTTT	GCCTTATTTG	120
AAAGACATCG	TAACGCAGCA	AAAAATCGCC	CTTGTAGATG	AAGACAATTC	CTTCCTTTCT	180
AGGCAATTAG	CCTTCATGGT	GCAAAGCTCC	AACGAGTTAG	AAATCGCTTT	CTTAGCCCCC	240
TCTATGCTGG	AAGCCAAAAA	GCTTTTAAAA	GAAGAAAAAA	TTTATGGGAT	CTTACACATT	300
CCCTCTCAT	TTGAAGCCAA	TATTTATAAA	CAAAGTGCCT	GTAACGATAG	ATTTTATGTC	360
GAACGCCAAT	TACTTTTGA	TTTATGGTGC	GTTAGCGAAT	GCGGTGGTGG	GGAGCATCAA	420
CGCCTTAAAC	GA					432

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...219

166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89

GTGGGGGGCT	TAGCCATGCT	GGGCTTTTTT	TATAATATTG	AAAAAATTTT	GCTCGCCACA	60
GCGACGGCTT	TCTCGCAATG	CGCGCCTAWT	TATACGGTGC	TCCTTTCCCC	TTTGCTTTTG	120
AAAGAAAAGC	TCAAAAGAAG	CGCGTTAATT	TCCGCATGCA	TCGGGCTAGT	GGGGGTGGTG	180
TTGATTTCAG	ATCCTAGCGT	GGAAAATGTA	GGACCTAGT			219

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 933 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90

GTGTGCTGGA	CGGATTGAT	TCAAGGGCTT	TTGATGATGA	GCGCTTTAAT	CGTGGTGCCG	60
ATTGTTATGA	TAATCCATCT	TGGAGGGGAT	GGAGAGGGGA	TTAAAATCAT	TAGAGAGATC	120
AAGCCTGAAA	ACCTWTCTTT	CTSGCAAGGC	TCTAGCGTAG	TCGCTATTAT	TTCAAGCCTT	180
GCTTGGGGGT	TAGGCTATTT	TGGGCAACCC	CATATTTTAG	TGCGCTTCAT	GTCTATCCGC	240
TCCATTAGAG	ATGTGCCTAA	AGCGACCACT	ATTGGGATTT	CTTGATGGT	TATTTCTTTA	300
ATTGGGGCAT	GCGTTATGGG	GCTTTTAGGC	GTTGCTTATG	TACATAAATY	TGACTTGAGT	360
TTAGAAGACC	CTGAAAAGAT	TTTCATTGTA	ATGAGTCAAT	TGCTCTTTAA	CCCTTGGATC	420
ACAGGCATTT	TATTGAGCGC	GATTTTAGCG	GCGGTGATGA	GCACGGCCAG	TTCGCAACTG	480
CTTGTAAGCT	CTTCTACCAT	TGCTGAAGAT	TTCTATGCGA	CGATTTTCAA	TAAAAACGCC	540
CCCCAAAAAT	TAGTGATGAC	GATTTCTAGG	CTTTCGGTTT	TAGGGGTGGC	TTGCATCGCT	600
TTTTTCATTT	CAACGGATAA	AAACGCTAGC	ATCCTCAGCA	TCGTGAGTTA	CGCATGGGCT	660
GGCTTTGGCG	CGAGTTTGGG	CTCTGTGATT	TTGTTTTCAC	TTTTTTGGTC	AAGAATGACG	720
CGCATTGGCG	CGATTGCTGG	CATGCTCTCT	GGGGCTAGCA	CGGTGATTTT	ATACGATAAA	780
TTTGCCAAAA	GCTTTTGGGA	TATTTATGAA	ATCGTTCCGG	GCTTTATTGT	AGCGAGCGTA	840
GCTATTGTTG	CGTTTAGTTT	GTTTCTAGC	GTGCGATCAG	GCACTAAAGA	GGCCTTTGAA	900
ACCATGCTTA	AAGAAATTGA	GAGCTTAAAG	CAT			933

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

167

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91

GTGGGGCTTT TTATCGTTTT GTTTTAAATT ATAATGAAGC ACCAAACCTC CCCCTATGCT	60
TTCACGCATA ATCAAGCCCT TGTCACCTCA ACCCCCCCTT ATTCACGCA ACTCACTATC	120
CCTAAACCAA ATGACGCTTT AAGCGCGCAT GCGAGCTCTT TAATCAGCTT GCCTAACGAC	180
AATCTTTTGA GCGCTTATTT TAGCGGCACT AAAGAAGGGG CAAGGGATGT GAAAATCAGC	240
GCGAATCTTT TTGACAGCAA GACTAATCGC TGGAGCGAAG CCTTCATTCT TTTAACCAA	300
GAAGAGCTTT CTCATCATTC GCATGAATAC ATCAAAAAA TTAGG	345

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92

ATGCTGTAG GGCCAACAGG CGTGGGGAAA ACGACGACTT TGGCTAAATT AGCCGCACGC	60
TATTCTAGAA TGCTGGCTAA AAAATACAAG GTGGGCATTA TCACTTTAGA CAATTATCGC	120
ATTGGGGCTT TGGAGCAATT GAGTTGGTAT GCTAATAAAA TGAAAATGAG TATAGAAGCG	180
GTGATTGACG CTAAGGATTT TGCTAAAGAA ATTGAAGCTT TGGAATACTG CGATTTTATT	240
TTAGTGGATA CGACAGGGCA TTCGCAATAC GATAAGGAAA AAATTGCCCG TTTGAAAGAG	300
TTTATAGATG GGGGTATATA TATTGATGTA TCCTTAGTGC TTTCGGTTAC CACTAAGTAT	360
GAAGACATGA AAGATATTTA TGATTCTTTT GGGGTGTTAG GGATTGACAC TTTAATCTTT	420
ACGAAATTAG ATGAGACTAG GGGGTAGGG AATTGTTTT CTTTAGTGCA TGAAAGCCAA	480
AAGCCTATCA GTTATCTTTC TGTCGGCCAA GAAGTGCCTA TGGATTTGAA AGTGGCTACT	540
AATGAGTATT TAGTGGATTG CATGCTAGAT GGCTTAGTA ACCCTAATAA GGAACAAGCA	600

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 792 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

SUBSTITUTE SHEET (RULE 26)

168

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93

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GTGGGAGGAG CGAGCTTTAT TTCTGGGGGC AATGGCACGC TTTATGGCTT GAATGTGGGC      60
TATGACCGAT TGGTTAAAAG CGTGATCCTT GGGGGTTATG TGGCTTATGG CTATAGCGGT      120
TTTAACGGGA ACATCATGCA TTCTTTGGCT AATAATGTGG ATGTGGGGAT GTATGCGAGG      180
GCTTTTTTGA AAAGAAACGA ATTCACTTTG AGCGCGAATG AAACCTTATG AGGCAATGCG      240
AGTCATATCA ATTCTTCTAA TTCCTTGCTC TCTGTGTGA ACCAACGCTA CAACTACAAC      300
ACCTGGACAA CGAGCGTGAA TGGGAATTAC GGCTATGATT TCATGTTCAA AAAAAAAGC      360
GTGGTGCTAA AACCTCAAGT GGGCTTGAGC TATCATTTCA TAGGCTTGAG CGGGATGAAA      420
GGTAAAATGC AAAATCCAGC TTACCAACAA TTCGTCATGC ATTCAAACCC TTCTAACGAA      480
TCGGTTTTAA CGCTCAACAT GGGGTTAGAG AGCCGTAAAT ATTTTGGTAA AAATTCCTAT      540
TATTTTGTAA CGGCGAGGTT GGGTAGGGAT CTTTGTATCA AAGCTAAAGG CGACAATGTG      600
GTGCGTTTTG TGGGTGAAAA CACTTTATTG TACCGCAAGG GGGAAATTTT TAACACTTTT      660
GCGAGCGTGA TCACAGGAGG CGAAATGCAT TTGTGGCGTT TGATGTATGT GAATGCGGGG      720
GTGGGGCTTA AAATGGGCTT GCAATACCAA GATCTTAATA TCACTGGGAA TGTGGGCATG      780
CGAGTGGCGT TT                                     792

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(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1017 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94

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ATGGACGGCT ATGGGTTTAA AATGCAAGAC TTGGGCCAAA AAACCTCAAGT TATCCAACAC      60
ATCTTTGCCG GGGATGATGT GAGCGCTTTA GAAGTCAAAG AAAATGAATG CGTTAAAATC      120
RTGACTGGAG CGATGGTGCC AAAGGGGAATA GAAACGATTG TTCCCATAGA ATGCATGCTA      180
GAGAGTCATA AAGATTTCCG CCTAGCTCCT AAAGATTTTA AAATTCACGC TAATATCCGT      240
CAAAAGGGCG AGAACGCTTC TTAAACAGC GTTTTAGTCC CTAAAAATAC CCGTTTGAAT      300
TATGGCCATA TCGCGCTCAT TGCCTCTCAA GGGTTCAAAG AAATCAAAGC GTTTAGAAAA      360
TTAAAAATCG CTCTCTTTAG TAGCGGCGAT GAATTAGTGC CTTTAGGGCA AAACGCCCTA      420
GAGTGCCAGG TTTATGATGT TAATTCAGTG GGTGTTTTTA ACATGCTTAA AAACCTACAAC      480
ACGCATTTTC TAGGGGTTTT AAAAGATGAT AAAAATTTAC AGCTTAAAT ACTTGAATTG      540
CAAGGCTATG ATGTCATCCT TTCAAGTCG GGGGTGAGCG TAGGGGATAA AGACTTTTTT      600
AAAGACGCTT TGAAAGAAAG AAACGCCCTT TTTTATTACG AAAAAGTCAA TCTCAAACCT      660
GGAAAGCCGG TAACTTTAGC CCAACTCAAT CAAAGCATT AATTATAGGCTT ACCGGGTAAT      720
CCTTTAAGTG GCTTACTGGT TTTACGAGTT TTGATTCTAC CCTTATTGGA GCGCTTATCC      780
TTAAATAAAG GTTTTAAATT AAAACCCCTT AAGGCTCAAA TCAATGCCCC TTAAAGCTT      840
ATAACAAAC ATGACGCATT AATCTTAGGC AACTATTCAA ACCACCAATT CATTCCCTAC      900
AACACCGCT ATGAATCAGG AGCGATTCAA GCCCTTGCGC AAGTGGATT TATCRCTTTA      960
ATTGATGAAG GAGTGGGATT GGTTCAGGGC GAAATTGAAA TTTTAAGGTT TGAAAAAT      1017

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SUBSTITUTE SHEET (RULE 26)

169

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95

ATGCCATACG CCTTAAGAAA AAGATTTTTC AAACGCCTTT TATTGTTTTT TTAAATTGTT	60
TGTATGATAA ATTTGCATGC CAAAAGCTAT CTGTTTTCTC CTTTGCCCCC AGCGCACCAG	120
CAAATCATTA AGACAGAGCC TTGCTCTTTG GAGTGCTTGA AAGACTTGAT GCTGCAAAAT	180
CAAATCTTTT CTTTGTATC CCAATACGAT GATAACAACC AAGATGAGAG CCTTAAAACT	240
TATTACAAGG ACATCTTAAA CAAACTCAAC CCCGTATTCA TCGCTTCTCA AACTCCAGCT	300
AAAGAAAGCT ATGAGCCTAA GATTGAATTA GCGATTTTAC TGCCTAAAAA GGTGGTGGGC	360
CGTTATGCGA TTTTAGTGAT GAACACCCTT TTAGCGTATT TTGAACACCA GAAACAACGA	420
TTTCAATATC CAAGTCTT	438

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96

ATGCCATTAA ACCCTCTCTA TCTTTTCCCC AATCTTTTTA CCGCTAGCAG TATTTTTTTA	60
GGCATGATGA GTATTTTTTA CGTTCCAGT TACCAATTTG TCATGGCGTG TTGGTTAGTG	120
GTGGCGAGTC TTATTTTAGA TGGGCTTGAT GGGCGTGTG CAAGGCTTAC CAAACACCAC	180

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

170

- (A) LENGTH: 699 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...699

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97

ATGCTTTCAG	CCITGCTTTC	TAAATGGGG	ACTTACGCCT	TATTACGCTT	CTTGCTCCCG	60
CTTTTTCCTG	AACITTCAGA	AATTTATTTA	ACCCCATAG	CCATTGTGGC	GCTGTGCATG	120
ATCATTTATG	GAGGTTTTCT	AGCCTACGCT	CAAAAAGATT	TAAAAACCT	CATCGCTTAT	180
AGCTCTTCT	CGCATGGG	AGTCGTGGTG	CTTGGGGTTT	TTTCTTTCAA	TGTTGAAGGG	240
GTTCAGGGG	CGGTGTTTAT	GATGTTTGGC	CATGGCGTTA	TCGTCATGGG	ATTATTTTAA	300
CTCGCTGGTA	TCITGGAAGA	ACGCGCCAGC	AGTTTAGAAA	TCGCTCGCTT	TGGATCGATC	360
GCTAAAAGCG	CTCCTGTTTT	TGCAGCCTTT	TTTATGATCG	TTTTAATGGC	GAATGTGGGC	420
ATGCCTTTAA	GCATGTGTTT	TGTGGGAGAG	TTTTTGARCT	TGTTAGGGTT	TTTTGCCACT	480
TACCCTCTTT	TGGCTATCAT	TGCCGGGACA	AGCCTCATTC	TATCAGCGGT	TTACATRCTC	540
ACTTCATATA	AAGATGTGTT	CTTTGGCAAC	TTAAAAACCG	GGAACAACCA	AATCAGCGTG	600
TTTGAAGATT	TAAACGCTCG	TGAGGTAGGG	GTTTTAAGCG	TGATTTTAGC	CTTTGATCTT	660
AATTTTAGGG	ATTTATYCYA	AAGCGCTTTT	AAAACCGAT			699

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...96

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98

GTGGAATTGA	TTAGCAATAA	CCCTAACGCC	AGCCAACAAT	CTATCGTTAT	TCCTTTGGAG	60
ACTTTTGCCT	TGGCGCGAGC	GTTAAAGGGA	ATCTTT			96

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs

SUBSTITUTE SHEET (RULE 26)

171

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99

ATGAAATTT TTGGGACTGA TGGCGTGAGG GGTAAAGCAG GGGTGAAACT CACCCCCATG	60
TTTGTGATGC GTTTAGGCAT TGCTGCCGGA TTGTATTTTA AAAACATTTC TCAAACGAAT	120
AAAATTCTAA TCGGTAAAGA CACCAGAAAG AGCGGCTATA TGGTAGAAAA CGCTTTAGTG	180
AGCGCTCTCA CTTCATAGG CTATAATGTG ATCCAAATAG GGCCTATGCC TACCCCTGCG	240
ATCGCTTTT TAACCGAAGA CATGCGCTGT GATGCGGGCA TTATGATAAG CGCGAGCCAC	300
AACCCTTTGG AAGACAATGG CATCAAGTTT TTCAATTCCT ATGGTTATAA ACTCAAAGAA	360
GAAGAAGAAA GAGCGATTGA AGAAATCTTT CATGATGAAG AATTACTGCA TTCTAGCTAT	420
AAAGTGGGCG AGAGCGTCGG TAGCGCTAAA AGGATAGACG ATGTGATAGG GCCGCTATAT	480
CGCGCATTTG AAGCACTCTY TYCCCAAACA TTT	513

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...99

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100

GTGCGAGCCG TGTTTGCTTT TGGTTTGAAA GCGGCGTTTT GTATAGGGAT TTTTCTAT	60
GCGGCTTATT ATTTCTAGA TGAGTTTTTA ATCAAGCTC	99

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

172

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...210
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101

GTGAGGAGCG GTAAAAGATT AGGCTATACC AATCAAGTGA TCACCGATAT TGTCATATC	60
GGTATTGGGG GGTACAGATT AGGCGCTTTA ATGGTTTGCA CCGCCCTAAA ACGCTACGGC	120
CACCCAAGAT TARRAATGCA TTTTGTGTCT AATGTGGAAT GGCACGCAGA TTTTAGACGT	180
TTTGGAAAAA ATCAACCCGG CCAGCGCGCT	210

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 390 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...390
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102

ATGAATCTTG TCTTTTGTG GGCCGCTCTA GGAGGGGCTA TAGGGAGCTC GTTAAGGTAT	60
TTTGTGGGCA AAATGATGCC CAGTAAATTT TTAATGTTTG AAAGTTTCCC TTTAGGGACT	120
TTTAGCGTGA ATCTCATAGG GTGTTTATC ATCGGCTTTA TGGGGCATTT GGCCGCTAAA	180
AAAGTTTTTG GTGATGATTT TGGGATTTTC TTTGTAACCG GAGTTTTAGG GGTTTTACG	240
ACCTTTTCTT CTTATGGGTT AGACACTTTA AAACCTTGC AAAAATCCCA ATACCTTGAA	300
GCCATTTCTT ATGCTTAGG CACTAACCTT TTAGGCTTA TTGGGGTAGC TATCGGTTGG	360
TTTTTGCTA AGAATTTTGT AGGCGTTAAT	390

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 237 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

SUBSTITUTE SHEET (RULE 26)

173

- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...237
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103

ATGTTGGA	AACTGATTGA	AAGAGTGTG	TTTGCCACTC	GTTGGTTGCT	AGCCCCTTTA	60
TGCATTGCCA	TGTCGTTAGT	GTTGGTGGTT	TTAGGCTATG	TGTTTCATGAA	AGAGTTGTGG	120
CACATGCTCA	GCCATTARA	CACCATTAGT	GAAACGGATT	TGGTTTTATC	AGCCTTAGGT	180
TTAGTGGATT	TGTTGGTTCA	TGGCCGGGCT	TGTTTIGATG	GTGCTGCTCG	CCAGTTA	237

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 306 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...306
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104

ATGCACTATC	AATTACAAG	TTTCAATATA	ATACAAGATC	TTTTTATAAC	TTGTCATGTG	60
TTAAGGATCA	AAATGCGCGT	GTTTGTTTGC	TTTTTAGGGG	TTTTTGATC	TAACGGCTTG	120
GCTCGTTTGG	GCTATGTGGT	TTTAATCCCC	CTACTCATT	TATCAGGGAG	TTTAACCCCA	180
CACCAAAGCT	TCCAAGTGGG	TATTGCGGTG	CTAATGGGCT	ATGTTTTTGG	GAGCTTTTGA	240
ATCCAATTTT	TAAGCCCGTT	AATGTCATTA	SAAAGCATCG	CTAAAATCAG	TTTTAAATTA	300
ACACTT						306

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

174

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105

GTGGATATGA AAGACGCTGT AGGGACTTAT AAACATYTCA GGGCT

45

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3081 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...3081

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106

GTGTGTTT	AGCATCAGGT	TGGAGCAGGC	AAGACTTTGT	GCGCTATAGC	CAGCTGCATG	60
GAACAAAAAC	GCATGGGATT	AGTGAATAAA	ACGCTCATTG	CCGTGCCTAA	CCATTTAACC	120
AAGCAATGGG	GCGATGAATT	TTATAAGGCT	TACCCTAACG	CTAATGTGTT	AGTTGTTGAT	180
AGCAAGGACA	CCACTGAAAA	AGAAAGAGAA	CTTTTATTCA	ATCAAATCGC	TAACAACAAT	240
TATGACGCTG	TGGTTATCGC	GCACACCCAT	TTGGAATTAT	TGTCTAACCC	TAGAGGAATC	300
ATAGAAGAAT	TGAAAGAAGA	AGAGCTAGTG	AATGCTGAAA	AAAACTTTGA	AAGGCAAGAA	360
TTAGCTTTATA	AAAAATAACCC	TAGAGAAACT	AAAAAACCCA	ATGAAAGAGC	CTTTAAAAAC	420
AAGTTGGATA	AAATCCGTGC	TAAATACGAT	GCGATTTTAG	AAAAACAAGG	CTCTCATATT	480
GATATTAGTC	AAATGGGGAT	TGACAAATTTG	ATTGTGGATG	AAGCCCACTT	ATTCAAAAAT	540
CTAGCCCTTG	AAACTTCTAT	GGAAAAAATT	GCAGGACTTG	GTAACCAACA	AGGCTCTAAT	600
CGCGCTAGAG	ATTTGTTTAT	TAAAAACGCGC	TACTTGCATC	AAAACGATAA	GAAAAATCATG	660
TTTTTAACCG	GCACGCCTAT	AGCTAATTCC	TTGAGTGAAA	TGTATCACTT	GCAACGCTAT	720
TTAACCCTTG	ATGTGTTAAA	AGAAAGAGGG	TTAGAATTCT	TTGATGATTG	GGCTAAGACT	780
TATGGGGAAG	TGGTGAATGA	TTTTGAATTA	GACACTTCCG	CTCAAAGTTA	TAAAATGGTT	840
AATCGCTTTT	CTAAATTTAG	CGATGTGCAA	GGCTTAAGCA	CCATGTATAG	AGCTTTTGCG	900
GATATTGTCT	CTAATGATGA	TATTTTAAAG	CATAACCCCC	ACTTTGTGCC	TAAAGTGAT	960
GGGGATAAAC	CTATCAATGT	GGTGGTGAAA	AGAAGCGAAG	AAGTGCTCA	ATTCATGGGA	1020
GTGGCTTTAG	AAAATGGAAA	ATATAATGAA	GGCTCTATCA	TTGATAGGAT	GCAAAAATGC	1080
GAGGGCAAGA	AAAGCCAAAA	AGGGCAAGAC	AATATCCTTT	CTTGCAACAC	AGACGCTAGA	1140
AAAGTGGCTT	TGGATTACCG	CTTGATTGAC	CCTAACGCTA	AAGTAGAAAA	AGAATTTTCT	1200
AAAAGCTATG	CTATGGCAAA	AAATATCTAT	GAGAATTATT	TAGAAACTCA	TGCCACTAAA	1260
GGCACACAAC	TTGGTTTCAT	AGGGCTATCC	ACACCCAAAA	CCCATAGCCA	AAAAGTCAGT	1320
TTAGAAGCGC	TAGATAACGC	TCACGAAACT	GAAAATAAAA	ATCCCCTAGA	TAAAGCTCAA	1380
GAACTTTTAG	AAAGCTTGTC	TAGTTATGAT	GAAAAGGGCA	ATCTTATCGC	TCCTAGCAAG	1440
AAAGAATTAG	AGAACGAGCT	CAAAGAGAAA	GAAGCTAAAA	GCGTCAATTT	AGATGAAGAG	1500
ATAGCTAAAG	GCTGTTCGTT	TGATGTTTAT	AGCGATGTTT	TAAGGCATTT	AGTCCAATG	1560
GGTATCCAC	AAAATGAAAT	CGCTTTCATC	CATGACGCTA	AAACCGAAGA	GCAAAAGCAG	1620
GATTTGTTTA	AAAAGCTCAA	TCGTGGCGGA	GTCAAGGTAT	TATTGGGCAG	TCCTGCTAAA	1680
ATGGGCGTAG	GCACTAATGT	GCAAGAAAGA	TTAGTCGCTA	TGCATGAATT	AGATTGCCCA	1740
TGGAGACCTG	ATGAATTGTT	GCAAAATGGAA	GGGCGTGGGA	TAAGGCAAGG	CAATATTTTA	1800
CACCAAAATG	ATCCTGAAAA	CTTTAGAAATG	AAAAATCTATC	GTTACGCCAC	TGAAAAGACT	1860
TACGATAGCC	GTATGTGGCA	AATCATAGAA	ACTAAATCTA	AAGGCATAGA	GCAATTTAGA	1920
AACGCGCACA	AATTAGGCTT	GAATGAATTA	GAAGACTTTA	ATATGGGTAG	CTCTAATGCG	1980

SUBSTITUTE SHEET (RULE 26)

175

AGCGAGATGA	AAGCAGAAGC	GACAGGCAAT	CCCTTGATTA	TTGAAGAAGT	CAAATTGAGA	2040
GCGGAGATTA	AAAGCGAAGA	ATCAAAATAC	AAAGCCTTCA	ATAAAGAGCA	TTACTTCAAT	2100
GAAGAAAGCT	TAAAAAACAA	CGCTTCTAAA	TTGGATTATC	TAAAACAGGA	ATTGAAAGAT	2160
TTAGAAACGC	TTCAAAGATC	CGTAATAATC	CCCACTCATA	CAGAGATCAA	GCTCTATGAT	2220
TTGAAAAATG	AAGAAAGTAA	GGATTATGAG	CTTATCAAAG	TTAAAGAGGT	AGAGCCTTTA	2280
AAAGAAAACG	CCTCTATGAG	TGAAGAATTA	ACGCACAAGA	AACTCAAAGA	ACAAAACAAG	2340
CAAAATAGCCG	AACAAAATAA	AGAAAAGCTA	GACGCTATTA	AAAAGCAATT	TGCAAGCAAT	2400
TTGAACACCT	TGTTTGTGAA	TGAAGAAGAA	GATTATAAGC	TTTTAGAATA	CAAGGGCTTT	2460
GTGGTGAATG	CTTATAAAAC	TAAGTATCAA	GTGGAGTTTA	GTTTAAGCCC	TAAAGACAAT	2520
CCCAATATTG	CCTATAGCCC	TAGCAATATG	GTTTATAAAA	ACGATACTAT	CAACATGTTT	2580
AGCTCTTATA	ATTTCTGCGC	TGAGATCAAG	TTTGATGGGT	TTTTAAAAAG	GTTGGATAAC	2640
GCTATCACTA	AACTCCCTGA	AAAAATCAAG	GAATTAGAAA	ACTCCATTGA	AATCACGAAA	2700
AAAAATATCG	CTAAATACAC	AAGATTAGTG	GAGCAAAAAC	CTTCTTACCC	ACGACTAGAA	2760
TACCTGCAAG	CTTTAAATG	GGATCATAAA	ACTCTAATAG	ATGATTTAGC	TAAAATGAGC	2820
AAAGACAGAA	ATTATAAGCC	TGCGTTCAAC	CCTAAATCTA	AAGAAGTCTT	AAAGAATTTG	2880
AACGCTGAAA	AAAGAGCGAG	TTTAGAGAAT	GAGAGGGAAG	AGCAAGGGGT	TAAGGGGAAC	2940
ACAAAGAGTC	ATGATGAAAT	AGAGCCAGCT	ACAGAACAAG	TGATTGAAAA	AGAAATAGAA	3000
AAAGGAGATG	AAATCGCTAA	TAATGTTGAT	TACTACGAGA	ACGAACAAGA	AGTGGAATT	3060
ACTAAATCAA	TGGGTAGAAG	A				3081

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107

ATGCGCGAAG	AAGAAAAGAC	CGAACTCCCT	AGCGCGAAAA	AAATCCAAAA	AGCCAGAGAA	60
GAAGGCAATG	TGCCTAAAAG	CATGGAAGTG	GTGGGGGTTT	TTAGGGTTAT	TGGCTGGGCT	120
AATGAGTATT	TTTGTTTTTT	TTATATGGTG	GGTGGGATGG	CTTTAGCGAG	ATGTATCGCC	180
ATGTGT						186

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

SUBSTITUTE SHEET (RULE 26)

176

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108

```

ATGAAAACAC TCGTGAAAAA TACCATATAT TCTTTTTTGC TATTGTCTGT TTTGATGGCA      60
GAAGATATAA CAAGCGGCTT AAAGCAACTG GATAACACCT ACCAAGAGAC CAACCAACAA      120
GTGCTCAAAA ACCTAGATGA GATTTTTTCA ACCACTAGCC CTAGCGCTAA TAATAAAATA      180
GGTCAAGAAG ATGCTCTAAA CATCAAAAAA GCGGCCATTG CTTTGAGAGG AGATTAGCG      240
TTATTGAAAG CCAATTTTGA AGCGAATGAG TTATTTTCA TCTCAGAAGA TGTGATTTTT      300
AAGACTTATA TGTCTAGCCC TGAACCTTTA TTAACCTATA TGAAAATCAA TCCCTTAGAC      360
CAAAGACTG CTGAGCAACA ATGCGGAATA TCCGATAAAG TTTTAGTTCT TTATTGTGAG      420
GGGAAGCTGA AAATCGAGCA AGAAAACAA AATATAAGAG AGCGTTTAGA AACTTCTCTA      480
AAGGCATATC AGAGCAACAT TGGAGGTACA GCTTCCTTAA TCACTGCTTC ACAGACGCTT      540
GTAGAAAGCC TAAAAAATAA AAATTTTCATC AAAGGAATCA AAAAGCTTAT GTTAGCTCAC      600
AACAAAGTCT TTTTAAATTA TTTAGAGGAG TTGGACGCAT TAGAAAGATC CCTAGAACAA      660
AGTAAGCGAC AATACCTACA AGAAAGGCAA TCAAGTAAGA TCATTGTAA A              711

```

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109

```

GTGAGCGAAA AAGACAGGGC GTTCTTTTGA GCGAGCTTGT CTTGCGTGGA TTATGTTGTG      60
GTGTTTGGAG AAGACACGCC CATAAAATTG ATTCAAGCCC TAAAGCCTGA TATTTTAGTC      120
AAGGGAGCGG ACTACCTCAA TAAAGAAGTC ATAGGGAGCG AGTTGGCTAA AGAAACCCGT      180
TTGATAGAAT TTGAAGAAGG TTATTCCACA AGCGCTATCA TAGAAAAAAT TAAAGGACA      240
CATAATGAT

```

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

177

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110

```

GTGTATGACA AATCCTTGTG TAAGACCATG GCGCTAGCGT TGAAGGCTTT AGGCGTTAAA      60
AGGGCGATGG TGTTAATGG AGGGGGGACA GGTGAAATCG TGTGTCATGA CATTACGCAT      120
GCGTGCGAAT TGAAAAATAA CGAAATTTTA GAGTATGATT TGACGCTAA AGATTTTGRT      180
TTRCCCCCT CA                               192

```

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 684 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111

```

ATGCTAGTAG AAATAGAGAA TTTGACTAAA ACTTATGGGA GTTTAAAAGC GCTAGACAAT      60
ATCAGTTTGA AACTACCCAA ACAGCAATTT ATAGGGCTTT TAGGGCCTAA TGGGGCGGGT      120
AAAACCACTC TGTAAAAAAT TTTAGCCGGA TTGAATTTGA ACTATCAAGG GGAAGTGAAA      180
ATTTTAAACC AAAAGATTGG TATAGAGACT AAAAAAAGCG TGGCGTTTTT AAGCGATGGC      240
GATTTTITAG ATCCTAAATT AACGCCCTTA AAAGCGATCG CTTTTTATAA GGATTTTTTT      300
AGCGATTTTG ATGAATCAAA AGCCCTAAAT TTGTTAAAAC GCTTCAGCGT GCCTTTAAAA      360
AGAGAGTTCA AAGCCCTTTC AAAAGGCATG AGGGAAAAAT TGCAGCTGAT TTTAACCCTA      420
TCACGAAACG CTTCTTTGTA TCTTTTGTAT GAGCCGTGGG CTGGGATTGA CCCTATTGCA      480
AGAGAAGAGA TTTTGTAGTT AATCGCTAAG GAGTTTAGCC AAAACGCAAG CTTGCTAGTC      540
TCTACGCATT TGGTGTGGA TGTGAAAAAG TATTTAGACA GCGCGATTTT TTTAAAAGAA      600
GCTAAAGTGG TGGCTTTTGG GGATGTGGGG GAATTAAAAA AAGGGTATAG CAGTTTGGAG      660
GCAGCGTATA AAGAAAGGTT GAAA                               684

```

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 819 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

SUBSTITUTE SHEET (RULE 26)

178

- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...819
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112

ATGAACAAGC	TTTTTTTAGC	TTTATTGTT	GGGGAATGC	TTTTAAGTC	TGATGCTTA	60
AACGATAAGA	TTGAGAATTT	AATGGGGGAG	CGATCCTACC	ACATGAACAA	GCTTTTTTTA	120
GAGCGTTTGT	TTAAAAATCG	TAAGGATTTC	TATGAAATGG	GGCGTTTGGA	TTCTTAAAA	180
CTACTCAACA	CTCTCAAAGA	AAACGGGCTT	TTATCGTTTA	ATTTTGACAA	ACCAAGCGTG	240
TTAAAAATCA	CTTTCAGGC	TTCAAGTAAT	CCCCTAGCGT	TTGCCAAAAG	CATCAACAAT	300
TCTTTGAATA	TGATGGGGTA	TTCGTATGTT	TTGCCTATTA	GAATGCAAAG	CTCTTCAGGC	360
GAGAATGTTT	TTTCATACGA	GCTTAAAACG	GAATACGTTT	TAGACCCTAA	CATTTTGATA	420
GAGACGATGA	AAAGGCATGG	TTTGTATTTT	ATGGATATTA	GACGGGTGTC	TTTAAAGGAG	480
TGGGAATACG	ACTTTGCCTT	ACAAAAGATC	AAGCTCCCTA	ACGCGAGAGC	CTTAGTTTTG	540
AGTAGCGATC	CTGTGGAGTT	TAAGGAAGCG	AGCGGGAAAT	ATTGGCTGAG	CGTGAATCAA	600
AACGCGTATT	TAAAAATAAG	CTCCAATAAC	CCTTTGTGGC	AACCCAAAAT	CATTTTTTAT	660
GATGAAACT	TAAAGATCAT	TCAAATCATT	GCTAAAGAAA	ACAGACAACA	AGAAATCGCT	720
CTTAACTTGC	TTGATGGCGT	GCCTTTTATC	CATATCACTG	ACGCAAAAAA	CCCTATCATT	780
TTAAAAATG	GGATTAGCGT	GGTTTTTGAT	GCGATGCCT			819

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...45
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113

GTGTCTCGCC CGTTCAAAAC GATCAAAAAA CCCCCACAAC CCCCT

45

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

179

- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...201
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114

ATGATCGCTG	TATTACCGCC	CTTGTTTTCT	ATGGGGAGCT	TTGATGAGTG	GATTTATAGG	60
GGGCTTGTGG	CTTTAATGGT	GAGCTGTCCT	TGCGCGTTAG	TGATTTCTGT	GCCTTTAGGG	120
TATTTTGGAG	GCGTGGGAGC	GGCGAGCCGA	AAGGGGATTT	TAATGAAAGG	AGTGCATGTT	180
TTAGAGGGTG	CTTACCCAAA	C				201

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 969 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...969
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115

GTGCAACACT	TCAATTTCCT	CTATAAGAT	TCTTTATTTT	CTATCGCTTT	ATTCACCTTC	60
ATTATCGCTC	TTGTGATTTT	ATTAGAACAG	GCTAGAGCGT	ATTTACCCCG	AAAGAGAAAC	120
AAAAAATTTT	TGCAAAAATT	CGCCCAAAAT	CAAAACGCCT	ATGCGAGCAG	CGAGAATTTA	180
GACGAGCTTT	TAAAGCATGC	TAAAATTTCC	AGTTTGATGT	TTTTAGCTAG	GGCGTATTCT	240
AAAGCGGATG	TGGAAATGAG	CATTGAAATC	TTAAAAGGGC	TTTTGAATCG	CCCCTTAAAA	300
GATGAAGAAA	AAATCGCTGT	TTTAGATTTA	TTGGCTAAAA	ATTATTTTAG	CGTGGGGTAT	360
TTGCAGAAAA	CAAAAGACAC	CGTGAAAGAA	ATTTTGCCT	TTTCCCAAG	GAATGTGGAA	420
GCGTTGTTGA	AGCTTTTGCA	TGCGTATGAA	TTAGAAAAAG	ATTATTCAAA	GGCTTTAGAA	480
ACTTTGGAAT	GTTTGGAAGA	ATTAGAGGTG	CCTAAAATTG	AAACGATTAA	AAATTACCTC	540
TATTTAATGC	ATTTAATAGA	GAATAAGGAA	GATGCGGCTA	AAATCTTGCA	TGTTTCAAAA	600
GCGTCGTTAG	ATTTGAAAAA	AATCGCTCTG	AATCACTTAA	AATCGCATGA	TGAAAATCTT	660
TTTTGGCAAG	AAATTGATAC	AACCGAACGG	CTAGAAAAATG	TGATCGATCT	TTTATGGGAT	720
ATGAATATCC	CTGCTTTTAT	TTTAGAAAAA	CATGCCCTTT	TGCAGGACAT	CGCGCGATCT	780
CAAGGGTTGC	TTTTGGATCA	CAAACCTTGC	CAAATTTTTG	AATTAGAGGT	TTTACGCGCT	840
CTATTGCATA	GCCCTATAAA	AGCGAGTCTG	ACTTTTGAAT	ACCGCTGCAA	GCATTGCAAA	900
CAAATCTTTC	CTTTTGAAAG	CCATAGGTGT	CCTGTGTGTT	ACCAGTTAGC	GTTTATGGAT	960
ATGGTGGCT						969

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

SUBSTITUTE SHEET (RULE 26)

180

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...30
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116

ATGGAACACC TTACAAGGGG AATTAAGCAC

30

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 153 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...153
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117

GTGGTTATCT TAGGCTCRCA TGGCAAGGAA GAGTATTACG CTAGCAAGAT TGCAGCCCCC	60
ATTTTAAAG AAATCACCGA AATTTTAGTG CGTTACAATT ACCTATCGCC CTCTATTGCG	120
ATTCAAAACG CTTTGGA AAAACCGCTTA AAA	153

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 237 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

181

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118

ATGAAAAAGG TTATGTGGC TTAGGCGTT TTGGCGTTCG CAAATGTTTT AATGGCAACC	60
GATGTTAAGG CTCCTGTAAA AGGTTGTGCC GCTTGCCATG GGGTTAAGTT TGAAAAGAAA	120
GCTTTAGGTA AAAGCAAAAT CGTTAACATG ATGAGCGAAA AAGAGATTGA AGAGGATCTT	180
ATGGCTTTTA AAAGCGGTGC CAACAAGAAT CCTGTCATGA CCCGCAAGCT AAAAAAT	237

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119

ATGGGGATTG CAACCACTCT CATCAGTGAG GTTCTAAGT TTTATTACGC TTTAAAATAC	60
CATGCGAAAT TTATGAGCTT GGGGGAGCTT GGGTGCTATG CGAGCCATTA TTCGTTGTGG	120
CAAAAATGCA TAGAGCTCAA TGAAGCGATC TGTATTTTAG AAGACGATAT AACCTTGAAA	180
GAGGATTTTA AAGAGGGCTT GGATTTTTTA GAAAAACACA TCCAAGAGTT AGGCTATGCG	240
CGTTTGATGC ATTTATTGTA TGATGCCAGC GTGAAAAGTG AGCCT	285

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120

SUBSTITUTE SHEET (RULE 26)

182

ATGCACCTTA	AAAGTGGGGC	TGTTTTTATC	TCTGATGCGC	ATTTTTTGCC	CAAAAGCCCT	60
CATTTAATCC	ATACGCTTAA	AGAACTTTTA	AGCGCCAAAC	CCCCGCAAGT	CTTTTTCATG	120
GGCGATATTT	TCCATGTTCT	TGTGGGCTAT	TTACCCCTAG	ATAAAGAGCA	GCAAAAAATC	180
ATTGATTTAA	TCCATGCGTT	GAGCGAAATT	TCACAAGTCT	TTTACTTTGA	AGGCAACCAT	240
GATTTTTTCCA	TGCGTTTTGT	ATTCAATTCC	AAAGTAATGG	TTTTTGAGCG	CCAAAACCAA	300
CCCGCATTTAT	TCCAGTATGA	TAACAAACGC	TTTTTGCTAG	CCCATGGGGA	TTTATTCATC	360
ACTAAAGCGT	ATGAATTTTA	CATCACGCAG	CTCACTTCCA	CTTGGGCTAG	ATTTTTTTTA	420
ACTTTTTTTAA	ATTTATTAAG	TTTTAAAACC	TTATACCCCTT	TT		462

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 939 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...939

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121

GTGCAACCGA	TGAAATCTAA	AAAACCTTTAT	TTAGCTTTAA	TCATAGGGGT	TTTATTAGCG	60
TTTTTAACCC	TATCTTCATG	GCTAGGTAAT	AGCGGTTTAG	TGGGGCGTTT	TGGGGTGTGG	120
TTTGCCGCAA	TCAATAAAAA	ATATTTTGGG	TATCTTTCAT	TGATTAATTT	ACCCTATTTG	180
GCGTGGGTTT	TATTCCTTTT	ATACAGGGCT	AAAAACCCTT	TTACAGAAAT	CGTTTTAGAA	240
AAAACCTTGA	GGCATCTATT	AGGCATTTTA	TCTTTACTCT	TTTTGCAATC	TAGCCTGTTG	300
AATCAAGGGG	AAATCGGCAA	CAGCGCGCGT	TTGTTTTTAC	ACCCTTTTAT	AGGGGACTTT	360
GGGCTTTATG	TGCTGATAAT	GCTTATGGTA	GTTATCTCTT	ATTTAATTTT	ATTCAAACCTG	420
CCCCCTAAAA	GCGTTTTTTA	CCCTTATATG	AACAAAACAC	AAAGCCTTTT	AAAAGAGATT	480
TACAAACAAT	GCTTGCAGGC	CTTTAGCCCT	AATTTTAGCC	TGAAAAAAGA	GGGTTTTGAA	540
AACACCCCAT	CAGATTCTCA	AAAAAAGAA	ACCAACAACG	ACAAAGAAAA	AGAAAACCTC	600
AAAGAAAAAC	CTATTGATGA	AAACCACAAC	ACCCCTAACG	AAGAATCGTT	TTTAGCGATC	660
CCTACCCCTT	ATAACACGAC	CTTAAATAAT	TCAGAGCCGC	AAGAAGGCTT	AGTCCAAATT	720
TCCCCACACC	CCCCTACCCA	TTACACCATT	TACCCTAAAA	GAAACCGATT	TGATGATTTG	780
ACTAACCCCA	CTTTAAAAGA	ACCTAAGCAA	GAAACCAAAG	AAAGAGAACC	CACGCTAAAA	840
AAAGAAACGC	CCACCACACT	CAAACCTATC	ATGCCCATAT	CCGCATCCAC	ACAGAAAAATC	900
ATGACAAAAC	RGAAAACCAC	AAAACCCCTA	ACCACCCCA			939

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 957 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

183

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122

GTGATGTTAA GTAGAGACAT TGTCCAATAT TCCAAGATCC GCACCGAGTT ATACGCCTAC	60
CTCACTTATT TGTTTTCGCA CAATATCCGC AACCACCTTC CTGAAATCAC TTTGGATTAT	120
TTAAACAGGC AAATCAGTAA GATGCAAGCT GAAATCAAAA TGGCAAAAAG TTTTTTGT	180
TTAGACGCTA AGGGCATGCT CATGCTTAAG CCAAGCCAAT TTAAAGAGCA GGGGCATAAG	240
GAAGGGCTAT TAGAGCATGA TTAAACAGAA GGGATTGAAT TAGAATCGCA TGTCAGTTTT	300
AGCGATAAGT ATTATTTTAA TCAAGCCGTG AATGAAAAGC GTTGCATTTT AACCGACCCC	360
TATCCTTCTA AAAAAGGGAA CCATTGTGTA GTGAGCGCGT CTTACCCGGT GTATGATCAA	420
AATAACGATC TAGCGTTTGT GGTGTGCTTG CAAATCCCTT TGAGGGTGGC GATTGAAATC	480
AGCTCGCCTT CAAAGTATTT TAAACTTTT AGCGAAGGGA GCATGGTCAT GTATTTTATG	540
ATTTCTATCA TGCTCACTTT AGTGTGCTG CTTTATTTCG TGAAATGCAT TTCTAGCTTT	600
TGGACAGCGA TCGTGCATTT TAGCAGTTTT GACATTAAAG AAGTGTTCCTA CCCCATTGTG	660
CTTTTAACCC TAGCTTTAGC CACCTTTGAT TTGGTCAAGG CGATTTTGA AGAAGAAGTG	720
TTGGGTAAAA ATAGCGGGGA CAACCACCAT GCGATCCACC GCACCATGAT CAGGTTTTTA	780
GGCTCTATCA TTATCGCATT AGCCATTGAA GCGTTAATGC TCGTGTATA ATTACGCGTG	840
AGCGAGCCGG ATAAATCAC TTATGCGGTG TATTGGCTA TCGGCGTGGC GGTGCTTTTG	900
ATCAGTTTGG CGATTATGT TAAATTCGCT TATAGCGTGT TGCCCAAACG AGAACGC	957

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 354 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123

ATGGTTATAC ATGAAAAAAT CAAAAGCCGC TTTTCTAGGA ATTGGTCTTT AAGGAATAGG	60
GGCAGGCATT TTGCATCTC AAGCGTGTAT TTTTCTCAC TTCTTGTCAT TACAGCGGTT	120
AATAGAAGTA GTGCAGTTG TTGTTATTG ATGCCTGAAC ATTTGATTGG GTGGTTTTTG	180
ATTTCTTTTA GTGGGAATT TGTAGCAGAC ATGGCGTTTG GCAAAAAAAG TAAGATTTT	240
AAAACCCGCT TTGGAATTC TATTGTGAGC GCGTTTCAC TATTGCTTGG CGCTTACCAG	300
CGCTTTTATT TTTGTATGG TTTGGCTTTA TTAATTGGTG GGCTGTCTTT TTTA	354

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 276 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

SUBSTITUTE SHEET (RULE 26)

184

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...276
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124

ATGTTTAAAA GCAGATTAAA TTCATGGATT TTATTAGGGA TTTTAGGGGT TTTAGTGGTG	60
GTTTTTTGGG ATGTCATAAA ATACAAAATA GAAGATTTC AACATGATCA TTATCTATCA	120
CAAGTGAAAG AAAGGGAAGA ATATTATAAA AACCACATAG AAGAAGCTTT GAAAAAGGAT	180
AGCGAATGCT TTGAAAAAGG AGGCGATAAA GTGGATTGCT CGGCTGCTAT GAGAATAGCT	240
GCTGGTGAAA GAAATAGAAG AATGTTAGAG ATTAAA	276

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 414 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...414
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125

ATGGTATTTT GGGGCGCTGT TTTCTTTTGA TGGGATCGAA CGGCATGGAA GCGCTTAATG	60
GTGTTTTTGA ACAGCTTGAW TTYCATGCTT GCGGCCTTGA GTTTGGGGTC GTTTTTAGGG	120
GCGATGGATCA AAAATGAAGC CCACACCACT CAAATCGTTT TGATTTCTTC TTGCCCCTTG	180
ATTTTTATGA TGGGTTTTGT GTGGCCTTTT GAATCCTTGC CCTCTTATTT GCAAGTCTTC	240
GTTCAAATAG TGCCTGCTTA TCATGGGATC AGTTTGCTCG GGCGATTGAA TCAAATGCAT	300
GCGGAATTTA TAGATGTTTC TATCCATTTT TACGCGCTTA TTGCGATTTT TATCGTGAGT	360
TTTATAGGGT GCGTGTTCAA ACTCAGCTCT TTAAAGAAAG CTTGTGAAAA CGCT	414

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 762 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

185

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...762
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126

ATGCATGAGC	AAGGTTCTAT	AAGCTTTT	TAAGGCGACAGG	GAGCTAAAAG	ATTATTATAC	60
ATACTCTACA	AGCTCGCATT	TAATGCTAAG	TCTAATAAGA	TGCCCCTAGA	TAGACATTAC	120
GCCAAAATGT	TTTTGCAAGT	TGTAGCAAGA	ACTCTAATAA	AGAATGTCAA	TATATTAGAA	180
GAGCAAGGTT	TTATTGAAGT	CATTAAAGGA	AAACAAAGAT	ACTTGTATGT	GTATCTTAAA	240
GATTACAGAG	AATTAGAATG	CTTAGTGAAG	AGCAAGATGG	CTAAGTATGT	GATGTATTTA	300
AGACAATTCT	TTGATTATTT	GGATAGAAAA	AGGCGTTATG	GCTTTGATTT	TACGCTTAAA	360
AACCTAGCCT	TTGCTAAGAC	CAAAGAAAGC	TTACCCAGAC	ATTTAAACGA	TAAAGACTTA	420
AAGAGTTTTT	TAAAAACACT	CTTAGACTAT	AAGCCAGCTA	CAAGCTTTGA	AAAACGCAAT	480
AAGTGATTC	TACTTATTGT	AATACTTGGG	GGACTTAGAA	AATGCGAAGT	GTTAAACATA	540
GAATTA AAC	ACATTCAAGT	AGAAGAGCAA	AACACTCTCTA	TTTTAATTCA	AGGTAAAGGT	600
AGAAAAGAGA	GAAAAGCTTA	TATTA AAAAG	AGTTTGTTAG	AACCAAGCTT	GAATGCTTGG	660
ATTAGTGATG	ATTACAGACT	AAAATATTTT	AATGGAGCAT	ATCTCTTAA	AAAGGATAAG	720
CAAAAATCAC	AAAATTCCTT	AACGCTTTAT	AATTTATCCC	CT		762

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 555 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127

GTGGTCTTTA	AAATTTTAAG	TTTATGGTTA	GGGGTGTTTT	GTTTCCTTAG	GGCTACGCAT	60
TTATACITAG	GCGAAGAACC	CAAATATAAA	GACAATTTC	CGCATTTTGA	ATACGCTAAC	120
CCTAACGCTA	GAAAAGGCGG	TGTTTTGAGA	AATGACGCTA	TAGGGACTTT	TGATAGCCTT	180
AACCTTTT	CGCTTAAAGG	CACTAAAGCC	GAAGGCTTGG	ATCTCATTTA	TGACACTTTA	240
ATGGTGCAAA	GCTTAGACGA	ACCTTTTGCA	GAATACCCCT	TAATCGCTAA	AGACGCCGAA	300
GTGGCTAAGG	ATAACAGCTA	TGTGATTTTT	ACCCTAGATA	AAAGAGCGAG	ATTGAGCAAT	360
AACGCTCCCA	TTTTAGCGAG	CGATGTGAAG	TTTAGCTTTG	ATACGATAAT	GAAATTAGGA	420
TCGCCCCCTT	ATAGGCAGTA	TTACCAAGAT	GTTAAAAAGG	CGGTTATCTT	AGACAAGCAC	480
CATGTTAAAT	TCATTTTCAA	AACCACTGAA	AATAAAGAAT	TGCCCCTCAT	TTTAGGGCAG	540
TTGCAGATCT	TTTCC					555

(2) INFORMATION FOR SEQ ID NO:128:

SUBSTITUTE SHEET (RULE 26)

186

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 198 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128

GTGGCCATGA TAGATTGCGC GATTATTGGA GGTGCTCCTG CAGGTTTGAG TCGGGGGCTT	60
TATGCCACTA GAGGCGGTGT TAAAAACGCC GTTTTATTG AAAAAGGAAT GCCTGGGGGG	120
CAAATCACTG CCACTAGTGA GATTGAAAAT TATCCGGGCG TTAAGGAAGT GGTGAGCGGA	180
TTGGATTTC A TGCAACCA	198

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 546 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129

GTGGGGAAAA GCTTGAGATA CAGCTTGAAT TTAGATCTCA ATCAAAAAGC CGATTTGTTT	60
TTCACCGAAT TAGAGCCAAC AGGTCTCACC CTCTCCCCCA TCATGAAACG CTTTACTATC	120
AAAGGCGATT TTGATTCAGG GCTAAAATCC TATGACATGA GCTACATGTA TGCGAGCCTT	180
CAAGCTATAA GCGCGATCAG GAGATTACCC TTAGGGCTTT ATGATGGGGT GCATGTCTAT	240
TCTAAAACGC CCATGAAGGA TATTGAAAAA TTACGCAACG CTTTAAAAAC AATCAACCAC	300
CATGGCATAG GCATTGAAGG GTGGTGSCAA CAAAACGGGA ATTTTCTCTC GCGATGGAA	360
TTGGAAAAAA GAGCGTTATT CATGTGCTC ATGCTCATT TTTTAATGGC GTCTTTGAAT	420
ATCATCAGCT CGCTTTTAAAT GGTGGTGTG AACAGGCGTA AAGAAATCGC CCTACTCTTT	480
AGCATGGGGA GCAGTCAAAA AGAAATCCAA AAAACCTTTT TTTATTGGG TAATATCATT	540
AGTTTA	546

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

187

- (A) LENGTH: 741 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130

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ATGAAAAAAA CTTTTTIGAT CGCTTTAGCG CTTACGGCTT CTCTTATAGG CGCTGAAAAC      60
ACCAAATGGG ATTATAAAAA TAAAGAAAAT GGGCCGCACC GCTGGGACAA ATGACACAAA      120
GATTTTGAAG TGTGCAAAAG CGGTAAAAGC CAATCGCCCA TCAACATTGA GCATTACTAC      180
CACACGCAAG ATAAAGCCGA TTTGCAATTG AAATACGCCG CTTCTAAACC TAAAGCGGTC      240
TTTTTCACCC ACCATACTTT AAAGGCTTCG TTTGAGCCGA CTAACCACAT CAATTATAGA      300
GGGCATGACT ATGTGTTGGA TAATGTGCAT TTCCACGCCC CTATGGAGTT TTTAATCAAT      360
AATAAAACCA GGCCTTTGAG CGCGCATTTC GTGCATAAAG ACGCTAAAGG GCGTTTGTG      420
GTGTTAGCGA TTGTTTGA AGAAGGGAAA GAAACCCCA ACCTTGATCC TATTTTAGAA      480
GGCATTCAAA AGAAACAAA TCTTAAAGAG GTGGCTTTAG ACGCTTCTT GCCTAAAAGC      540
ATCAATTACT ACCATTTTAA CGGCTCTCTC ACCGCTCCTC CTTGCACAGA GGGGGTGGCA      600
TGGTTTGTCA TAGAAGAACC TTTGGAAGTT TCTGCCAAC AATTGGCTGA AATCAAAAAA      660
CGCATGAAAA ATTCGCCCAA CCAACGCCCC GTCCAGCCTG ACTACAACAC CGTGATCATT      720
AAAAGCTCGG CTGAGACCCG C

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(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131

```

ATGAAAATTT CTTTATTGGG GCATGGAAAA ACCACTCTAG CCCTAGGGCG TTTTITTTAAA      60
AAAAACCATA ATGAAGTCAA ATTTTITGAT GATAAATTCC CTGCATTTT TAAGGATAGC      120
GAGGGTTTTT TTTGCTACCC TAGTAAGGAT TTAAACCCTA ATGATTCCCA ACTAGAAATC      180
GTCAGCCCTG GCATTAGTTT CACGCACCCT TTAGTCATGA AAGCCAAGCA TTTAATGAGC      240
GAATACGATT ATATTGATAG TTTGTTTIGAT CATTCTTTCA CGCTACGAT GATAAGTATT      300
AGCGGCACTA ACGGGAAAAC CACCACGACC GAAATGCTCA CCACACTTTT AGAAGATTTT      360
AAGGCTGTGA GTGGGGGGAA TATCGGCACG CCCTTGATTG AATTGTTTGA AAAACGATCC      420

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SUBSTITUTE SHEET (RULE 26)

188

CCCTTGTTGGG	TGCTAGAAAC	AAGCTCCTTT	TCTTTGCATT	ACACTAATAA	GGCTTACCCT	480
TTAATCTACT	TGCTCATCAA	TGTGGAAGCC	GATCATTTGA	CTTGGCATTG	CAATTTTGAA	540
AATTATTTGA	ACGCTAAACT	CAAGGTTTTA	ACATTGATGC	CTAAAACCTC	GCTCGCTATC	600
CTCCCTTTAA	AATTCAAAGA	ACACCCTATT	GTTCAAAAC	CGCAAGCGCA	AAAAATCCTT	660
TTTGACAAAA	GCGAAGAGGT	TTTAGAGTGT	TAAAAAATCC	CTTCTAACGC	CCTTTTTTTT	720
AAGGGAGCGT	TTTTATTAGA	CGCGGCTTTA	GCCCTTTTAG	TTTATGAGCA	ATTTTAAAAA	780
ATAAAGAATT	TAAAAATGGCA	AGATTATAGA	GAAAACGCCC	TTAAAAGACT	GAACGCTTTT	840
AAAATCGGCT	CGCATAAAAT	GGAAGAATTT	AGGGATAAAC	AAGGGCGTTT	GTGGGTAGAT	900
GACAGCAAAG	CCACGAATAT	TGATGCCACC	TTACAAGCCC	TAAAAACCTT	TAAAAACCAA	960
AAAAATCCATT	TGATTTTAGG	GGGCGATATT	AAAGGGGTCA	ATTTAACCCC	CCTTTTTTGAA	1020
GAGTTAAAAA	ACTATAAAAT	AAGCCTTTAT	GCCATAGGAT	CAAGCGCTTC	TATCATACAA	1080
GCCTTAGCGT	TAGAATTIAA	TGTTTCTTGT	CAGGTTTGT	TGAAGTTAGA	AAAAGCGGTT	1140
CAAGAAATTA	AAAGCGTTTT	ATTACAAAAT	GAAGTCGCTT	TGCTTTCACC	TAGCGCGGCC	1200
AGTTTGGATC	AATTTTCTTC	GTATAAAGAA	AGGGGTGAAA	AATTCAAAGC	GTTTGTTTTA	1260
AAAGAT						1266

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132

ATGAAAGAAA	TCATTGTCGC	CCTTGTTGGG	CAGCCTAATG	TGGGGAAATC	GTCCTTAATC	60
AACGCTTTGA	GTAACSCCCA	TTTAAAGTG	GGGAATTTTA	CCGRGGTTAC	CGTGGATAAA	120
ATGGAAGTGA	GTTTGATCCA	WAAAGATCAT	CAARTSWYTM	TC		162

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...333

SUBSTITUTE SHEET (RULE 26)

189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133

GTGCATCGTT TTTCTAGAAA CCCATGCGCA TCTTGCAATC GCGCTCGCTC TTGTTTCGAGA	60
CTATCTCGCT CATTAGTGAG CGCGGTAAC TGGTGGTTGA GCTTGTCGTT TTCGGTGGTT	120
AGTGCTTTAT TTTCTTTAGT CAGCTCGGTG ATTTTATGGG TTAGCTCGGT GTTTTCTCTT	180
TTTAGCCTTT CTTTTCTGT TGTCAATTCT CTTTTTCTT CAGTCAGCCG ATCTCTGGCT	240
GCTAATAAGC GTGTGTTTC TTTAGCTAAA ATGTCCTTTT CCGTTTTTCAG TTCTGCTTTT	300
TCTTTAGTGA GCTTGTTATT GTTTGCCAT AAT	333

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134

ATGCAAAAAA TGGGCGTTGT CTCTTATTCC GTGTTTCAAG CGTTTGAAAA GCCTTTGAGT	60
CGGTTTAAAG AGGGCGTTGT TTTGATTGTG GATTCTTTAA GGCGTTTGAT TATGGGGAGC	120
GCTTCAGTTA AAGAATTGAG TGGGGTAATA GGCATTGTGG GGGCGTTAAG CCATGCCAAT	180
AGCGTGAGCA TGCTTTTGTT GTTTGGGGCG TTTTATCTA TCAATCTAGG GATTTTAAAT	240
TTATTACCCA TTCCAGCCTT AGATGGGGCG CAAATGCTAG GGGTCGTTTT TAAAAATATT	300
TTTCATATCG CTTTGCCAAC GCCCATACAA AATGCGTTGT GGCTAGTGGG GGTGGGGTTT	360
TTGGTTTTTG TCATGTTTTT AGGGCTTTTT AATGACATTA CTCGTTTGCT A	411

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135

SUBSTITUTE SHEET (RULE 26)

190

GTGATGGCTT	TGTTGAAAT	TAGTGTGGTA	GTTCTGAGG	GGGAAGTTTA	TACAGGAGAG	60
GTTAAAAGCG	TGTGTTGCC	AGGAGTGGAA	GGGAATTTC	GGGTGCTTTA	TGGGCATAGC	120
AACATGATCA	CCTTGCTTCA	GGCGGGAGTG	GTTGAGATTG	AAACCGAAAA	CCAAAAAGAG	180
CACATTGCTA	TCAATTGGGG	TTATGCAGAA	GTTACTAATG	AACGGGTGGA	TATTTTAGCC	240
GATGGAGCGG	TCTTTATTAA	AAAAGGATCA	GATGACAGAG	ATGATGCTAT	CTCTAGGGCT	300
AAAAAGCTTT	TAGAGGACGC	AAGCTCTGAC	AGGTTAGCGG	TCTCTAGCGT	GCTGGCTAAG	360
ATTGAGTCTC	TT					372

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136

ATGTATTCTT	TGCTCTTAGA	TTTGAATAAA	AAGACCGCTC	TTTTAGGCAC	AAGAGGGTTT	60
TTTATCGACG	ACAAACACAT	CAAAGAAAAG	GGCTTGACCA	CGCCCACTCT	TTTAGAGCTT	120
TATAGCGATT	TGGAAGAAGC	GATTGCTTTA	AAATGCGAAT	ACTTCATTAT	GGAGGTGAGC	180
TCCCATGCCA	TTGTCCAAAA	CGCATCGCTG	GGCTTGATTT	CGCTCTTAAA	ATTCTCACCA	240
ATATCACAAAG	CGATCATT					258

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137

ATGAAAACGA	ACTTTTATAA	AATTAAATTA	CTATTTGCTT	GGTGTCTTAT	CATTGGCATG	60
TTTAACGCTC	CGCTTAACGC	TGACCAAAAC	ACGGATATAA	AAGATATTAG	TCCTGAAGAT	120

SUBSTITUTE SHEET (RULE 26)

191

ATGGCGCTAA ATAGCGTGGG GCTTGTTTCT AGAGATCAGC TAAAAATAGA GATCCCTAAA	180
GAAACCCTAG AGCAAAAAGT GACCATACTC AATGACTATA ATGATAAGAA TGTTAATATC	240
AAGTTTGACC ACATAAGTTT AGGGAGTTTC CAACCTAATG ATAATCTAGG TATCAATGCG	300
ATGTGGGGCA TTCAAAATCT TCTM	324

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138

ATGATTGATA SCCTTGATGG GGCAAAAGAT GCACAATTGA TAAAAAAGC TTACGCGTTT	60
TTGTGTTT TAGAGCGATGG CACGATTTTA GGGGCTTTAA GAATGACGCA TGCTCACAAT	120
AAGCCATGCT TTGGGGTGAG GATTGGGAAT TTAGGGTTTT TGAGCGCGGT TGAATTGAAC	180
GGGTTGAAAG ATTTCTTACA AGATCTCAAG CAAACAGGA TCAAATTAGA AGAGCATTTG	240
GCTTTGGAGG GCCGTATTGG AAACACTTCT TTTTATGCGA TCAATGAAAT CGTGATCGCT	300
AAAAAAAAG CTTTAGGGGT TTTAGACATC AAAGCGTGCG CGGGCCATAC GCCCTTTAAC	360
ACTTATAAAG GCGATGGGCT TATCATTGCC ACGCCCCTAG GCTCAACCGC TTATAATTTG	420
AGCGCTCATG GGCCCATGT GCATGCTTTA AGCCAAAGCT ATATTTTAAC GCCCTTGTC	480
GATTTTCTT TAACGCAACG CCGTTTAGTG TTAGGGGCGG AATTTTGCTT GAGTTTTTGC	540
GCTCATGAAG ACGCTCTGT GGTATTGAT GGGCAAGCCA CCTACGATTT AAAAGCCAAC	600
CAACCCCTAT ACATTCAAAA AAGCCCCACG ACCACCAAGC TCTTACAAAA AAATTCAAGG	660
GATTATTTTA AAGTGCTTAA AGAAAAGCTG TTATGGGGGG AAAGCCCTAA CAAAAAAGA	720

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139

192

ATGATAGTGG	TTTTGATAGG	GGTTGTGGAA	AAAATCTCTG	CTTTAGAAGC	GCATATAGAA	60
GTGCAAGGGG	TTGTTTATGG	GGTGCAAGTT	TCTATGCGAA	CGGCTGCTTT	GCTCCAAACG	120
GGCCAAAAG	CGCGTTTGAA	AATCTTACAA	GTGATTAAAG	AAGATGCGCA	TCTTTTATAC	180
GGGTTTTTAG	AAGAGAGCGA	AAAAATTCTC	TTTGAAAGGC	TTTTGAAAAT	CAATGGGGTA	240
GGGGGGCGTA	TCGCTTTAGC	CATTCTTTCA	AGCTTTTCGC	CGAATGAATT	TGAAAACATT	300
ATCGCTACTA	AAGAAGTCAA	AAGACTCCAG	CAAGTCCCAG	GCATAGGGAA	AAAGCTCGCC	360
GATAAGATCA	TGGTGGATTT	GATTGGCTTT	TTCATTCAAG	ATGAAAACAG	ACCCGCGCGC	420
AATGAAGTCT	TTTtagccct	AGAGAGTTTG	GGCTTTAAAA	GCGCTGAAAT	CAATCCAGTT	480
TTAAAAACCC	TAAAACCCCA	TCTCAGCATA	GAGGCAGCGA	TTAAGAAGC	CTTACAGCAA	540
CTGCGCTCT						549

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 462 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140

GTGGGGGTTT	TGTTTRGCGTT	GTTTTTCTTT	TATGCGAAAA	ATAACCTTTT	GGAAAACACC	60
CAAATACGCA	TGCAATACAC	CGCTGATGCG	ATCGCTAAAA	GCCTTTTAGA	ATTAAATAAT	120
GCCTCTTCTT	TAGAGCCTTT	AAAAATCTTA	GAAGAACGAT	TCAAAAACAC	CCCCTTTGTT	180
TTGTTGGACG	CAGACAACAG	AGTCAAGTTT	TCTAATATCG	GGGTGTTTGT	GGCCTCTTTT	240
AAAAATGACG	CCTTAATCAA	AACCCCTTAT	TTTGCGCTTA	AAAAACAGGG	CTTTTACCTC	300
ACAGACAGCG	CCCCAACTAA	CCGCTTAGGG	GTTTCTAAAA	TCATTATTGC	AGAAGAAGAA	360
ATTCAAAAAA	TCTTTATCCC	CCTTTATAAA	ATGATAGGCT	ATGTGTTTTT	GGGCGCGAGT	420
TTGTTTGTCTG	CGCTAATAGC	CATGTGGCTT	TATAAAATCC	CA		462

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 864 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

193

(B) LOCATION 1...864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141

GTGGTAATAA	TGATTTTAGT	CTGCTTTTTA	GCTTGCTCGC	AAGAGAGCTT	TATCAAAATG	60
CAAAAAAAG	CCCAAGAGCA	AGAAAATGAC	GGCTCTAAAC	GCCCCAGCTA	TGTGGATTCTG	120
GATTATGAAG	TCCTTTAGCGA	AACGATTTTT	TTACAAAACA	TGGTGTATCA	GCCTATAGAG	180
GAAAGAAACG	CTTTTTTCCA	ACTGACTAAA	GATGAAGACA	ATTCTTTTAA	CCCTGAAAAT	240
TCCGTGATTT	TACTGAATGA	GCCAAGCGAT	AATAGTGAAA	AAAACCTACT	CTCATACCCA	300
AACGATCCCA	ATAACAATGA	AGACAACGCT	AATAATAGTC	AAAAAAATCC	GTTCCCTTTAC	360
AAGCCCAAAA	GAAAAACAAA	AAACCCAAAA	CTCATTGAAT	ATTCCTCAAC	AGATTTCTAC	420
CCCCTAAAAA	ATGGGGATAT	TATCATGAGT	AAAGAAGGGG	ATCAATGGTT	GATAGAAATC	480
CAATCCAAAG	CCTTGAAGCG	TTTTTTAAAA	GATCAAAACG	ATAAAGATCG	CCAGATCCAA	540
ACTTTCACCT	TTAATGACAC	TAAAACGCCA	ATCGCGCAAA	TTAAGGGCAA	AATTTCTTCG	600
TATGTTTATA	CCACCAATAA	CGGTAGCTTG	AGTTTAAGGC	CYTTTTATGA	ATCGTTTTTG	660
TTAGAAAAAA	AGAGCGATAA	TGTTTATACG	ATAGAGAATA	AGGCTTTAGA	TACTATGGAG	720
ATTTCAAAGT	GTCAAATGGT	GTTAAAAAAG	CATTCAACCG	ATAAATTAGA	CAGCCAGCAT	780
AAAGCCATCA	GTATTGATTT	GGATTTTAAA	AAAGAGCGCT	TTAAGAGCGA	TACGGAACCT	840
TTTTTAGAAT	GTCTTAAGGA	AAGT				864

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142

ATGGCCGCTC	CACTACTTGC	TCTGCCCTTT	CTTTCTAACC	CTTTAGTGCT	TGGTGCTTTA	60
GCTGTCTAG	GAGTGGGTGC	TTACTTGTAT	CCCAATAAGC	AAGATTCTTT	AGTTGTGCAA	120
GCAGATGGGC	TTTATAGTGA	AATTCTTGGG	TTTTTCATTT	CGTTTTCTAG	CAAGATCTTG	180
AAAGGAATTG	GTGAGCCTTT	AGCCAATGTT	ATCCAACCTT	TGGTATGGT	TTTAGGAATG	240
CTTTTAAATC	TTTTGTATTC	CTTTAAACGC	TATCAAAACA	ATGATTTATT	TGAAATCAAA	300
ACCTTTTTAA	TGCTTTTTGT	GTTTGTAGGA	TACCTTTCTT	TGTACCATTA	TGCTTTTAAA	360
TCTGATGGTT	CTAGTAGCGG	TAATGGTCGC	TCCAGTTTTG	CCTTTCAAAA	TCATGTAACA	420
GAAATTTTTG	ACACGCCTGC	TAACTTGCTA	AATGCTGGGA	TTTCTAATGT	GGTTAAGGAA	480
TATCAAACAA	ATAGTGCAAG	AGAACACAAG	AATATAGACA	CGCACCACAG	TATCACTAAC	540
GCTAATATTT	CATTCCATGT	CAGACAAATT	TTAACGAGTT	TGAATAAACT	ATATGAAGAC	600
TTCAAATTA	ATAATGGACT	ATCGCTAAAA	ACCCTTATTG	CAGCTGTTTT	GTTATTAGTT	660
ATTTTAGGAT	TAGAAITGTT	TTTATTGTTT	AAAGTTTCTT	GTTATGTTTT	TATGACTTAT	720
TTAGAAAAAA	TTATTTACTT	GTCTTTGGTT	ATTTTCATGC	TACTGCTAGG	GTTTTTTTCAG	780
CAGACTAGAG	GTTTTTTAGT	GTCTTATGTG	AAAAAAATTA	TTTCATTGAC	TTTTTACATG	840
CCTTTGTTGT	TGCTATTAGT	GTTATTCAAC	TCTTTTGTCAT	TACAATACGC	AATCAAAGTG	900
GGAGGGAGCA	ATGAAATAGT	GGCTAAATTT	GGCATTATTG	TAGCAATAGG	AATTTCACTG	960
ACATTTATTC	AAAAAGTCCC	CGAAATGATT	AACGCTATCT	TTGGCACACA	AGGTGGTCTA	1020
ACGGATGCTA	AAAGCTTCAT	ATATCAAGGT	GTGCAAAATG	CTAGTGCTGG	AGCTGGAGCC	1080
ATAGCTGGAA	GTCTTAAGAG	TGTGGGTCGT	TCAGATTGTT	GTAGAACGCT	AGAAGCTTAT	1140
AAAGACGCAA	AATCTACGAT	AAACAGCACT	ACGGCTAACA	TGAGAGACAT	GCCAGGACAT	1200
CCTGTGTTTA	GAGTGGGTGT	GGAGACGATT	GAACCTCCCA	AGTCTCATAG	AGCTAGCAAA	1260

SUBSTITUTE SHEET (RULE 26)

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143

GTGTTAAAAT TTCAAAAATT ACCCTTATG TTTGTTTCCA TTCTTTATAA TCAAAGCCCT	60
TTATTGGCTT TTGATTATAA GTTTAGTGGG GTAGCGGAAT CTGTTTCTAA AGTGGGGTTT	120
AACCATTCCA AACTCAATTC CAAAGAAGGG ATTTCCCTA CAGCCACCTT TGTAACCGCC	180
ACGATCAAGC TTCAAGTGRA TTYCAAATCT GCTCCC	216

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144

ATGGGTAATC ATTTTCTAA ATTAGGATTT GTTTACGCG CTTTAGGGAG CGCGATAGGT	60
TTAGGGCATA TCTGGCGCTT CCCCTATATG ACTGGGGTGA GTGGTGGGGG TGCTTTTGTT	120
TTATTGTTTT TATTTTATC CTTAAGCGTT GGTGCGCGA TGTTTATCGC TGAAATGCTA	180
TTAGGACAAA GCACGCAAAA AAATGTAACA GAAGCTTTA AAGAGCTTGA CATTAAACCT	240
AAAAACGCT GGAATACGC AGGGATCATG CTTATTTCTG GACCTTTAAT ACTGACTTTT	300
TATGGCACTA TTTTAGGTTG GGTGCTTAT TATTTGGTGA GTATTAGTTT TAATTTGCCT	360
AGCAGTATCC AAGAACTCGA ACAAATTTT ACTCAAACCT TGCAGTCTAT AGGGTTACAA	420
TCCATAGGGC TTTTATGCGT TTTATTCATA ACCGGATGGA TTGTTTCTAG GGGGATTAAA	480
GAAGGCATTG AAAAATCAA TTTGGTTTTA ATGCCCTTAC TCTTTGCCAC TTTTITGGT	540
TTGCTTTTTT ATGCGATGAG CATGGATTCT TTTTCTAAAG CTTTCCATT CATGTTGATT	600
TCAAGCCAAA AGATT	615

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 984 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145

ATGGAAGAAAG	TTTGCCTGAG	CGCATGGGGG	TTGCCTAAGA	TTTTAGAAGA	AAGATTAAAA	60
GAAAAATATG	GCGATGATTG	GGAAAAACAT	GTTAAGGCTA	AAGCAATAAA	CGAAGAAGAG	120
CTTGAAGAAC	AAGTCAAAGC	TAAAGCCAAA	GAGCAACAAA	AGACACAAAG	AGAAAAAACA	180
CTCAATGGAT	TTTTAAAAAA	AGTTGGTTTA	AAAAAGCGTG	ATATGTTACA	AAGCACTATG	240
TTATTTTGATG	AAGTCAAAGA	AGCTGATGTG	CTTTTCAAG	CAGAGCGTAA	AATTGGCGAT	300
TGGATTTTTA	GCAGTGCGGT	GTTCTTTTTT	GCTCTAGCCC	TTATAGAAGC	CATTATTATT	360
GTATGCTTAT	TGCCGTTAAA	AGAAAAAGTG	CCTTATTTAG	TAACCTTTTC	AAACGCTACA	420
CAAAATTTTG	CCATAGTCCA	AAGAGCAGAC	AAGAGCATCC	GTGCTAATCA	AGCGCTTGTC	480
AGACAAATGG	TAGCGTCTTA	TGTTAATAAT	AGAGAAAATA	TTTCAAGTAT	AAAAGAGCAA	540
AACGAAATAG	CCCACGAAAC	CATTAGGTTG	CAAAGCGCAT	TTGAAGTGTG	GGATTTTTTT	600
GAAAAACTGG	TTTCTTATGA	GCATAGCATT	TACACTAATA	TAAATCTAAC	ACGAAAAATT	660
AGCATTATCA	ATATCGCTTT	AATCAGTAAA	ACCCAAGCCA	ATATTGAAAT	ATCCGCACAA	720
CTTTTTCATA	AAGAAAAGTT	AGAAAGCGAA	AAGCGTTATA	GAATAATTAT	GACCTTTGAA	780
TTTGAACCTA	TTGAAATTGA	TACAAAATCT	GTTCCCTTAA	ACCCTACAGG	CTTTATTGTT	840
ACAGGTTATG	ATGTAAGTGA	AATTGCGATT	TTAAAAGATT	TAGATGAGAA	AAATAAAGTC	900
AAAGATGATG	GTGTGAAATC	TAGGATTATC	CATGTGCGAG	AAAAAGACCC	TCATATGAGC	960
CAGTATAAAG	ATGTTAAGGA	GCAA				984

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...228

196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146

ATGCTGCATA AGGCTAAGGT GGGCATCGTG TTTCAGGCGC TTTTAGGGAT TTTTGCCTG	60
TTTTTATTGT TGTTTTACTT GAGCGCGTTT TTAATGGTGG CTTTTAAAGA CACTAAACGC	120
ATGTTTATAA GCGTTTAAAT AGGGAGCGTG GTGTTCTTT GGAGCGATCT ATGGTCTTT	180
GTAGGGTTA AAAATATCAG CTTTGTTTTG GATATTGGTT ATGAAATC	228

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147

ATGCCGTTTT TGAAAACTG GATCTGGAGT TTAAAGATGG CTTTGAGCGC GATTAGTGGG	60
GCTAGTGGGG TGGGAAAAG CGTCCTTATT GCGAGCCTTT TAGGGGCGTT TGGGCTTAAA	120
GAGAGCAACG CTTCAAACAT TGAAGTGGA TTGATCGCGC CTTTTTTAGA CACGGAAGAA	180
TACGGCATT TTAGAGAAGA TGAGCATGAA CCCTTAGTTA TTAGCGTGAT TAAAAAAGAA	240
AAAACACGCT ATTTTTTAAA CCAAACAAGC CTATCTAAAA ACACGCTCAA AGCGTTATTA	300
AAGGGGCTTA TTAAACGCTT ATCTAACGAC AGATTGAGCC AGAATGAAC CAACGATATT	360
TTAATGCTCT CTTATTAGA TGGCTATATC CAAAATAAAA ATARGCGTTT AGCCCCCTTT	420

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 924 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148

ATGCCACAAA ACCAGCTTGT GATCACCATC ATTGATGAAT CAGGCTCTAA GCAACTCAAA	60
TTTTCTAAAA ATTTAAACG CAACCTCATC ATTTCTGTTG TCATTCTTTT ATTGATCGTG	120

SUBSTITUTE SHEET (RULE 26)

197

GGGCTTGGCG	TGGGGTTTTT	AAAATTTT	ATCGCTAAAA	TGGATACGAT	GACAAGCGAG	180
AGGAATGCGG	TTTAAAGGGA	TTTTAGGGGT	TTGTATCAAA	AAAATTACGC	CCTAGCGAAA	240
GAGATTAAAA	ACAAGCGAGA	AGAGCTTTTT	ATTGTGGGCG	AAAAGATCCG	TGGGCTAGAA	300
TCCTTGATTG	AAATCAAAAA	GGGGGCTAAT	GGGGGAGGGC	ATCTCTATGA	TGAAGTGGAT	360
TTAGAAAATT	TGAGCTTAAA	TCAAAAACAT	TTAGCACTCA	TGCTCATTCC	TAATGGCATG	420
CCCCTAAAA	CTTATAGCGC	TATCAAACCC	ACTAAAGAAA	GGAACCACCC	CATTAAAAAG	480
ATTAAGGGCG	TTGAATCCGG	GATCGATTTT	ATCGCGCCAT	TGAACACGCC	TGTGTATGCG	540
AGCGTGATG	GGATTGTGGA	TTTTGTGAAG	ACTCGTTCTA	ATGCGGGGTA	TGGGAACCTG	600
GTGCGCATTG	AACATGCGTT	TGGTTTCAGC	TCCATTTATA	CGCACTTAGA	TCATGTCAAT	660
GTGCAGCCTA	AAAGCTTCAT	CCAAAAAGGG	CAGTTGATTG	GCTATAGCGG	GAAGAGCGGT	720
AATAGCGGCG	GCGAAAAATT	GCATTATGAA	GTGCGGTTTT	TGGGTAAAT	TTTAGACGCA	780
GAAAAATTCC	TAGCATGGGA	TTTGGATCAT	TTTCAAAGCG	CTTTAGAAGA	AAATAAATTT	840
ATTGAATGGA	AGAATCTGTT	TTGGGTTTTA	GAAGACATCG	TCCAGCTCCA	AGAGCATGTG	900
GATAAAGACA	CCTTAAAAGG	TCAG				924

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1017 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149

ATGATCACTG	GCTCTCACAA	CCCCAAAGAA	TACAACGGCT	TTAAATCAC	GCTCAATCAA	60
AACCCGTTTT	ATGGCAAGGA	CATTCAGGCT	TTAAAAACA	CGCTTTTAAA	CGCAAAGCAT	120
GAAATAAAGC	CCCTAAAAGA	AACGCCAGAG	AAAGTCAATG	CCCTAGAAGC	GTATCATCGC	180
TATTTGATCA	AGGATTTTAA	GCATTTAAAA	AATCTTAAAT	ACAAAATCGC	CCTGGATTTT	240
GGTAATGGCG	TGGGGGCGTT	AGGATTAGAG	CCGATTTTAA	AGGCTTTTAA	CAITGATTTT	300
AGCAGCCTTT	ATAGCGATCC	TGATGGGGAT	TTTCCTAACC	ACCACCCAGA	CCCTAGCGAA	360
GCGAAAAACT	TAAAAGACTT	AGAAAAACAC	ATGCGAGAAA	ACGCTATTTT	AATAGGCTTT	420
GCTTTTGATG	GCGATGCGGA	TAGGATTGCG	ATGCTAAGCT	CTCATCATAT	CTATGCGGGC	480
GATGAATTAG	CGATTTTATT	CGCTAAACGC	TTGCATGCTC	AAGGCATCAC	CCCTTTTGTG	540
ATCGGCGAAG	TCAAATGCTC	TCAAGTGATG	TATAACGCAA	TCAATACTTT	TGGTAAGACG	600
CTCATGTATA	AAACCGGGCA	TAGCAATTTA	AAAATCAAGC	TCAAAGAAAC	TAATGCGCAT	660
TTTGCGGCTG	AAATGAGCGG	GCATATCTTT	TTTAAAGAAC	GCTATTTTGG	CTATGATGAC	720
GCTCTTTACG	CATGTTTAA	GGCTTTGGAG	TTATTGCTTG	AACAAAGTCC	AAGCGACTTG	780
GAAAACACCA	TTAAAACCT	CCCCTATTCC	TACACCACGC	CTGAAGAAAA	AATCGCCGTG	840
AGCGAAGAAG	AAAAATTTGA	AATCATTCGC	AACTTACAAG	AAGCGCTTAA	AAACCCGCCA	900
AGCCATTTCC	CTACAATCAA	AGAAATCATC	AGCATTGATG	GCGTGAGAGT	GGTTTTTGAA	960
CATGGCTTTG	GGCTTATTCG	CGCAAGCAAC	ACCCACCCCC	TATTTAGTCA	GCCGCTT	1017

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

SUBSTITUTE SHEET (RULE 26)

198

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...621
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:150

ATGTCCAAGA	ACCTTCAAAA	GAAGAATCCA	AAGAAGAGTT	TYCCACAAGC	CCAGAAAGCC	60
ATAAGGGAGA	TGAAAATGTT	TGAAACCATT	GCTTTTATT	TCTTTGCGAT	CCTTACTTTA	120
AGCATGGCGT	TAGTGGTGAT	CACAACCACA	AATATCCTCT	ATGCCATTAC	CGCTCTCGCT	180
AGTAGCATGG	TTTTTATPFC	TGCTTTTTTC	TTTTTACTGG	ACGCTGAGTT	TTTGGGCGTG	240
GTGCAAAATCA	CGGTGTATGT	GGGTGCGGTC	ATTGTGATGT	ATGCGTTTGG	CATGATGTTT	300
TTCAACTCCG	CTGCAGAAAGT	AGTTGAACGC	AAGCAAAGCC	CTAAATCTT	GTGCGTTCTT	360
TCATTTGGCG	TGGCGCTGTT	GCTCACCTTG	ATTTTAAAGC	CTCCTAGCAT	TGSSGAAAAC	420
CTTTCTAAGC	AAGTCAATTC	CAACGCTATT	GATGCGCAAA	TYCCYAACAT	TAAAGCGATT	480
GGTTATGTGC	TTTTCACCAA	TTACCTCATT	CCCTTTGAAG	CGGCGGCTTT	AATGCTTTTA	540
GTGCTATGG	TTGGAGGCAT	CGCTACAGGG	ATTCAAAAA	TCCATGGGAA	AAATCACACG	600
CAATTTATAA	AGGAATCTCT	A				621

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 753 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151

ATGGGTGCAA	TTTTATCTAT	TTTAAACTTT	GAAATCAAAT	CTTATCTCAC	CAATACAAGC	60
GCGCTATTTT	GGACTTTTAT	TTATCCTATT	TTAATGCTCC	TATTACTAAT	TTTGTTTTTT	120
TCAAAAAATA	CCACTGAAAT	TTTTTACTTT	AATAACATTA	TAGGTCTAAT	GGGACTTCTT	180
ATTATTTCTA	GCGCGATCTT	TGGTCTCACA	CAAGCTATAA	CAAGCTCTAG	ATCGCATAAT	240
ATATTCTTAT	TCTACATGCT	ATCACCAGCA	ACTTTCAAAC	AAATAACTCT	AGCATTAAATC	300
GCTTCAAGAC	TAATCGTTGT	AATCCTATAT	GCTTTTATCT	TTATTGTTCT	CTCTTTTTAT	360
GCGCTCAATA	TCATCACTAT	TCTTAATTTT	AAAGCGCTTA	TTTTGGGGTT	TATTAGCATT	420
TTTTCAAGCG	CATTGTTTTG	TTTTTGCTTG	GCAATTTTGG	TAGCTAGAAT	TTTTCAAAAC	480
GAACAAAGCA	TCTTAGGATT	TTGTAATATC	ATCAATCTCT	ATGCGCTAAT	GTCTTGTAAT	540
GTTTTTGTTT	CTTTAGAATA	CCTACCTAAT	ATTGGTCAAT	TATTTATCAA	AACATCTATT	600
TTTACTACC	TTAATCAACT	TCTAATCAAA	GCTTTTCAAG	GGATTGATAC	TATACTGGTT	660
TTAGCAACTT	CAACATTTTT	CATTATTGGT	GGCATTATTT	TATTTTACT	AAGCGCTAAT	720
CGCATGTTAC	TAAACCAAAA	AGAACGCATG	CCT			753

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152

ATGGCAGGCA CACAAGCTAT ATATGAATCA TCTTCTGCAG GATTCTTATC GCAAGTCTCC	60
TCAATCATCT CAAGCACAAG TGGTGTGCGA GGGCCATTG CAGGAATAGT AGCGGGCGCT	120
ATGACAGCAG CGATTATTCC TATTGTTGTG GGATTTACTA ATCCGCAAAT GACCGYTATY	180
ATTRACCCAA TAYAATCAAA GCATCGC	207

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153

GTGAGCCGTA TTTTAGGCTT GAGCGATGAT TTAGCGATGA CTTTATGCGC TGAATCCATC	60
CGCAATCAAG CCCCTATCAA AGGTAAAGAT GTCGTTGGTA TTGAAATCCC TAACAGCCAA	120
AGCCAAATTA TTTATTTAAG AGAAATTTTA GAAAGCGAAT TGTTTCAAAA ATCCAGCTCG	180
CCTCTAACCC TAGCTTTAGG CAAAGACATT GTGGGTAACC CTTTCATCAC GGATTTAAAA	240
AAGCTCCCC ACTTGCTCAT CGCCGGCAGC ACAGGGAGCG GTAAGAGCGT GGGCGTGAAT	300
CGGATGATTT TATCCTTACT TTATAAAAAA CCCCCC	336

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

200

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154

ATGGATGAAA	GSCTCGTTTA	TGGGGTGATT	TGCATGCCCC	GTCAGGTTTT	TGCCAACACC	60
GGCACTAACG	TSAGCATCAT	CTTTTITCAA	AAAACGCCAA	GCGCAAAGGA	AGTGATCTTG	120
ATTGACGCTT	CCAAACTCGG	CGAAGAATAC	ACCGAAAACA	AAAACAAAAA	AACGCGCTTA	180
AGGCCAAGCG	ATATGGATTT	GATTTTAGAA	ACTTTCCTAA	ATAAAGCCCC	AAAATCGGAT	240
TTTTCGCTC	TGGTTTCTTT	TGATGAAATT	ACAGAAAAAA	ATTATTCTCT	AAACCCCGGG	300
CAGTATTTCA	CTATAGAAGA	CACGAGCGAG	ACAATCAGCC	AAGCGGAGTT	TGAAAACTTG	360
ATGCAACAAT	ATTCAAGCGA	ACTAGCGAGC	CTTTTGTATG	AAAGCCAAAA	TTTGCAACAA	420
GAGATTTTAG	AAACTTTTAA	AGGGGTTAGG	TTTGAG			456

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155

ATGAGAAGAA	TTATTAAAAA	CACACTTTCA	CGCTTAGGCT	ATGAAGATGT	TTTAGAAGCT	60
GAGCATGGGG	TGGAAGCTTG	GGAAAACTA	GACGCTAATG	CGGACACTAA	GGTGCTTATT	120
ACGGATTGGA	ACATGCCTGA	AATGAACGGG	TTGGATCTCG	TTAAAAAGGT	GCGTGCGGAT	180
AACCGATTTA	AGGAAATCCC	TATCATTATG	ATCACCACAG	AGGGCGGTAA	AGCTGAGGTC	240
ATTACGACTT	TAAAAGCGGG	CGTGAATAAC	TACATTGTGA	AACCTTTTAC	CCCCCAAGTT	300
TTGAAAGAAA	AATTAGAGGT	TGTTTTAGGG	ACAAACGAT			339

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs

SUBSTITUTE SHEET (RULE 26)

201

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156

ATGGCAGAAG AACAAAGAAA TACCGCGCAA CAACCCCAAA AAAAAAGCAA AGCCCTTTTA	60
TTTGTCATTA TTGGAAGCGT GCTAGTGATG CTTTTATTGG TGGGGGTGAT TATCATGCTG	120
CTTATGGGGA ATAAGGAAGA ATCTAAAGAA AACGCTTCTA AAAACACCCA AGAAGTCCAA	180
GCTAATCCTA TGGCGAACAA GAATCAAGAA GCCAAAGAAG GCTCTAATAT CCAGCAATAT	240
TTGGTGCTTG GGCCTTTGTA TGCGATTGAT GCGCCTTTTG CGGTGAATTT GGTCTCTCAA	300
AATGGCAGAC GCTACCTTAA GGCTTCTATT TCGCTAGAAT TGAGCAATGA AAAGCTTTTG	360
AATGAAGTCA AGGTTAAAGA CACGGCGATT AAGGACACGA TTATAGAAAT TCTATCGTCT	420
AAAAGCCTGG AAGAAGTGGT TACTAACAAA GGCAAAAACA AGCTTAAAGA TGAAATTAAG	480
AGCCATTGA ATTCGTTTTT GATTGATGGC TTTATTAAAA ATGTCTTTTT CACTGATTTC	540
ATTATCCAA	549

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157

ATGGGGTGTT TTAGCACCAT TTGTTGTAAG GGTTTAACGC TTAGCGTTGG TGGATTTTTG	60
GTGATGATGA GATTCTTAAT ATTCAAAGAT TTTTGCAAAG ATTTT	105

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2106 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

SUBSTITUTE SHEET (RULE 26)

202

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2106
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158

GTGGCGCGTC	TTGTGGTTAA	AAGGCGTAA	ATTGATTATA	AACAAAGCAT	TCAATCTGAC	60
TCTCAATACT	TGCAAGCGAS	CTTGAATCAG	TTTGAAAATA	AAGAAGTGTA	TGAGAATCAG	120
TATTTTITAG	TTTAGAAAG	CACTCACTCT	TTGCATGGCG	TTTTGGAGCA	TAAGAAAAAA	180
TCTTTCATGC	ACGCTAATAG	AGAAAATTTT	AAGGATATTC	TCTCTTATA	AGCGCATTTT	240
TTGCAAGAAA	CTTTAAAAAG	CTTAGAAATC	CAGCTCAAAA	ACTATGCCCC	CAAACCTCTA	300
AACTCTAAAG	AGGTTTTGAA	TTTTTATGCA	GAATATATTA	ATGGGTTTGA	ACTCCCTTTA	360
AAACCCCTAG	TAGGGGGGTA	TTTGAGCGAT	AGCTATATCG	CTAGTCTAT	CACTTTTGAA	420
AAAGATTATT	TCATTCAAGA	AAGCTTTAAT	CAAAAAACCT	ATAACCGCTT	GATTGGCATT	480
AAAGCTTATG	AGAGCGAAAG	GATCACTTCT	ATAGCGGTGG	GAGCGCTTTT	ATACCAAGAG	540
ACGCCTTTGG	ATATTATCTT	TTCCATAGAG	CCTATGAGCG	TCAATAAAAC	GCTGAGTTTT	600
TTAAAGAGAG	GGGCCAAGTT	TAGCATGTCT	AATCTTGTTA	AAAACGAGCT	ATTAGAATAC	660
CAAGAATTAG	TCAAAACCAA	ACGATTATCC	ATGCAAAAAT	TCGCCCTAAA	CGTTCCTATC	720
AAAGCCCCCA	GTTTGGAGGA	TTTAGACGCT	CAAACCAGCT	TAATTTTAGG	GCTTTTATTT	780
AAAGAAACT	TAGTGGGCGT	TATAGAAACT	TTTGGCTTGA	AAGGGGGGTA	TTTTTCCTTT	840
TTCCCTGAAC	GCATCCATT	AAACCACCGC	TTGCGTTTTT	TAACCTCTAA	AGCCCTAGCG	900
TGTTTGATGG	TGTTTGAAG	GCAAAATTTA	GGTTTTAAGG	CTAATTCATG	GGGGAATAGC	960
CCTTTGAGCG	TGTTTAAAA	TTTGGATTAT	TCCCTTTTTT	TATTCAATTT	CCACAACCAA	1020
GAAGTGAGCC	ATAATAACGC	TAAAGAAATT	GCCAGAGTGA	ATGGGCATAC	TTTAGTTATA	1080
GGGGCAACCG	GAGCGGTAA	AAGCAGCTG	ATTAGCTATT	TAATGATGAG	CGCTTTAAAA	1140
TACCAAAACA	TGCGCCTTTT	AGCTTTTGAC	AGGATGCAAG	GGTTGTATT	TTTCACCGAA	1200
TTTTTTAAAG	GGCATTACCA	TGACGGCCAA	TCTTTTAGTA	TCAACCCCTT	TTGTTTAGAG	1260
CCTAATTTCG	AGAAATTTAG	ATTTTTCGAA	TCCTTTTTTT	TGAGCATGTT	GGATCTTGCC	1320
CCTTCAAGGG	ATAAGAAGC	CTTAGAAGAC	ATGAATGCGA	TTTCTGGCGC	GATTAAGAGC	1380
CTTTATGAGA	CCTTATACCC	CAAAGATTTT	AGTTTGCTGG	ATTTTAAAGA	AACGCTTAAA	1440
AGAACCTCAT	CTAACCAATT	GGGCTTGAGT	TTAGAGCCGT	ATTTGAATA	CCCCCTTTTT	1500
AACGCTTTGA	ATGACGCGTT	CAACTCCAAC	GCTTTTTTAA	ATGTGATAAA	CCTAGATGCG	1560
ATCACCCAAA	ACCCTAAAGA	CTTAGGGCTT	TTAGCCTATT	ACTTGTTTTA	TAAGATCTTA	1620
GAAAGAGTCT	AGAAAAACGA	CAGCGGCTTT	TTGGTTTTTT	TAGACGAATT	TAAATCCTAT	1680
GTGAAAACG	ATTTGTTAAA	CACTAAAATC	AACGCTTTAA	TCACGCAAGC	CAGGAAAGCT	1740
AATGGCGTGG	TGGTGTGGC	CTTGCAAGAC	ATTTACCAAC	TTAGCGGGGT	TAAAAACGCC	1800
CATAGTTTTT	TAAGCAACAT	GGGACTCTC	ATTTTGATC	CGCAAAAAAA	CGCTAGGGAA	1860
TTGAAACACA	ATTTCATGT	GCCTTTGAGC	GAAACTGAAA	TTTCTTTTTT	AGAAAAACCC	1920
CCTCTGTATG	CCAGGCAGGT	TTTAGTCAAA	AATCTGGGTA	ACGGGAGTTC	CAACATGATT	1980
GATGTGAGTT	TGGAGGGCTT	GGGGTGTAT	TTGAAAATCT	TTAATTCAGA	TTCCAGTCAT	2040
GTCAATAAAG	TGAAAGCGTT	ACAAAAAGAC	TACCCTACAG	AGTGGCGTGA	GAAACTTTTTG	2100
AAGAGT						2106

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 879 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

SUBSTITUTE SHEET (RULE 26)

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...879

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159

ATGCAAGAAG	ACTGGCAAGC	CGTCCAAGAC	ACCATTAAAG	TGGTTTCAGA	TGTGAAAGCG	60
GGGAATTTTG	CGGTGCGCAT	CACGGCTGAA	CCCGCAAGCC	CTGATTTGAA	AGAATTGAGA	120
GACGCGCTAA	ATGGGATCAT	GSAYTATTTG	CAAGAAAGCG	TAGGGACTCA	CATGCCAAGC	180
ATTTTCAAAA	TCTTTGAAAG	CTATTCTGGC	TTGGATTTTA	GAGGGCGGAT	CCAAAACGCT	240
TCGGGTAGGG	TGGAATTGGT	TACTAACGCT	TTAGGGCAAG	AAATCCAAAA	AATGCTAGAA	300
ACTTCGTCTA	ATTTTGCCAA	AGATCTAGCG	AACGATAGCG	CGAATTTAAA	AGAATGCGTG	360
CAAAATTTAG	AAAAGGCTTC	AAACTCCCAA	CACAAAAGCC	TGATGGAAAC	TTCCAAAACG	420
ATAGAAAATA	TCACCACTTC	CATTCAAGGC	GTGAGCTCTC	AAAGTGAAGC	CATGATTGAA	480
CAAGGGAAAG	ACATTAAAAAG	CATTGTAGAA	ATCATTAGAG	ATATTGCCGA	TCAAACGAAT	540
CTATTAGCCC	TAAACGCTGC	TATTGAAGCC	GCACGAGCCG	GCGAGCATGG	CAGAGGCTTT	600
GCGGTGGTGG	CTGATGAGGT	GAGGAAGCTC	GCTGAAAGGA	CGCAAAAATC	CCTCAGTGAG	660
ATTGAAGCCA	ATATTAATAT	TCTCGTTCAA	AGCATTTCAG	ACACGAGCGA	AAGCATTAAA	720
AACCGGTTA	AAGAAGTAGA	AGAGATCAAC	GCTTCTATTG	AAGCCTTAAG	ATCGGTTACT	780
GAGGGCAATC	TAAAAATCGC	TAGCGATTCT	TTAGAAATCA	GTCAAGAAAT	TGACAAAGTC	840
TCTAACGATA	TTTTAGAAGA	TGTGAATAAA	AAGCAGTTT			879

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160

ATGCCTAAAA	GTTTCACCTT	ACCGACTTTC	GTGTGGTGTT	TGTTTGTGGG	GTTTATCTTA	60
AGGAACGCTT	TGTCGTTTTT	TAAAATCCAT	AGCGTGTTTG	ACAGAGAGGT	TTCAGTTATA	120
GGGAATGTGA	GCTTGAGCCT	GTTTTTAGCT	TACGCT			156

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 546 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

204

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161

GTGGGGCTTT	TAAATTCTAA	GGCGTTCAAA	CCCTACCGCA	AGATTTTGCA	AATGGTGTTT	60
CAAGACCCCT	ACGCATCATT	AAACCTCGC	TTAAGCATTC	AAAGCATTTT	AATAGAAGCT	120
TTGCGCTTTG	CTTACCCTAA	AGCTTCACAA	CAAGAATGGC	ACCATTTAGC	TGAAC TTGC	180
TTAGAAGAAG	TGTGTTTAAA	CCCTGAATTG	CTTAAC TT T	ACGCTTATGA	GCTCAGCGGA	240
GGGAGCGGCC	AAAGAGTGGC	GATCGCTAGA	GCGATTGCCT	TAAAACCTAG	AATCATTCTT	300
TTAGATGAGC	CAACCTCTGC	TTTAGACAAA	AGCATTCAAA	AAAGCGTGTT	GGAATTATTG	360
TTGAATTTAC	AAGAAAAGCA	GGATTTGAGC	TATTIGTTTA	TCAGCCATGA	TTTAGATGTG	420
ATCAAAGCTT	TTTGCATAG	GGTGTTAGTG	GTGAGTGAGG	GGAAATCGT	GGAAACAGGC	480
GCTATTGAAG	AGGTGTTTGA	CAACCCCAA	CACGCTTATA	CCAAGCGTTT	GTTGGAATCC	540
AGGCTT						546

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 753 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162

GTGAGTTTGA	TTAAAGTTAG	TGGTGATAAA	AAAGTGATTG	AGGTTTCTAT	TCCTTTAACT	60
TCCATTTTCAG	GCAAAGCGCG	TGTGAAAATC	AGACATGCCT	TTAGCGATTA	TGGTATTTCA	120
ACAGCGACTA	GAAAAATCCC	TTTAGTTTAA	AAGCATTATG	TAGAGTGGCA	GATCGGTTAT	180
GATGTCCCCA	TTAAAGATAA	AGAAAAATTT	GAAC TCACTA	CTTTAAAAGA	TGAAAAATAT	240
CATTTT TTAG	GGGCTAATAA	TAAAGTAAAA	ACTCTTTATG	AATTGAGCGA	AATGATTTAT	300
TACGCTAAGC	GATTGGGTTT	AATCAGTTTA	GAAAATTTAG	AAAA TACTTT	AAAA TTTTAA	360
GAAAAACAAA	AACAATTTAT	AGAAGATAAT	TTTATGATTA	CAAGAGAAAG	ATTTAGATCG	420
CATCAATTTG	GTGGCATGGA	TTTTGAACTC	TCACGCATTT	CTTATCCTTT	GCTCATTCAT	480
TCTTTTGATG	ATAATGAGTT	GAGCGAAATA	GTTATTAAGG	AACAACAATA	TGGCTCTAAA	540
ACCCAAGCCA	TGCTGTATTT	TGCTTTTCT	ATTTTGGAGT	TAAAAACCGC	TACCCCTTAA	600
TTAAACAGAA	CCGCTATGCC	CAAAGAACAT	GCCCTTTTGA	TTATCCATGA	AACCAACGCT	660
CTTGTTGTTT	TAGAAATGCT	TAAAATTTT	GGACTTTTAA	GCCAAGTGCA	CCATAACGAT	720
GTGTTWAAGA	TTTGWAAAA	AATACTTCAA	AAT			753

SUBSTITUTE SHEET (RULE 26)

205

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163

```

GTGATCACGG CGTGTTTTAA TAGYGAAAAA ACCATTGAAG ACACCATCTT TTCCGTGCTT      60
AATCAAACTT ATAAAAACAT TGAATACATC ATTATAGATG GGGCTAGCGC GATAGCACTT      120

```

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164

```

GTGTTTGTAG GGCTTTATCA TGGGGCAAGC ATCTTTGATT TAAAATTGTA AGTCTATCTT      60
ACTATGCTAA TCTCTTTAAT GCCCTTTGTG GCTACGATTT ATATCAATTT CCCAAAACC      120
ACAGAACTT CGCATGGCTA TGCAGATGG GCTAATGTTA AAGATATAGA ATGCTTTAAA      180
ATTTTAGCA AAGAGGGCTT TTGTAAAGTG GTGCATAGAT TAGGGGTGCA ATTTGATAAT      240
GGCTTTATTC TAGGTAAATT TGGTTTCCCA AAGCTTAGAA ATGTGTGCTA TGACAAGCCC      300
TTAGGAACGA TGATTGTTGC ACCCCCTGGT GCGGAAAAC TGCATGTGTG GCTTTGCCAA      360
ATTATAT

```

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

SUBSTITUTE SHEET (RULE 26)

206

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165

ATGAAACGCC	TTGCTGTTGC	GCTTATTTTG	GTGTTGGGAG	TGGTGTGGGG	GAAATCCTTG	60
CCTAAGTGGG	CAAAAGATTG	CTCAAAAGAG	ATGCGGATTG	AAAAGACCCA	AACCAAAGAT	120
GAAAAAATT	TAGTGTGTGG	GATGAGCGAT	ATATTGCTTT	CAGATATGGA	TTATAGCTTG	180
TCCTCAGCCA	GACAAAACGC	CTTAGAGAAA	GTGATGGAAG	CTTTCAAGGG	GGATAGAATA	240
GAGATTAAGG	CTGGTGAGCT	AAAGGCCACT	TTTATTGATA	CGGATAAAGT	TTATGTGCTT	300
CTAAGAATCA	CTAAGAAGCA	TGTCGCTTTA	ATGAATGAG			339

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1311 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166

ATGAACCCCC	AGATTCAACC	CGCCACTAAA	AAACCCTTAA	AATCCCTTTT	AGCCGCTAGT	60
TCAGGCAATT	TAGTGGAAATG	GTATGATTTT	TACGCTTATG	CGTTCCCTGC	TCCTTATTTC	120
GCTAAGGAAT	TTACCCACAC	CAATGACCCT	ACTCTAGCGC	TCATCTCAGC	TTTTTTAGTT	180
TTTATGCTAG	GGTTTTTCAT	GCGCCCTTTG	GGGAGTTTGT	TTTTTGGTAA	ATTGGGGGAT	240
AAAAAGGGGC	GTAAACTTTC	CATGGTGTAT	TCCATTATCC	TTATGGCGCT	AGGCTCTTTC	300
ATGCTCGCAT	TGCTCCCCAC	TAAAGAAATC	GTAGGGGAAT	GGGCGTTCTT	GTTTTTATG	360
TTAGCCAGGC	TTTTACAGGG	CTTTAGCGTG	GGAGGAGAAT	ATGGCGTGGT	CGCCACTTAT	420
CTCTCTGAAT	TAGGCAAGAA	TGGTAAAAAA	GGTTTTTATG	GCTCTTTTCCA	ATATGTAAC	480
TTAGTGGGAG	GGCAACTCTT	AGCTATTTTT	TCGCTCTTTA	TCGTTGAAAA	CGTTTACACG	540
CATGAGCAAA	TCAGCGCGTT	TGCTTGGCGT	TATTTATTCG	CTTTAGAGGG	TATATTAGCC	600
CTACTCTCGC	TCPTTTTGAG	AAATATCATG	GAAGAACTA	TGGATAATGA	AGCGACTCCT	660
CAAAAAAAGA	CTAATGTAAA	TAATACAAAA	GAAACCCATA	TCAAAGAAAC	CCAAAGAGGC	720
AGTTTAAAGG	AATTGCTCAA	CCATAAAAAA	GCCTTAATGA	TAGTCTTTGG	GCTAACTATG	780
GGAGGGAGTT	TGTGCTTTTA	CACTTTTACG	GTGTATTTAA	AAATCTTTTT	AACCAACAGC	840
TCATCGTTTA	GCCCTAAAGA	AAGCAGTTTT	ATCATGCTTT	TAGCGCTCTC	TTATTTTCATC	900
TTCTTACAAC	CCTTATGCGG	GATGCTTGCG	GATAAAATCA	AACGCACCCA	AATGCTGATG	960
GTTTTTGCGA	TCACAGGGCT	TATTGTAACG	CCTATTGTCT	TTTATGGTAT	CAAGCATGCG	1020

SUBSTITUTE SHEET (RULE 26)

207

ACTAGCGTGT ATGAAGCCCT ATTTTATGAA ATACTCGCAT TGAGCAGCAT GAGTTTTTAC	1080
ACTTGCAATTG CTGGGGTTAT TAAGGCGGAA TTATTCCTG AACATGTGCG AGCGCTTGGC	1140
GTGGGTTTAG CCTATGCGAT CGCCAATGCG CTTTTTGGAG GGAGCGCGAG TTATATAGCG	1200
TTAGAGTTCA AACAGCATGG TTTTGAAGAG GGGTTTGTGG GCTATGTCAT GTTGAGTATT	1260
GTTATCTTTA TGGTTATGGT TATCATATTC CCTAAAAAA CCTATTTGGA G	1311

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167

ATGGACATTA GCATTTTTAG AGAATACGAT ATTAGAGGCA TTTACCCAC CACTTTAGAT	60
GAAAATACGG CTTTTAGTAT CGGCGTGGAG TTGGGAAAA TCATGCGAGA ATACGATAAA	120
AGCGTGTTG TAGGGCATGA CGCAAGGGTG CATGGGCGTT TTTGTTTGA AGTTTGTAGC	180
GCGGGGCTGC AATCAAGCGG CTTGAAAGTG TATGATTAG GGCTAATCCC CACACCGGTA	240
GCGTATTTTG CGGCCTTTAA TGAAATAGAC AATATCCAAT GGCCC	285

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168

GTGTGCGACA TTTTTTCTGA TGGCGTTTAA TTGGACAAAG CGTTAGTGAT TTATTTCAAA	60
GCCCCCTATA GTTTCACCGG TGAAGATGTG TGCGAAATCC AATGCCATGG AAGCCCCCTT	120
TTAGCGCAAR ATATCCTTCA AGCTTGCTTG AATTTAGGGG CTAGGCTCGC TAAAGCGGGG	180
GAATTTAGCA AAAAAGCCTT TTAAACCAT AAAATGGATT TGAGCGAGAT TGAAGCGAGC	240
GTTCARCTCA TCCTTTGTGA AGRTGAAAGC GTTTTAAACG CTCTAGCCAG GCAGCTTCAA	300

SUBSTITUTE SHEET (RULE 26)

GGGGGA

306

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169

ATGTTTAAAA	AAATGTGTTT	GAGCCTGCTA	ATGATAAGCG	GTGTTTGTGT	GGGGGCAAAG	60
GATTTGGATT	TCAAGCTGGA	TTATCGCGCG	ACTGGGGGGA	AATTCATGGG	GAAAATGACG	120
GACTCTAGTC	TTTAAAGTAT	CACCTCTATG	AACGATGAAC	CGGTGGTGAT	TAAAAACCTT	180
ATGTCAATA	GGGGAAATTC	AGTCGAAGCG	ACTAAAAAAG	TAGAACCCAA	ATTTGGCGAT	240
AAGTTTAAAA	AAGAAAAACT	CTTTGATCAT	GAATTAAAT	ACTCGCAACA	GATATTTTAC	300
CGCTGGATT	GCAAGCCTAA	CCAATTGTTA	GAAGTTAAAA	TCATCACGGA	CAAGGGCGAA	360
TATTACCATA	AATTTTCCAA	A				381

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170

ATGACCTTGA	AGCCATATCC	AACCAAAGAG	ACTGGTCTTG	CTAGCCAATT	ATCTGGGCAC	60
TGGTTTTTTC	AGCTTTCGTT	ATTTAATAAA	ACAAACTTTA	ATCCTAATAA	AATTTGGATT	120
CCTTTAGAGT	TCAATAAAAG	ATCAAAAATA	AAGTTTGATA	AAGATTTAGA	AATCTATTTT	180
GATAGTCATG	AATCGTTCAA	TATCTCTAAA	AAATACTTGC	AAGAAATAGA	TCAAGAATCA	240
CTAAAAAGA	TCAACAATC	AAAAGATTTT	TTTTCAATTC	AAAAAATAGA	GAGTAAGCAT	300
GATAATAACG	ATATACTGCA	ACTTGAAATT	TTTGAGAATG	ATACAAGTTT	TCTTTTGTCT	360
AAAGGAAGTT	TTGCAGAAAT	TTTAGAATAC	AACATGCAAT	TAAAAATAGA	TTCTTTAATT	420

209

ACAAAAGAAT	TTAATAAGCT	TTAGCGATC	GTTCAAGATA	GTCCCAAGA	TAGTTACCAA	480
TTAAAAATT	GTGTCCGACA	TAACAATAAG	CTTCTAGAG	AGAAATATAC	GGAACATGAA	540
ATAAAACTTG	AAGTTTATGA	TGCGAGAAAA	TCCCACGATC	ACAATGAGCC	AATCATCTTA	600
AGCCAGCAAA	GCACCGGCTT	CCAATGGGCG	TTTAATTTCA	TGTTTGGCTT	TCTTTATAAT	660
GTGGGATCAC	ATTTTAGTTT	TAACCATAAT	ATTATCTATG	TCATGGACGA	GCCAGCCACT	720
CATTTGAGCG	TGCCAGCCAG	AAAGGAGTTT	AGGAAATTTT	TAAAAGAATA	CGCTCATAAA	780
AATCATGTTA	CTTTTGT TTT	AGCCACCCAT	GACCCCTTTT	TAGTGGATAC	GGATCATTTA	840
GATGAAATAA	GGATTGTGGA	AAAGGAAACA	GAAGGCTCTG	TAATTAAGAA	TCACTTTAAC	900
TATCCCCTAA	ATAATGCAAG	CAAAGACTCC	GACGCTTTGG	ACAAAATCAA	ACGCTCTTTA	960
GGAGTGGGCC	AGCATGTTTT	TCATAACCCC	CAAAAACACC	GAATCATTTT	TGTAGAAGGC	1020
ATCACGGATT	ATTGTTATTT	GAGCGCTTTT	AAATTGTATT	TGCGTTACAA	AGAATACAAG	1080
GACAACCCCA	TTCTTTTCAC	TTTCTTACCC	ATTTTCAGGC	TTAAAAACGA	TTCAAACGAT	1140
ATGAAAGAAA	CCATTGAAAA	ACTTTGCGAG	TTAGACAATC	ACCCTATTGT	TTTGACAGAC	1200
GATGACAGAA	AATGCGTTTT	TAACCAACAA	GCAACGAGCG	AACGATTTAA	AAGAGCTAAT	1260
GAAGAAATGC	ATGATCCCAT	CACCATCCTA	CAACTCTCAG	ACTGCGATAG	GCATTTCAAA	1320
CAAATTGAAG	ATTGTTTCAG	CGCAAACGAT	AGAAACAAAT	ACGCTAAAAA	TAAGCAAATG	1380
GAATTGAGCA	TGGCTTTTAA	AACAAGGCTT	TGTATGGCG	GAGAAGATGC	GATAGAAAAA	1440
CAAACAAAAA	GAAATTTTTT	AAAATTATTC	AAATGGATTG	CATGGGCTAC	AAACTTGATC	1500
AAAAAC						1506

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171

GTGTATTTTT	TTCTGGCATT	GAGCGGGGAA	AAAGTCTTAC	TGCCCGTCAT	TGGCGGTTTA	60
GAACAAAAACG	CGCTAGAAGC	CGGGCTGTTA	AAGGGGGATA	GAATCCTTCT	ATCAACCATC	120
AAAAAA						126

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1050 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172

ATGGAAATTT	TTAAACTCAT	CAACTTTTTT	ACCGGTCAAA	ACGATGCGGG	TAAAACCAAT	60
CTTTTAGAAG	CTCTTTATAC	CAACACAGGC	CTTTGTGATC	CTACTGCCAA	TCAAGTCAGT	120
CTTCCTCCTG	AACATGCCGT	GAATATTAGT	GAATTCAGAA	AAATCAAAC	CGATGCCGAC	180
AACCTAAAAA	CCTTTTTTTA	TCAAGGAAAC	ACCGCTAATC	CCATTAGTAT	CCGCACTGAA	240
TTTGAACATG	CTACTATCCC	TCTTACTATC	CAATACCCCA	CACAAACCAG	TTACAGCAAA	300
GACATCAATT	TGAATAGCGA	TGATGCTCAT	ATGACAAACC	TTATAAACAC	AACAATAACG	360
AAGCCACAGC	TCCAATTTTC	CTACAATCCA	TCCCTTTCCC	CCATGACAAT	GACTTATGAA	420
TTTGAAAGGC	AAAACCTAGG	TTTAATCCAT	TCTAATTTAG	ATAAAATCGC	TCAAACCTAT	480
AAAGAAATG	CGATGTTTAT	TCCTATAGAA	TTATCTATTG	TTAATTCTCT	TAAAGCATTG	540
GAAAATTTAC	AATTAGCAAG	CAAAGAAAAA	GAATTGATTG	AAATCCTACA	ATGTTTCAAC	600
CCTAATAATT	TAAATGCTAA	TACAATAAGA	AAGTCTGTCT	ATATCCAAAT	CAAAGATGAA	660
AACACACCGC	TAGAAGAAAG	TCCCAAAAGG	CTTTTAAATT	TGTTTGGTTG	GGGTTTTATC	720
AAATTCTTTA	TTATGGTGAG	CATTCTTATA	GACAAATCGT	TCAAGTATCT	TTTTATTGAT	780
GAAATAGAAA	GCGGTTTGCA	CCATACAAAA	ATGCAAGAGT	TTTTAAAAGC	TCTGTTTAAG	840
TTAGCTCAAA	AATTACAGAT	TCAAATTTTT	GCCACCACGC	ACAATAAGGA	ATTTTATTAT	900
AACGCCATCA	ACACGATATC	CGATAATGAA	ACGGGAGTTT	TTAAAGACAT	AGCCTTGTTT	960
GAGCTTGAAA	AAGAAAGCGC	TTCTGRCTTT	ATCAGACACA	GCTATTCTAT	GCTAGAAAAA	1020
GCGCTTTATA	GGGTATGGA	GGTTAGAGGC				1050

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1395 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173

ATGGATTTTA	AAAAATGCCC	TAATTTTGAA	AAAAAATGTG	CGTTTCTTTG	TTTCTCAAAT	60
TTGGTTTAC	TTATTGAAAT	CCACTCTAAA	GGACTACACA	TGCAAAAAAA	GAAACCCAAG	120
AACCCGCAAC	CGAATTTTAT	TAGCATCTTA	GATAAGGGCG	ATGTTGCAAC	AAACAATCCT	180
GTTGAAGAGT	CAGACAAGGC	CAATAAAATA	CAAGAGCCAC	TCCCTTATGT	CGTGAAAACG	240
CAAATCAATA	AAGCAAGCAT	GATTTCTAGA	GATCCTATTG	AATGGGCAAA	GTATTTAAGC	300
TTTGAAAAAC	GAGTCTATAA	GGATAATAGT	AAAGAAGATG	TCAATTCTTT	TGCCAATGGT	360
GAGATAAAAG	AAAGTTCTCG	TGTTTATGAA	GCGAATAAAG	AAGGGTTTGA	AAGGCGCATC	420
ACTAAAAGAT	ACGATCTGAT	TGATAGAAAT	ATTGATAGAA	ATAGAGAATT	TTTTATAAAA	480
GAAATTGAAA	TTCTAACCCA	CACAAACAGC	TTAAAGAAT	TGAAAGAGCA	AGGGTTAGAA	540
ATCCAATTGA	CCCACCATAA	TGAAACGCAT	AAGAAAGCCT	TAGAAAATGG	CAATGAAATC	600
GTTAAAGAAT	ACGACCATCT	TAAAGATATT	TACCAAGAAG	TAGAAAGAAC	AAAAGATGGT	660
GGATTGCTAA	GAGAAATAAT	CCCCAGTATT	TCTAGCGCTG	AGTATTTCAA	GCTTTACAAC	720
AAACTGCCTT	TTGAATCAAT	AAACAATGAA	AATACCAAAC	TGAATACTAA	CGACAATGAA	780
GAAGTTAAAA	AACTAGAATT	TGAATTAGCT	AAAGAAGTGC	ATATTTTAAT	CCTAGAGCAA	840
CAATTGCTTT	CAGCAACAAA	TTATTATTCT	TGGATAGATA	AAGATGATAA	TGCGAATTTT	900

211

GCTTGGAAAA TGCATAGGCT TATCAATGAA AATAAACTCA AAGAAAACCA TCTCAGCGCC	960
AATAACGCTA ATAAGATTAA GCAATTTTTC TTTAATAATG GTTCTATTTT AGGCTGGACT	1020
AAAGAAGAAC AAAGCGCTAT ACAAGAAAAC AGAGATTATT CTTTAAGAAG CGCTCTTTTA	1080
AGTTTAGAAG AAATCGCTCA AGCAAAAATT GAATTGCAAA AATACTATGA AAGCGTTTAT	1140
GTTAATGGTG ATGGGAATAA AAGAGAAATC AAGCCTTTTA AAGAAATTTT AAGAGACACC	1200
AACAATTTTG AAAAAGCTTA TAAGGAGCGT TATGACAAAT TGGTAAGCTT GAGTGCAGCA	1260
ATCATTCAAG CTAAAGAGGG TGGTAATGAG CGACAAAATT CTAGTGCAAA TAACAATAAC	1320
CCTATTAAAA ATACAATAGA GACTAATACT TCTAACAAATA TTATTCAAAA TAATGATAAT	1380
ATAATCATCC AAATT	1395

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174

ATGGCGCTTG AAGTGGTTTT ATGGGATTTT GATGGCGTGA TTTTGGACAG CATGCATTTA	60
AAATATGAAG GGTTTAAGGC GTTGTTCCTAA AAGCATGGCA ACGATAGTAA AGAGGGTTTG	120
AAACAATTTG AAGTTTATCA CTATCAAAGT GGGGGGATTT CAAGGAATGA AAAGATCCAA	180
TATTTTATA ACGAGATTTT AAAAACCCTT ATCGCTCAAG AAGAAATAGA TGCATTAGCC	240
CTAGAGTTTG GCGCTATCAT AGAGCAAAAG CTTTTTGATA GGGGGCATTT GAATAGCGAR	300
GTGATGGCGT TTATTGATAA GCATTATCAA AATTATATTT TCCATATCGC TTCAGCGGCC	360
TTGCATAGCG AATTGCAAGT GTTGTGCGAG TTTTTAGGGA TTAATAAGTA TTTTAAGAGC	420
GTGAAGGGA GTCCGCTTGA TAAACCCAAAG ATTATCGCTA ATATCATTCA AAAATACGCC	480
TATGACCCAA GCCGTATGCT AATGATAGCG ATAGCGTCAA TGATTATGAA AGCGCTAAGG	540
CTAATAAAGT GGCGTTTTTG GGCTATAACA GCAAGGTTT	579

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

212

(B) LOCATION 1...423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175

ATGCTCAAAA	AAAAGATTGA	TTTGCAATAA	GATTCTATTA	GGAAGCTCTT	TTTTTATTAC	60
TTCATCCCTT	TAGTTTTTTC	TATGATCTCA	CTTTCTACTT	ACTCTATGGT	AGATGACATG	120
TTTGTGGGCA	AAAAACTGGG	TAAAGAAGCT	ATCGCTGCGG	TCAATATCCG	ATGGCCTATT	180
TTTCCAGGAC	TCATTGCGTA	TGAATTGCTT	TTTGGTTTIG	GGGCAGCGAG	CATTGTGGGG	240
TATTTTTTAG	GTCAAAATAA	AACCCATAGG	GCTAGGCTTG	TGTTTAGCAG	CGTGTTTTAT	300
TTTGTGCTC	TAAGCGCCTT	TATTTTGAGC	ATGGCGTTAT	TGCCTTTTAG	CGAAAATATC	360
GCGCAGTTT	TTGGGAGCAA	TGACGCTTAA	TTGAACATGT	CAAACGCTAT	ATTGAAATCA	420
TTT						423

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176

GTGAAATGTT	TATTAATAAA	AAAATCACTT	CTATTTGCAC	TGAAACCATT	GCCGGACCTA	60
AAAACGACTA	CCCCTATTTT	AGCGCCTATG	AGCGTGCTGG	CTGGGAGGTT	GRCTSCSCAT	120
TTAGTCCAGC	ATTATTTACT	GGCTTTAGAG	CATGTTAAAG	GCTTTATGGG	TAAGGGGGTC	180
ATACTAGGGG	GTTTGTGCGG	TGCSCAAAGG	GCTAAAATCG	TCGTAATTGG	AGCCGGTGTG	240
GTTGGCATGG	AGAGCGCGAA	AGTCTTAARC	CAAAATGGGR	CTAAAGTAAC	GATTTTAGAA	300
TTAGACTACG	CTAAATTACA	AAACCACCCT	TATTATCATT	TGTATGATTT	AGAAGTCTTA	360
AGCGTGAAATG	AAGCCAATAT	CATTCAAGCC	TTAAACGGGR	CGGTGGGGCT	AGTGGGAGCG	420
GTRCTGGTTA	CARCAGACCA	AACCCCTAAA	GTGRTCTTAA	GAAGGCATTT	AAAATAC	477

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

SUBSTITUTE SHEET (RULE 26)

213

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177

ATGCTTGCAA	AAATCGTTTT	TAGCTCATTG	GTTGCGTTTG	GAGTTTTGTC	GGCTAATGTG	60
GAGCAGTTTG	GTTTCATTTTT	CAACGAGATA	AAAAAAGAAC	AAGAAGAAGT	GGCCGCAAAA	120
GAAGACGCTC	TTAAAGCTCG	CAAGAAGCTC	TTAAACAATA	CGCATGATTT	CTTAGAAGAC	180
TTGGTTTTTA	GAACAACAAA	AATCAAAGAG	CTTGTGGATT	ACAGAGCTAA	AGTTCTTTTA	240
GATTTAGAAA	ACAAGTACAA	AAAAGAAAAA	GAGGCTCTAG	AGAAAGAGAC	AAGAGGTAAA	300
ATCCTTACTG	CTAAGTCAAA	GGCTTATGGT	GATCTAGAGC	AAGCCTTAAA	AGATAACCCCT	360
CTTTATAAGA	AACCTCTTCC	TAACCCCTTAT	GCTTATGTTT	TAAACCAAGA	AACATTTCAG	420
CAAGAAGATA	AGGAGCGTTT	GAGTTATTAC	TACCCCCAAG	TGAAAACGAG	CAGTATTTTT	480
AAAAAACTA	CCGCTACCAC	TAAAGATAAG	GCTCAGGCTT	TGCTTCAAAT	GGGTGTGTTT	540
TCTTTAGATG	AAGAGCAAAA	CAAAAAGCG	AGCCGATTAG	CTTTATCTTA	CAAGCAAGCG	600
ATTGAAGAAT	ATTCCAATAA	CATTTCTAAT	TTATTGAGCA	GAAAAGAATT	GGATAATATA	660
GATTATTACT	TGCAGCTTGA	AAGAAACAAA	TTTGACTCCA	AAGCAAAAAG	TATTGCTCAA	720
AAAGCCACCA	ACACGCTTAT	TTTTAACTCG	GAACGCTTGG	CGTTTAGCAT	GGCGATTGAT	780
AAGATCAATG	AGAAATACTT	AAGGGGCTAT	GAAGCTTTTT	CTAACTTGTT	GAAAAATGTC	840
AAAGATGATG	TGGAGTTGAA	TACTTTGACT	AAAAACTTCA	CCAATCAAAA	ATTGAGTTTC	900
GCACAAAAC	AAAAATTGTG	TTTGTTGGTT	TTAGACAGCT	TCAATTTTGA	TACCCAATCC	960
AAAAATCTA	TATTAATAAA	GACTAATGAA	TACAATATCT	TCGTAGATAG	CGATCCTATG	1020
ATGAGCGACA	AAACAACAT	GCAAAAAGAA	CACTACAAGA	TATTTAATTT	CTTCAAAACA	1080
GTGGTTTCTG	CATACCGGAA	CAATGTTGCC	AAGAATAACC	CCTTTGAA		1128

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1056 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1056

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178

ATGGATTTTCG	TAGGGTTTGA	AGATTTAAAA	TGCAAAGACA	AAGAAAACCTC	TCAAAAAGTT	60
TTTGTGATCC	GTAACGATAA	GTTAGGCGAT	TTTATTTTAG	YGATTCCCGC	TTTAATCGCT	120
CTCAAGCATG	CTTTTTTAGA	AAAAGGCGTA	GAAGTGATTT	TGGGCGTGGT	TGTGCCTAGC	180
TATACCACCC	CAATTGCTTT	AGAATTCCTT	TTCATTGATG	AAGTTATCAT	AGAAGACAAC	240
CATTTAGCCA	CCACCCYCAA	AAACCGCTCC	ATTGACGCTC	TTATCTTTTT	ATTTTCTAAT	300
TTTAAAAACG	CCAAACTCGC	TTTCAGTTTG	AGAAAATCCA	TCCCTTATAT	CCTAGCCCCA	360
AAGACCAAAA	TCTATTCTTG	GCTTTATCAA	AAGAGAGTGC	GCCAAAACCG	CTCTTTATGC	420
TTAAAAACCG	AATACGAATA	CAATTGCGAC	TTAATCCATG	CGTTTTGTAA	AGACTACGAT	480
CTCCCTAAGC	CTCAACTTAA	AAAAATCGCA	TGGAAGCTTA	AAGACAAATC	CAAAGAGCGA	540
TCCATCATCG	CTTCAAAACT	CAACGCTAAT	GTTGATCTAT	TGTGGATTGG	CGTGCATATG	600
CATAGCGGAG	GCAGTTCGCC	CGTATTGCC	GCTTCGCATT	TCATTGAGTT	GATTGCAATC	660
TTGCATGAAA	AATTAAGTTG	TGAGATCATT	CTTATTTGCG	GGCCAGGCGA	GAGAAAAGCC	720
ACAGAAGAAC	TCCTTAAAGA	AGTCCCTTTC	GCTCACCTCT	ATGATACGAG	CCATAGTTTA	780
GTGGATTTAG	CCAAATTGTG	CGCGAATTTA	AGCGTCTGTA	TCGGGAACGC	TTCAGGCCCT	840
TTGCATGTGA	ACGCTTTATT	TGACAACCAA	TCTATCGGGT	TTTACCCTAA	CGAACTCACC	900
GCCTCTATTG	CCAGATGGCG	GCCTTTCAAC	GAACAATTTT	TAGGCATCAC	CCCGCCTAAT	960

SUBSTITUTE SHEET (RULE 26)

214

GGCTCAAACG ATATGGGTTT GATTGACATT CAAAAAGAAA GCGAAAAGAT TATGGGATTT 1020
 ATCACAAAAA ATCTTTCTCA TCACATGCAA GAAAGA 1056

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179

GTGGGTGTCT TATCCCTCAA AATAGAGGCA ATTTCTAATT TTTATGGGTT ATGCGTTTTA 60
 GGGGTGTTGT TAGCATGTTT TTATCTTTTA GACGCTTATT ATCTCATGCA AGAAAGGCTG 120
 TTTAGGGAGC AATACCAATG GCTAATAAAA AACCGACTTA AAACCGATGA AAGGCTGTTT 180
 GAAGTCITCC CTATTCATCA AACTTGCCAA TCAACGCAAT TCTTATCGCC ATGCGTTCGT 240
 TTAGTCTTTT CCCCTATTGG GCGT 264

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180

ATGTCTTTAG GGGCAGTGGT CAGCTCACTC CTTTGCCATA AGTTAGAGGG GGCAATATTA 60
 GATCTGAGAG CGTATCGTTS RARAGCTTAT TATCAGGAAA ATAAAGATAC YTTGCTTATT 120
 AAAGGCAAAA AACGCCTTCT TTACAATTAT ATTAAGCCCC ATATTGYTTT AAAGTTGCTA 180
 TGGACAATTA GAAATCGCAC GTRATCATTG GGAAAATTTA CTCAAAATCC AACCGAACAA 240
 CCGCCCACGA ATAACCACAC CATTCAATGG AAAAACRGAA AACATTCTAA TGGACAGAAT 300
 TTTAGTGATT GGTAT 315

SUBSTITUTE SHEET (RULE 26)

215

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181

ATGAAAAAA CAACCCTCTT TGTATTGGGC TTATTATTCA ATAGCTCTTT AAGCGCTGTT	60
GATGGGATT CTCAAACCGA GCCTTCTTCT TTGAATTTGG CTGAAGATAG CCTGCCTTTG	120
AACCATTTCTA ACGCCCAAAA ACTCTCTTTA AAAAACGCAT GGAATAGGGT GTTGTCTAAT	180
CATGAAGGCT TGCATGCGCA GAATACGCCA TTAAGCGAGC GAGTAAAA	228

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182

GTGAAAAAAG TAGAATCCAT GAATGTGGTG CCTTTCATTG ACATCATGCT TGTGTTGTTA	60
GTGATCGTGC TCACAACGGC GTCTTTTGTG CAAACTTCAA AGCTTCCTAT TAGCATTCTT	120
CAAGTGGATA AGGATAGCAC TGATTCTAAA GATGTGTTGG ACAAAAAACA AGTTACGATC	180
GCTATTTCTA ATAAGGGTTC TTTTATTTT GACGATAAAG AAATCAGCTT TGAAAATTTA	240
AAACACAAGG TTTCCACTTT GGCTAAAGAC ACCCCTATTG TCTTTGCAAG GCGA	294

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

SUBSTITUTE SHEET (RULE 26)

216

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183

ATGGGATCTT ACACATTCCC TCTCATTTTG AAGCCAATAT TTATAAACAA AGTGCCTGTA	60
ACGATAGATT TTTATGCGAA CGCCAATTAC TTTTGGATTT ATGGTGCGTT AGCGAATGCG	120
GTGGTGGGGA GCATCAACGC CTTAAACGAT GAAATCAGGT TCAAACGCAA CGCCCAAATA	180
GAAGAAGCTG AATTAGGGAC AGACGGGATT AAGATTAAGC CTATCGCTTT GTATAACCCT	240
AGTGAGGGGT ATTTGAATTA CGCGCTCTCT AGCGTGTTTA TTTTCATCTT ACACCAGGTG	300
ATGCTCATTT CAAGCAGCAT GTTTACTAGC TCCAGGCGTT TGGAAATGGC CCTTTTAGAC	360
AAGAAACAAA TCGCTTTAAG GCTGTGCGCA AGACTCTTGG TGTTTCATGGG GCGGTTTAGC	420
GTTTTTGTTT TATGGTATTT TGGGCGCTG TTTTCITTTT ATGGGATCGA ACGGCATGGA	480
AGCGCT	486

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184

GTGATTATGA CTAAGCTTGA TGGCACTTCT AAGGCGGAG CGATTTTARG CGTGCTGTAT	60
GAGTTGAAAT TACCCATTCT TTATTTAGGA ATGGGCGAAA AAGAAGACGA TTTGATCGCT	120
TTTGATGAAG AACGCTTTAT AGAAGATTG GTTGATGCGG TGTTGTGGA ACAA	174

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

217

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...198
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:185

```
GTGTGTGGGG CTCATGGAAA GAGCAGTATC ACGGYCATGT TGAGCGCGAT TTGCCCCGCT      60
TTTGGASSGA TTATTGGGCG GCATTCTAAA GAGTTTGATT CCAATGTSSG AGAGAGCGCG      120
GATATGAGTT TGGTTTTTGA ASCCGATGAA AGTGATTCAA GTTTTTTTAT TTTCCAACCC      180
TTTTTGCGCG ATTGTGCC                                     198
```

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...231
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:186

```
GTGAATGAGT TAAAAAACTC TAAGCAASTT TTAGGGAATG GGAAAGCCGA TCTGAGCAAC      60
GAAAACACCA AGGTAAGGCA GACTAAAACA RATCTGACTG AAAAAAATCA AAGGCTAACC      120
ACAGAAAAAA CAGAAATAAA TAACAAGATT ACTGGGTTAG CCACAGAAAA AGAAAGGTTA      180
GCCGCAGACA AAGAAAACCT AACTAAAGAA AGCAGACAAA GAAAACCTAA C                231
```

(2) INFORMATION FOR SEQ ID NO:187:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 555 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

218

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187

```

ATGGATTAC AACAAATGA TGAGCTAGAA AATAAGTTTG AAGAACAAGA AGAACAAGCC      60
CAAGATACCC CCCTAAAACA AGAGCCTAGC ACAAAGGAAG TAAAAATCCC TAAAAAAGG      120
GGGCGTAAAA AAAGCTTGTT AGATGAAGAT AAGAAAAAGA GCTTTAACAT TGCCTTTAGT      180
CCTTGTGTGA TAAAAGAACT TAATGAATTT TTGCTAGAAT TTGGCTCATT TAAAGAGACA      240
CGAAGCACTT TTATTGAAGA AGCGCTTATT AGGCATTTAA AACACAGAAA AAACACCCAA      300
GAGCAAAAGC TTTTAAAGCA ACTAGAAAGA TTACAAAACA AAGAAAAGGG AATAATGAAA      360
ACAATGAAC TGAATGAATT TTTTACGCAT AAGATAATCT ATAAAGACAC CCCTTTAAAG      420
TTTAAGGATA CACTAGAACA AGAAATCAGC CAAGCTAGTT TAGTAGAGAA GTTAATCTTA      480
GCTAATATCT TAGCCAATAT GGTGTTTGCT AAGATAAGCA ATGAGAATGC CCCTAAAATT      540
CTTATTTTCA CGGCT

```

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188

```

ATGGGGTGCT ATGGGATAGG CATTAGCCGG TTGCTCAGCG TGATTTTAGA GCAAAAAAGC      60
GATGATCTAG RCTGTGTGTG GACGAAAAAT ACCGCTCCTT TTGATGTGGT GATCGTGTT      120
TCTAACCTGA AAGATGAAGC GCAAAAAAAA CTCGCTTTTG AAGTGTATGA AAGACTGCTC      180
CAAAAGGGCG TTGATGCGCT GTTAGATGAC AGAGACGCTC GTTTTGGGGC GAAGATGAGG      240
GATTTTGAAT TGATTGGGGA ACGATTAGCC TTGATTGTTG GGAAGCAAAC TTTAGAGAGT      300
AAGGAATTTG AATGCATCAA ACGCGCTAAT TTAGAAAAGC AAACGATCAA AGACATAGGA      360
ATTAGAAGAA AAAATTTTAG AAATGTTAGC GAGCGAATAA GGGGAGGGAA TGGAAAAAYT      420
AGTGATTGGC TC

```

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

219

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189

ATGGAATAC AACAAACACA CCGCAAAATC AATCGCCCTT TAGTTTCTCT CGTTTATGCA	60
GGAGCGTTGA TTAGCGCCAT ACCGCAAGAG AGTCATGCCG CCTTTTTCAC GACCGTGATC	120
ATTCCAGCCA TTGTTGGGGG TATCGCCACA GGCACCTGCTG TAGGAACGGT CTCAGGGCTT	180
CTTAGTTGGG GACTCAAACA AGCCGAAGAA GCGAATAAAA CCCCAGATAA ACCCGATAAA	240
GTGTTGGCGCA TTCAAGCAGG AAAAGGGCTT	270

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 804 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190

ATGTCAGAAA AAGAAAGACT GAATGAAGTG ATCTTAGAAG AAGAGAATAA TGGGAGTGGT	60
ACTAAAAAGG TGTTTTGTAT CGTGGCCATA GCCATTATCA TTTTGGCGGT GCTTTTAATG	120
GTGTTTTTGA AAAGCACCAG AGTCGCTCCT AAAGAGACTT TTTTACAAAC CGATAGTGGC	180
ATGCAAAAAA TAGGCAACAC TAAAGATGAG AAAAAAGACG ATGAGTTTGA AAGCTTGAAT	240
ATGGATTCTC CCAAACAAGA AGACAAGTTA GACAAAGTGG TGGATAATAT TAAAAAACAA	300
GAGAGTGAAA ATTCTATGCC CATTCAAACC GATCAAGCTC AAATGGAGAT GAAAAACAAC	360
GAAGAAAAAC AAGAATCTCA AAAAGAATTA AAAGCTGTTG AGCCTATTCC CATGAGCACT	420
CAAAAAGAAT CTCAGGCTGT GGCTAAAAAA GAAACCCCCC ATAAAAAGCC TAAAGTAGCG	480
CCAAAAGATA AAGAAGCGCA TAAAGRTAAA GCTAAGCATG CAGCTAARGA GCCAAAAGTC	540
AAAAAAGAAG CTCGTAAAGA AGTTTCTAAG AAAGCTAATT CTAAAACCAA TCTTACTAAA	600
GGGCATTATT TGCAAGTGGG GGTTTTGGC CACACGCCCA ACAAAGCCTT TTTACAAGAG	660
TTTAATCAAT TCCCCATAA AATTGAAGAT AGGGGGGCTA CTAAACGCTA CCTYATAGGY	720
CCTTATAAGA GCAAGCAAGA AGCCTTAATG CATGCCGATG AAGTCAGCAA GAAGATGACT	780
AAACCGGTTG TCATAGAACT GCGG	804

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 513 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

220

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191

GTGGAATATT	ATGCGTTTAA	TTTCAGCGTG	TTGGATTTTG	TCTTAATGGG	GAAAGCGACG	60
CATTTGAATC	TGTTTCGCTAT	GCCTAAAGCT	AAGCACATTA	AAGAAGCCAC	GAGCGTTTTA	120
GAGCGCTTGG	ATTTAGAGTC	CTTAAAAGAT	CAAGGCATTA	ACGATTTGTC	CGGCGGTCAA	180
AGGCAGATGG	TACTTTTAGC	CAGAAGCTTG	TTGCAAAGAA	CGCCCTTATT	GTTACTGGAT	240
GAGCCTACGA	GTGCGTTAGA	TTTAAAAAAC	CAAGCCCTTT	TTTTTGATGC	GATTAAAGAT	300
GAGATGAAAA	AACGAGAATT	GAGCGTTTTA	GTCAATATCC	ATGATCCCAA	TTTGGTTGCC	360
AGGCACTCCA	CGCATGTGGT	CATGCTCAAA	GATAAAAAAC	TTTTTTTGCA	AGCTTCCACG	420
CCAATCGCTA	TGACTTCACA	CAATTTAAGC	GCGCTTTATG	ACACGCCCCCT	ARAAGCGATC	480
TGGCATGATG	ATAAGCTTGT	GGTGATGCG	TTG			513

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 306 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192

ATGATGGCAC	ATTCACCTAT	TTTGGTTTCA	AAAACATCAC	TCTCCAACCT	GCTTATTTT	60
GTGGTTCAAC	CTGATGGGAA	ATTGAGCATG	ACTGATGCCG	CCATTGATCC	TAACATGACT	120
AATTCAGGAT	TGAGATGGTA	TAGAGTTAAT	GAAATTGCAG	AGAAGTTTAA	GCTCATTAAA	180
GACAAAGCCC	TTGTAACAGT	GATCAATAAA	GGCTATGGGA	AAAATCCATT	GACAAAAAAT	240
TACAATATCA	AAACTATGG	TGAATTGGAG	CGTGTGATTA	AAAAGCTCCC	TCTTGTGAGA	300
GATAAA						306

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 711 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

221

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...711
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:193

```

GTGCTGAATG AAGAGCAAAA TTCATTAGAA GAAAAAGGGG GCGAAAACAA AAACGAAAAA    60
GAAACCCCCC TAAAGGGCAT TCATTCTAAA ATCCCCTCTT TGAAGCAGGC TTGGGAGCAG    120
ACGATTAGTA AAATCAAAAAG CTCTAAAGAG TTTTCAAAC AGCTTCTACA CAATAAAAAA    180
AAGCTTTATA TCGCGCTTGG AATATTGCTT TCACTCATCG CGCTCATTGT GGCTTTGAGT    240
TTGTTACTAG GGCATAAAAA AGAAAATAAA CAAACTTCTT TACAAACTAA TACCGCCACC    300
ACCAATAACG AAACGCCTAA CGACACCAAT AACGCAGAAG CCGAAGGGCA AATAGAAAAT    360
TTAGACTTGC CTGATTTAAT CGGCAAAGAC TCTTTGAAAA GAAACGATGA AAGCCAAGTG    420
GATGCGATGA TGCAAAAAGC GAGCCTTTTG TATGAGCAAG GGCAAAAAGA TGAAGCCTTG    480
CATTTGTTTG ATAAGATCGC TTCTTTCTCG CAAGGGATTG CGAGCCATAA TCTAGGGGTG    540
ATTAAATTC AAGAAAAGGA TTTTAATGGG GCGTTGGATT TGTTTGATTG CAGTATCGCT    600
TCTAAAGAAA ACGCGAGCGT GRGCGCGATT GATGCGTTAG TTACGGCTTA TCATTTGCAA    660
GATGCGGATT TGTATTATCA TTATCTAAAA ATTGTRAAGA GACACTTTGT A              711
  
```

(2) INFORMATION FOR SEQ ID NO:194:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 675 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194

```

ATGAATACAA GCTTATTGAC CCAAGCACAG GTTTTAAGCT CTAAAGAAAA TCAAATCCAT    60
CGCCTTTTGT TAGAGCTTTT AGAAGAGGCT AAGCTTCATT TTGAGCCTAA GCTTTATATC    120
ATTAACGCCC CTTACATGAA CGCTTTTGCG AGCGGGTGGG ATGAATCTAA TTCCCTTATC    180
GCTCTTACAA GCGCTTTAAT AGAGAGGTTA GATAGAGACG AATTAAAAGC CGTGATCGCT    240
CATGAGCTCA GCCACATACG GCACAACGAC ATCCGCTTGA CCATGTGCGT GGGGATTTTG    300
AGCAATATCA TGCTATTGGT GGCTAATTTT AGCGTGTATT TTTTCATGGG GAATCGCAAG    360
AATAGCGGGG CGAATTTAGC CCGAATGATT TTATGGGTTT TACAGATCAT CTGCTTTT    420
TTAACGCTCC TTTTGCAAAT GTATTTGAGC CGCACACGAG AATACATGGC CGATAGCGGG    480
GCGGCGTTTT TAATGCATGA CAATAAGCCC ATGATCAGAG CCTTACAAAA GATTTCTAAC    540
GATTACACCA ACAACGATTA TAAAGAAATA GATAAAAATA GCACCCGATC AGCGGCCTAT    600
CTTTTAAACG CTGAAATGTT TAGCACCCAC CTTAGTATTA AAAATCGTAT CCAATCCTTA    660
AGAAAGCGTG TGATC              675
  
```

SUBSTITUTE SHEET (RULE 26)

222

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1605

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195

```

ATGTTTAATA TTAAAAGGAC TTTTAAATA ACGATCATAA GTTTTTTCT CATTCCTCT 60
AATTGGTTGA AAGCTATTGA TTGCCCCATT GTTTCAAATC TCAAAATTTA CCAAACAGTT 120
TATTGCATGC TGATACCGAG TTATGTTTAA ACCAACAAAA GTTTTGCAGA TATTTTGACA 180
GGCTATACAT CTATTGGTGC ATCAGGGAGT GGAAAGAGTT CAGGGCAGGG TGTGATCGAA 240
GCGCTTAGCA CACCATAGC CACAAGTTA GCCGCTAGCA ATCTGGTGAA ATATTTGAAT 300
ACTTTAGGTC CTTTATGGGG ATCGGCGTGG GCAAGTGTG CTACAGCTAT ACAAGGTTTT 360
GCTCTAACGC CATCAAGTGG CTGTAATTTT GGTGGAACG CATTGATAAA TAAAAACATA 420
GATGTATCCA TGGATAGCGT ACTAGACAAT TTGAGCAACA AGATTCAGAA TTTTACCAA 480
GGCGGTGTTG AGGACAATGT GAAAGGCAAT ATTCTTTTAC AAATAATTGG CTCAATAACC 540
GCTCAAGCTT CTACGAATAT TACAGCTGAT GGTTTAATTT GGCTGATTGG TAAAGAATTC 600
ACTGCAATAA AACTGCAAAA CAACACTATA GCCATGCTTG CTTTGGCCGC ATTAGAATCT 660
GTTGTCAAAG GAGCGGACGC TGCTGTTCTT CCTGCATATG GTGTAGTCAA TCTGCCTGAT 720
ATTATCATAG GGCAAGGGTC ATATCTTGAT TTTGTTTCTT ACCTAATTTA TATTGTTTTT 780
GGGATTTTTG TTTTATTTTC TTTTATGAAA TTGAGAGATA TTTCAAACGG CATTGAGATT 840
AACATAGGTT TTGAATACAT GCGATTGTGTT GGGGGGACAT TATTCAAAAT GGCGATGGTC 900
TCTTTTATCG CCTATGCAGG TTTTGGTTAT CTTTATAAAA TCTCTTATTC TATTATTTTT 960
GGTTTAGCAG GTGCTTTTGG GCTGAATCAA GTTCTTTTTT GGGCTTTAGA TTTAGTGCTG 1020
AATTACACTG TTAATTCAAT TTTACCTGCG GTAAGAGCTG TTTTCTTAA TGTGGCAAC 1080
AACGCTCCTA GTTTGTTACA AGGCTTGCAA GTGGCAGGTA TTTCTTTATT CGCTATTTTT 1140
ATGCAAGTAA CTATCATTAT GAGAATAAGC ACTGTTGTG TGAAACCTTT GATAGCGGGG 1200
GCTTTTAGCG GTATTGTTTT CCCTATTGCA GTATGTTTGA TCGTGCTAGA TTGGTTCAA 1260
GATTCTATGA AAAACATATT GATATGTTT ATTAATAATC TGTTTATCTT GGTCTTAGCT 1320
ATTCTATTTT TGCTCTTTGG TGTTTTGGCA TTATTGGCAT TCAATTTGAC CATAACGCCC 1380
TCTGTTGCTA TACAAAACAT CAATCAAGGG GGATTGGGTA TCGATTCAAC TATTGCGAGT 1440
TTGATCACTC TATTTATTTT AAAAGGTTTC ATAGAGACGA TTATTGAGAG CGTCAATGCG 1500
ATCGTTAACA CCATTTTCAG CTCTGTCTCT ATGGATGGTA GCAGAAATGGA TAGAGAAAGA 1560
GATGCCCTAA TGGTGGGAAG AGTTGGTGGA TCTATGTTA AAGGA 1605

```

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

223

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196

ATGGCGTTTT	GGCAGGCTAT	CCGGTGGTGG	ATTTTAAAGT	TACCCTTTAT	GATGGGAGCT	60
ACCATGATGT	GGATTCTTTC	AGAAATGGCG	TTTAAATCG	CTGGYTYTAT	GGCGTTTAAA	120
GAAGCGAGTC	GTGCGGCTAA	CCCGGTTTTC	CTAGAGCCTA	TGATGAAAGT	GGAAGTGGAA	180
GTCCCTGAAG	AATACATGGG	CGATGTGATT	GGCGATTTAA	ACAGAAGAAG	AGGGCAAATC	240
AATTCTATGG	ACGATAGATT	AGGTTTGAAA	ATCGTGAATG	CTTTCGTGCC	GTTAGTGGAA	300
ATGTTTGTTT	ATTCTACGGA	TTTGCGATCA	GCCACTCAAG	GGCGTGGGAC	TTACTCTATG	360
GAGTTTGACC	ACTATGGCGA	AGTGCCTAGC	AATATCGCTA	AGGAAATCGT	GGAAAAACGC	420
AAAGGC						426

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 459 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197

ATGCAGAATT	TGCCGGGTAT	GGCGAGAGCG	GCGATGCTAA	CCACATCATC	AGCCCCAGCC	60
CCTGAGGGTG	AAGGGGCTTT	TAGAGCCATG	AAAATGGCTT	CAGAAATGGC	GAAAGTGGAA	120
GTAGGCTATG	TGAACGCCCA	TGGGACAAGC	ACGCATTATA	ACGATTGGTA	TGAAAGCATT	180
GCGTTAAAAA	ATGTGTTGGC	TCTAAAGAAA	AAGTCCCTCC	TGTTAGCTCC	ACTAAAGGGC	240
AGATTGGGCT	TGCTTGGGTG	CTGCGGGGTT	AGAAGCCGTT	ATTCTATCAT	GGCCATGAAY	300
CAAGGGATCT	TACCTCCTAC	CATTAATCAA	GAAACGCCTG	ACCCAGAATG	CGAYCTGGAT	360
TATATCCCTA	ATACAGCCAG	AGAAAAGCAA	GTGAATGCGG	TGATGAGTAA	CTCATTGTTG	420
TTTGGTGGCA	CTAATGGTGT	TGTGATTTTC	AAAAAAGCC			459

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 279 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

SUBSTITUTE SHEET (RULE 26)

224

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198

ATGATACTAA AAAATTTGAT TTTGTTATTT TTAGCAAAGA GAAAACTTAT TTTCATAGAA	60
GCTAATTTTT ATACCATTAG TGGGAGCAAG CTTAATGAAG TCGCAAGATC CTATCAAGAC	120
TTAGCTTTTAA AATTGGAAGC ATTTCTTAAT TACGAATTTA TTGGGATAAC TGATGGCATA	180
GGTTGGCTAG ACGCTAAAAG CAAGCTCCAA GAAGCTTACA AATCTGTAGA AATCTATAAC	240
TTAAGCTATG TGAATGATTT TATATCAAAG GTGCAAAA	279

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199

ATGGAATCAC AACTCATGAA ACTCGCCATT GAAACTTATA AAATCACTTT GATGATTTCT	60
TTACCGGTAT TATTAGCGGG CTTAGTGGTG GGGCTGTTAG TCAGTATTTT TCAAGCGACC	120
ACCCAAATCA ATGAAATGAC TTTGTCTTTT GTGCCAAGA TTTTAGCCGT GATTGGGGTG	180
CTGATTTTAA CCATGCCGTG GATGACGAAC ATGCTTTTAT ATTACACCAA AACCTTAATC	240
AAGCTCATTC CTAAATCAT AGGC	264

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 345 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

225

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200

ATGAAATTTT TTACAAGAAT CACTGACAGC TACAAGAAAG TTGTAGTAAC TTTAGGGCTA	60
GTGGTAACAA CCAATCCTTT AATGGCGGTC ACCAGTCCTG CAACAGGCGT TACTGAGACT	120
AAAAGTTTGG TTATTCAGAT CATTTCTGTT CTAGCGATCG TAGGTGGTTG CGCTTTAGGG	180
GTCAAAGGCA TAGCAGATAT TTGGAATATC TCTGATGACA TCAAAAGAGG TCAGGCGACT	240
GTTTTTGCTT ACGCGCAACC CATAGCTATG TTAGCGGTGG CAGGTGGCAT TATCTATTTG	300
AGCACTAAGT TTGGCTTCAA TATTGGCGAG AGTGGAGGAG CTAGC	345

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201

ATGAAAAATC CCCAAGCTAA TGTTTTAAAA CTCTTTTAA ATCAAGTGGC TGACCAAAAA	60
TACATAGATA TGAATGATGA AAAAAACTAT GACCCAAGAG AACCTGAACC CCCTTATGGA	120
ACAAAAGGGG CGTTAGATGA GATTATAAGG ACAGATGCTA GGAGTTGGGC AAACACTCCT	180
GATGATGAAT TTGGGAGCAT TATGTCTTCT TTAAAGCGTT TTATGTATGT CTATAAAGAC	240
CCAAAAGTGC GTGAAGCTAC TTCTAAAATG AGCTTTGATT ATGAAGAATT AAGAACGGGC	300
AATATCAGTA TTTACATTGT AATCGCTCAA ATTGATATAG GCACACTTTC TTCTTTAGTA	360
AGAGCCTTTT TAGAGAGTAT TGCTAAAAAC CTTATGGTCA AAGAAAGCTC TAAACCTGAA	420
GAGCGTATTT TTATCATTCG TGATGAATTT GTTAGATTG GTAAGTTGCC TTTCTTGTTA	480
GAAATGCCAG CACTTTGTCT CTCTTATAAT GTTGTCCCCT TATTCATCAC GCAAGATTAT	540
GCTATGATTA GAAATACTAT AGCGATGATG ATT	573

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1053 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

226

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202

ATGATAAGTC	AGATTATTAA	GTTTCAATTA	AAAGGAATAA	AAATGATTAG	ATTAAAAGGT	60
TTGAATAAAA	CTTTAAAAAC	AAGCTTATTA	GCTGGGGTTT	TACTAGGTGC	TACTGCTCCC	120
TTAATGGCAA	AGCCTTTATT	AAGCGATGAA	GACTTATTGA	AACGAGTAAA	ACTACACAAT	180
ATCAAAGAAG	ATACGCTGAC	TAGCTGTAAT	GCTAAGGTGG	ACGGCTCTCA	ATACTTGAAT	240
AGTGGTTGGA	ATTTATCTAA	AGAATTTCGG	CAAGAATATA	GAGAAAAGAT	TTTTGAATGC	300
GTAAGAAGAG	AAAAACATAA	ACAAGCCCTT	AATTTAATCA	ATAAAGAAGA	CACTGAAGAT	360
AAAGAAGAAG	TTGCAAAAAA	AATCAAAGAA	ATTAAAGAAA	AAGCTAAAGT	TTTAAGGCAA	420
AAATTTATGG	CTTTTGAAAT	GAAAGAACAC	TCTAAAGAAT	TCCCAAATAA	AAAGCAACTT	480
CAAACCATGC	TTGAGAACGC	TTTTGATAAT	GGAGCTGAAA	GTTTTATTGA	TGATTGGCAC	540
GAACGCTTTG	GGGGTATAAG	TAGAGAGAAT	ACTTATAAAG	CACTTGGCAT	TAAAGAATAT	600
AGTGATGAAG	GAAAGATATT	AGCCTTTGGC	GAAAGAAGTT	ATATTAGACA	ATATAAAAAA	660
GATTTTGAAG	AAAGCACTTA	TGATACTAGA	CAAACCTTAT	CTGCTATGGC	TAATATGAGT	720
GGCGAAAACG	ATTATAAAAT	TACTTGGTTA	AAACCCAAAT	ATCAGCTCCA	TAGTTCAAAT	780
AATATTAAAC	CCTTAATGTC	AAACACAGAG	TTGTTAAATA	TGATAGAGCT	AACCAATATC	840
AAAAAAGAAT	ATGTTATGGG	CTGTAATATG	GAAATAGATG	GTTCTAAATA	TCCCATTTCAT	900
AAAGATTGGG	GATTTTTTGG	TAAGGCAAAA	GTCCCAGAAA	CTTGGAGAAA	TAAGATTTTG	960
GAATGTATTA	AGAATAAAGT	AAAGTCCTAT	GACAACACTA	CCGCTGAAAT	AGGAATAGTT	1020
TGGAATAAAA	ATACTTATTC	TATCTCTCAT	CAC			1053

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1053 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203

ATGGCTGATA	TTTTAAGCCA	AGAAGAAATT	GATGCGCTTT	TAGAAGTCGT	TGATGAGAAT	60
GTGGATATTC	AAAAATGTCCA	AAAAAAAGAT	ATTATCCCCC	AACGCAGCGT	AACCCCTCTAT	120
GATTTCAAGC	GCCCTAATCG	TGTGAGTAAG	GAGCAATTGC	GCTCTTTTAG	GAGCATCCAT	180
GATAAAATGG	CTAGGAATCT	TTCCAGTCAA	GTCTCTTCTA	TCATGCGTTC	TATTGTAGAA	240
ATCCAGCTTC	ATAGCGTGGA	TCAAATGACT	TATGGCGAAT	TTTTGATGAG	TTTGCCTAGC	300
CCTACGAGTT	TTAATGTCCT	TTCCATGAAG	CCTATGGGGG	GAACGGGGGT	TTTAGAGATT	360
AATCCTTAGC	TTCGCTTTCC	TATGATTGAC	AGACTATTAG	GGGGTAAGGG	GAGCGCGTAT	420
GATCAAAACA	GGGAGTTTAG	CGATATTGAA	TTGAATTTAT	TGGATACGAT	TTTACGCCAG	480
GTGATGCAAA	TTTTAAAAAG	AGTGTGGTCG	CCTGTGGTGG	AGATGTATCC	TACCATTGAC	540
GCTAAAGAAT	CCAGCGCGAA	TGTGGTCCAA	ATCGTCGCTC	AAAATGAAAT	TTCTATCATG	600
GTGGTTTTAG	AGATTATCAT	TGGGCATAGC	CGTGGGATGA	TGAATATTTG	TTACCCGGTG	660
ATTTCCATTG	AGAGCATTCT	TTCTAAAATG	GGGAGTAGGG	ATTTTCATGCT	TTCAGAAACC	720
AACTCCAAA	AGAGCCGTAA	TAAGGAATTG	CAAGCACTAT	TGAGCGGGGT	GAGCGTGGAT	780
ATGATGGTGT	TTTTGGGCGC	GGTGAATTG	AGTTTGAAAG	AAATGTTGGA	TTTAGATGTG	840
GGGATACTA	TCCGGTTGAA	TAAAGTCGCT	AACGATGAAG	TGAGCGTGTA	TGTACATAAG	900

SUBSTITUTE SHEET (RULE 26)

227

AAAAAGCGTT ATTTAGCGAG CGTGGGGTTT CAAGGGTATA GGAAAACCAT TCAAATTAAA 960
 GAAGTGGTTT ATAGCGAAAA AGAACGCACT AAAGAAATTT TAGAAWTGCT WGAAGAACAG 1020
 CGCAGGAGGC AAAGTTGGGC GRTGTTATGG AGC 1053

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204

ATGCCCACGA TGTTAGCGGT TGGTTTTTGG GTGTTGGTTT TTTTATCCAC GAGCAATGCG	60
GTGAATTAA CCGACGGGTT AGACGGATTA GCGAGTGTGC CTAGCATTTT CACCCCTCTTA	120
AGCCTTTCTA TCTTTGTGTA TGTGGCAGGG AATGCGGAAT TTTCTAAATA CTTGCTCTAT	180
CCTAAAGTCA TAGATGTGGG GGAATTGTTT GTGATTTCGC TAGCATTAGT GGGATCGCTC	240
TTTGGCTTTT TGTGGTATAA CTGCAACCCG GCAAGCGTGT TTATGGGCGA TAGCGGGAGT	300
TTGGCAATAG GAGGGTTTAT CGCTTATAAC GCTATTGTTT CGCATAATGA AATCTTGCTC	360
GTTTTAATGG GGTCTATTTT TGTAATAGAA ACTCTGTCTG TGATCTTGCA AGTAGGGAGC	420
TATAAAACCC GTAAAAACG CCTTTTTTTA ATGGCACCCA TCCATCATCA TTTTGAACAA	480
AAGGGTTGGG CAGAAAATAA GGTGATCGTG CGTTTTTGGA TCATTTCTAT GCTGAGTAAT	540
TTAGTCGCTC TTTTGAGCTT GAAGGTGTGT	570

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205

GTGCGTTTTG AAAATTTTCAT CAACCGCCTA GCCTTTTACA TGGCCACAGG GAGCGGTAAA	60
ACGATCGTCA TTATCAAACCT GGTAGAGCTT TTAAGCGTGG CTATGGGAAT GGGTTTGATC	120

SUBSTITUTE SHEET (RULE 26)

228

CCTAAGAAAA	ATATCATGTT	TTTAGCGCG	AACGAGCATT	TAATCAAGCA	ATTTGAAAAA	180
GAAATTGAAA	AATACAACCG	CAATAAGGAC	TATTCCAAAC	AAATTGATTT	CAAAAACCTT	240
AAAAGCGTTA	AGAATAAGGA	TTTTTATCGT	GCTCCAAAAG	ATTCTTTAAT	GAAAGAAATC	300
GCTCTTTTTT	ATTACCGCGC	AGATTTAATG	AGCGATGAAG	AAAGCAAGGA	AAACCTTTTA	360
AATTATAAGG	ATTGTTGGGA	TAATGGGGAA	AATTATGTGA	TTTTAGATGA	AGCGCATAAG	420
GGGAATAAGA	CTGAAAGCAA	AAGACAGGCG	ATTTTATGCC	TGCTGTCTTT	AAAAGGGTTT	480
TTATTCAATT	TCAGCGCCAC	TTTCACTGAA	GAAAGCGATC	TCATCACTGC	GGTGATAAT	540
TTGAGCGTGG	GCGAGTGGGT	GAAACTTGGC	TATGGTAAAG	AGTCTGTTTT	ATTGAAGAAA	600
AACAACCTTA	ACGCTTTTAA	GGAATTGAAA	GATTTAAACG	ACAGGGAAAA	AGAAATCGCT	660
CTTTTAAAGG	CGTTATTGCT	TTTAGGCATG	CAAAAACGCT	ATAAAGTAGA	AGGCTATTTT	720
CATGACCCTT	TAATGCTCGT	GTTACGCGAT	TCTGTGAACA	TGGAAAACAG	CGATGCGRAA	780
ATCTTTTTTA	AAACTTTAGC	GCGCGTGATT	GAAAATGATG	ATGAGAGCGA	TTTTTCAAAA	840
GCTAAGACG	ATTTATTAGA	GGAATTAAAG	AATCCGGAAT	TCCTTTTTAG	CGATGGCAAA	900
GATAAGAAA	AAGACTATAA	AATTGAGGTC	TTTAAAGAGA	GTTTAAAGGG	CATGGATTTT	960
AAAGGCTTAA	AAGAAGCAGT	TTTTTATGCC	AGTAATGGGC	ATATTGAAGT	CATCATTAAC	1020
CCTAAAAACA	ACCAAGAAAT	CGCTTTC AAG	CTCAACACGA	GCGATAAAGT	CTTTTGCCTG	1080
ATTAGAATAG	GCGATATTAC	AGAATGGATC	CGTGAAAAAT	TAAAGAGCGT	GAAGTGCGTG	1140
AGTAAGAATT	TGAGCTTCAA	AGAAGAGAGC	TATTTCAAGC	AGATTGATAA	GAGCAGTATC	1200
AATATCTTAG	TGGGGTCTCG	TGCTTTTGAC	ACTGGGTGGG	ATAGCACAAAG	GCCTAGCGTG	1260
ATTTTATTTT	TAAATATAGG	GCTTGATGAT	GACGCTAAAA	AGCTGGTGAA	ACAATCTTTT	1320
GGCAGGGGCG	TAAGGATTGA	AAGCGTCAAA	AACCAACGCC	AAAGGTTAGC	GTATTTAGAG	1380
ATAGATGAAG	CCATTAAAGA	ACAAGCTGAA	ACCAAACGCT	GCAATGCTGG	AAATGCTTTT	1440
TGTGATACCT	ACCAACCATG	CAAGCCT				1467

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206

GTGTTTAAAA	ATTCCCTCTT	TGGTATATCA	ATCTCCATGC	TTATCACTTG	GGTTTAAACC	60
GCTTGATATT	TGATTTTAT	CCTTTTGTG	CCGAATTTTA	CCCTTACGCA	TCCCAATTTT	120
CATTTCACTC	CGTTTGAAAA	AACCTATTTT	CAAATCTAG	GACTTGTTGG	TATTGTAAGT	180
TCTATTATTT	TCACCGGGTT	TTTGGCTGAT	AAAATCAAAC	CGCACAAAGT	TTGCATGGCT	240
TTAGCSCGA	CCTTTGGGTT	TTTGGCTTT	TTATCTTTTA	AGGAATTTTA	TTCTAACGCG	300
CCAAGTTTAG	TCAATACTAT	AATTTTATAC	TTTTTAGCTT	GCTTTTGC GC	GGGCATTATG	360
AATTTTGGCC	CCATTTTCAT	GAGCGATGTG	TTTAGCGCTA	RAATCCGTTT	TAGCGGGATT	420
TCCTTTGCTT	ATAACATAGC	CTATGCTATA	ACCGCTGGCT	TTACCCCTCA	ACTTTCAAGC	480
TGGTTAAACG	CAAAAGCTAT	AGCAGTGCCT	GAAAGTTTGC	AAAGTTATGG	TTTAAGCTTT	540
TATATCCTTA	TAGTTTCTTT	AATTGCTTTT	ATTACATCGC	TTTAAATGGC	GCCAATTTAT	600
CACAAATCTA	ATACCCAACA	CGAAGTGTCG	CCCACGGCA			639

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 base pairs

SUBSTITUTE SHEET (RULE 26)

229

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207

ATGAAAAGCG	ATAAACCCCTT	TTTAGAACGC	TATTTTATG	ACCCCACTCT	TTTGCAAAAG	60
GGGTGATT	TCGCGCTCTA	TCCTTTTCT	TTAATCTATC	AATGTATTGC	CACAATTAAA	120
CGAAAACCG	CTAAAAGCA	TGATTTTAAA	ATCCCCATTA	TCAGCATAGG	CAACTTGATC	180
GCTGGGGGAA	GCGGTAAAAC	GCCCTTCATT	TTAGAAATCG	CTCCAAGATA	CCAAGAAGTG	240
GCGGTTGTTT	CTAGAGGGTA	TCAACGGGAT	TCTAAAGGTT	TAGTGGTGGT	GAGCGTTAAA	300
GGAAACATTT	TAGTTCCTCA	AAAAACAGCG	GGCGATGAAG	CCTATCTTTT	AGCCTTAAAT	360
CTAAAACAAG	CGAGCGTGAT	TGTGAGCGAA	AAAAGGGAGC	TAGGCGTTTT	AAAAGCCCTT	420
GAATTAGGAT	CAAAGATCGT	GTTTTTAGAC	GATGGTTTTA	GGTTTAATTT	CAACCAATTC	480
AATGCGCTTT	TAAAACCCAA	AGTCCCCCCC	TACTACCCTT	TTTGTGTTGCC	TAGCGGGTTG	540
TATAGAGAAA	ATATTAAAAG	CTATAAGAA	GCCCATTTAG	TCATTACAGA	AGATAAGGAT	600
TATCAAAGAA	TCACCTCTAT	CACTAACCCC	ACCAAACGCA	TGCTTTTAGT	AACGGCTATC	660
GCTAACCTTA	GCAGGCTTGA	TGCGTTTTTA	CCCAAAGAAG	TGGTTAAAAA	ATTGTATTTT	720
AGAGACCATG	CCCTTTTGA	TTTGAAGCTT	TTAGAAAAAG	AGTTTTATCA	AAATAACGCC	780
ACCTCCTTAT	TGGTTACTTC	AAAAGATCTC	GTCAAATTAC	AAGATTGCAA	ATTGCCTTTA	840
AGCGTATTGG	ATTTAAACT	AGAAATTTGC	CCTAAAGTTT	TAGAGGAGAT	TGATCGTTAT	900
ATCCTTTCTT	ATCCTTGTA	TATAAAAGAA	CATCTA			936

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208

ATGTCTTTAG	GGGCAGTGAT	CAGGCTTATT	TTTTGTTATA	AGTTAGAGGG	GGTAATATTA	60
GATTTAAAGC	GCATCAATTT	CAAATCCTAT	TACCCCAATA	ATAAAAATGC	ATTATTATATC	120
AACAATAAGA	AAAATCCATT	ATCTAGTRCT	TCAAAGTTCA	TATTGCTT		168

230

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 684 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209

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ATGCTAGAAA CCACTATTGA TTTTCTCGT TACAGCAGCG TGAAAATCGG TCGCCTTTA      60
AAAGTGAGCG TTTTAGAAAA CGATAATGAA ATCTCTCAAG AACACCAGAT CATAGGATTA      120
GCGAACAACC TTTAATCGC TCCTGACGTG AAAAATCTCG CTTTATTAGG AAAAACTAC      180
GATTATATTT GCGATAAGGG TGAGTGGGTG GAGGTAGGGG GAGCGGCCAA TCGCTCTAAA      240
ATTTTTAATT ATTTTAGGGC GAATGATTTA GAGGGTTTAG AGTTTTTAGG GCAATTGCCT      300
GGCACTTTAG GGGCGTTAGT TAAAATGAAT GCTGGCATGA AAGAATTGA AATAAAAAAT      360
GTTTTAGAAA GCGCTTGCGT TAATGGCGAA TGGCTAGAAA AAGAAGCTTT GGGGCTAGAT      420
TATCGCAGCA GCGGGTTTAA TGGCGTTGTT TTGAGGGCTA GGTTTAAAAA GACGCATGGT      480
TTTAGAGAAG GGGTTTTAAA AGCGTGTAAG AGCATGCGCA AAAGCCACCC CAAATTGCCT      540
AATTTTGGGA GCTGTTTCAA AAACCCGCCT AACGATTATG CGGGCAGGCT TTTAGAGGGC      600
GTGGGCTTAA GGGGTTATTG TCTAAAAGAG TGGGCTTTGC CAAAGAACAT GCGAATTTTT      660
GGTGAATTG GGGGCGCAG AATT                                     684

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(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210

```

ATGCTCAAAA ATGGCGATAA GATTCCGGAC GCTATTTTAG TGATATTGA GATGCCTAAA      60
ATGGATGGCT AACTTTTCGC CTCTGAAGTG CGTAAATACA ATAAATTCAA AAACCTGCCC      120
TTGATCGCCG TTACCAAGTC GGTAATAAA ACGGACAGAA TGCGCGGCGT TGAATCCGGC      180
ATGACTGAAT ACATACCAA ACCTTATAGC GGTGAATATT TAACCACCGT AGTGAAGCGC      240
AGCATTAAAT TAGAAGGAGA CCAATCG                                     267

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SUBSTITUTE SHEET (RULE 26)

231

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211

GTGTTTGAGC CGGTTATCGC TTACAAGCTT TTCCATTCTT TTGTGATTTT AGGGTGCGCG	60
ATTGAAACTT TAACGACTAA ATGCGTGGAA GGCATCACGG CTAATGAAAA GATTTGCCAC	120
GATTATGTTT TTAACAGCAT TGGCATGTG ACCGCGCTCA ACCCTCATAT CGGCTATGAA	180
AAATCCGCTA TGATCGCCAA AGAAGCCTTA AAAAGCGATC GCTCTATCTA TGATATCGCT	240
TTAGAAAAGA AAATCTTAAC CAAAGAGCAA CTGGACGATA TTTTCAAGCC AGAAAACATG	300
CTAAGYYCTC ACGCTTTCAA AAAGCATAAA GAC	333

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212

ATGTTGCGTT TATTAGCCCA AAAAAGCGCT ATTAACTCA TTCTTATCCC CCCAAGCGCG	60
AACGCTTTAG GCATCGCTTC TATTTGCCGA TTGAGCGAAG AAGTTTTTGA ACATGAAAAA	120
ATCGTAGGCA TTCGCGCTCA AGGGGATTTC ACTATCAATA GCGACGATAG GGGTTTTTGG	180
GAAAGACGCT GTCAG	195

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

232

- (A) LENGTH: 804 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213

```

ATGAAAAAAC TTCTTTTACT CTTAGAGCAT AAGATCGTAA AAATTGGCTT AATTATTGTG      60
ATTGTGTTAG TGGGTTTTTT TCTTTTTTAT GAACAAGAAA TCAAAGAAAA AGCTGTTAAT      120
GTTTCTCAAG GTAAATTCCC CACTTCATCT TATTGTGTTT AAGCTTACGA AGGCATTAAG      180
AATAAAATAG ATACTATCAA TCAAGTGAAG CCAAACGATG AACTAAAAAG CGTTAATGAG      240
AATATAGAAA AAACACAAAA AGATTTAGAT GATTTTAATG CGCTAGTGCA AAAGTTACCA      300
AATTTGCCTA AGGACTTTAA TAAAACACTT ATTAAACCAC AAAGTCCATT TTTCAACTAC      360
AATACCGCTA ACGAAGATGA AAAAAACCGC CTGGTGATT TAGCGTCTCG TATTAGCAGC      420
CAAAAAGAAA CGCAACCTCC CATTTCTATA AAAAATAGCG TTTCTCACAT AAAATCCAAA      480
GAAAAACGAG AACTTGAAAA AGAATGGGCA AAACCTAGTG TTTCTTTTGG TTCCTTTTCC      540
TTGCTTTCCA GTTCTTCTTC TTTTCTTCT TTTGAAGTTT CTTTTTTATC AAGGGGAATA      600
GGATTGGATT GTGAGAAGCT CAAATCCTTT TTAAAAGCTT TTTCAAGTTC GCTATTTTCC      660
TTATTATCTT CATTGTTTTG CCATCCACTT TCTCTTTTTT GCTCTCTAAT AGGATTAATC      720
TTTTGTTTTT CTAAGTTTTC TAGAGAGCTA GTGAATGCGT CTAACAATTC GCTTGAGTTT      780
TCATCATTGT CAAGGCTAGG ATCA                                     804

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(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214

```

ATGGGAGCGA TAGCGAGTTG TTACGCGCAT CAAATCATCT TAACTTCAGA CAATCCTAGA      60
AGCGAAAACG AAGAAGACAT CATTAAAGAT ATTTTAAAAG GCATCAATAA TTCTTCTAAA      120
GTCATTGTAG AAAAAGACCG AAAAAAGGCC ATTTTAAACG CTTTAGAAAA TTAAAAGAC      180
GATGAGGTGT TGTGTATTTT AGGCAAGGGC GATGAAAACA TTCAAATCTT TAAAGACAAA      240
ACGATTTTTT TTAGCGACCA GGAAGTCGTT AAAGATTATT ATCTCAATTT AAAACAAGGA      300

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SUBSTITUTE SHEET (RULE 26)

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215

GTGATGGACA AACTCACTAA AAGCTTGCAA ACGCAAAAAA ACTTCGCTTA TTTAGGCAAA	60
ATCAAGCCCC AACAACTCGC TGATTTCATC ATTAACGAAC ACCCTCAAAC CATCGCCTTG	120
ATTTTGGCCC ACATGGAARC CCCTAATGCG GCTGAAACTT TGAGCTATTT CCCTGATGAA	180
ATGAAAGCCG AGATTTCAT TAGAATGGCG AATTTTAGGC GAAATATCGC CCCAAGTGGT	240

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216

ATGCCGTATT TTAGAAGCGC TTTTITATTA TTTTTCATGA CGCTTTTTTT TGTTCCTTGC	60
TCTAAGCACC CTTTTTCTAA GCAAACCCCT AAGACTAAGG AGCGGATCCG ACAAGAAGAA	120
GCCAATAAAA AAAGAGAAGA GACTTTGAAT GCCTTGCGCC AATTGAGACT CATTTACATT	180
AACACGCCGG TTTTTCGCTT TTATGATTAC GGCACGATCA AAACCGATAA AGACCACAAT	240
ACTGAAGTAA CCCTTTATAA GCTCAGCCAA AAAGTGGGCG ATATTTACAT GACTAAACGG	300
AGCATTGTGT TTAGCCAAAA ATGTTCCGCC AAATGGATTG CTGCAAGGGA TTGTTTGGC	360
AAGGTGAGCT ATGGGGATTG GTTTGATGAT ATTGTTTGTG GGAGGGATAT TTTTAAAGGT	420
TTAGGGAAAC GCCACCTAAC CCCTGAATAT GTGATCCAAA GGTTCAAAAA AAGCGGGGAA	480
ATTATCCTTT ATGAAAGAAA AAATGGCCTG ATTTCTTTCC AAAACTTGAC TCAAAAAATT	540
GCTATTAGGA TTGAACCCTA TGAGCCTTCT TTGCAAGATT TAGAAGACAA TGAAAACGCT	600
GATAGCGAGC TTCAA	615

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217

```

ATGCGCATG AAGAAATGG CGTGATTCT CTAGCCTTTA GTAACGGGT GGTAGAGCCG      60
GTCGCTCGCA TCGGTATTW AGCTTTCCT AACGATCAAG GCTTAAGGAA AATCGGCGGT      120
AACCTCTATG AAATGCAAGA AGGCACCAT TATGGCGAAA ACAGACCCCT AAGSGGTAAC      180
CCCATTTTAG GGTGGGACGA AGAGGGCAAG CTCAAGTTTG GAAAATCAG GCACAAATAT      240
TTAGAAACGA GCAACGTGAA TGCCGGGAAC GCCCTAACCA ATCTCATTTT AATGCAAAGA      300
GGCTATTCTA TGAACGCTAG AGCCTTTGGC GCGGGCGATG ACATGATCAA AGAAGCCATT      360
AGCTTGAAAA AA                                     372

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(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218

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GTGGAAGCGC GTTATTATTA TGGGGACACT TCATACTTTT ATTTGCATGT GGGAGTTTTA      60
CAAGAGTTTC CTCACCTTGG ATCGAATGAT GTGGCGTCTT TAAACACCTT TAAAATCAAT      120
GCCGCTCGCA GTCCTTTAAG CACCTATGCA AGAGCGATGA TGGGTGGGGA ATTGCAATTG      180
GCTAAAGAAG TGTTTTTGAA TTTGGCGGTG GTTTATTGTC ACAATTGAT TTCCAACGCA      240
AGCCATTTCG CTTCCAATTT AGGAATGAGG TATAGTTTC                                     279

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(2) INFORMATION FOR SEQ ID NO:219:

235

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219

GTGGAGGAGC	TAGCTAAATT	GATCAACAAT	AATAATAACA	ATAAAAAACT	GAGAGGCTTT	60
TTTTTGAAAG	TTCTCTTAAG	TCTCGTTGTT	TTCAGTTCGT	ATGGGTCAGC	AAATGACGAT	120
AAAGAAGCCA	AAAAAGAAGC	GCTAGAAAAA	GAAAAAACA	CTCCCAATGG	GCTTGTTTAT	180
ACGAATTTAG	ATTTTGATAG	TTTAAAGCG	ACTATCAAAA	ATTTGAAAGA	CAAGAAAGTA	240
ACTTTCAAAG	AAGTCAATCC	CGATATTATC	AAAGATGAAG	TTTTTGACTT	CGTGATTGTC	300
AATAGAGTCC	TTAAAAAAT	AAAGGATTG	AAGCATTACG	ATCCAGTTAT	TGAAAAAATC	360
TTTGATGAAA	AGGGTAAAGA	AATGGGATTG	AATGTAGAAT	TACAGATCAA	TCCTGAAGTG	420
AAAGACTTTT	TTACTTTCAA	AAGCATCAGC	ACGACCAACA	AACAACGCTG	CTTTCTATCA	480
TTGCACGGAG	AAACAAGAGA	AATTTTATGC	GATGATAAGC	TATATAATGT	TTTATTGGCC	540
GTATTCAATT	CTTATGATCC	TAATGATCTT	TTGAAACACA	TTAGCACCAT	AGAGTCTCTC	600
AAAAAATCT	TTTATACGAT	TACATGTGAA	GCGGTATATC	TA		642

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220

GTGGGGGGCA	TTGTGGCAAA	CATGAACGAT	CTTTCAACTT	ACATGGTTGA	GAATTTACTC	60
ATGGGTTTGT	ATCTTTTTTC	TAGCGCTTTA	GATTTGGGCG	TGAAAAAAGC	CATTAATCTA	120
GCGAGCTCTT	GCGCTTATCC	TAAATACGCC	CCTAACCCCT	TAAAAGAGAG	CGATTTATTC	180
AACGGCTCTT	TAGAACCAAC	GAATGAAGGC	TACGCTTTGC	CAAACTCTCT	GTRR	234

(2) INFORMATION FOR SEQ ID NO:221:

SUBSTITUTE SHEET (RULE 26)

236

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221

ATGAAGAAAA	GAAAACATGT	ATCCAAGAAA	GTGTTTAATG	TCATTATCTT	GTTTGTGGCA	60
GTATCACTC	TTTTAGTCGT	CATTACAAAA	ACCCTTTCAA	ACGGCATTCA	CATACAAAAAT	120
TTAAAAATTG	GAAAACCTGG	CATTTCTGAA	TTATACTTAA	AACTCAATAA	CAAGCTTTCT	180
TTGGAAGTTG	AGCGGGTTGA	TCTCTCTTCT	TTCTTCCATC	AAAAACCCAC	TAAAAAGCGT	240
TTAGAAGTTT	CTGATTGAT	TAAAAATATC	CGTTATGGCA	TTTGGGCGGT	GTCTTATTTT	300
GAAAAACTTA	AAGTCAAAGA	AATCATTTTA	GACGATAAAA	ATAAAGCCAA	TATCTTTTTT	360
GATGGGAATA	AATACGAGTT	WAGAATTTC	AGGAATCAAA	GGGGAATTTT	CCCTAGAAGA	420
CGATTAAAAA	TATCAAGCTT	AAAATCATCA	ATTGCTTTT	TAAAGATGTT	AAAGTCCAAG	480
TGGATGGCAA	CGCCCACTAT	TCRCCCAAAG	CCAGGAAAAAT	GGCGTTCAAT	T	531

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222

GTGTCATGTT	GGGGAGCGTC	AAAAAAGCGG	TTTTTAGGGT	TTTGTGTTTG	GGGGCGTTGT	60
GTTTTATCGG	GGGGGTTAAT	GGCAGAGCAA	GATCCTAAAG	AGCTTATATT	TTCAGGTATA	120
ACTATTTACA	CGGATAAAAA	TTTCACTAGA	GCTAAGAAAT	ATTTTGAAAA	AGCTTGCAAA	180
TCAAACGATG	CTGATGGCTG	TGCAATCTTA	AGAGAGGTTT	ATTCTAGTGG	TAAAGCCATA	240
GCGAGAGAAA	ACGCAAGAGA	GAGCATTGAA	AAAGCTCTTG	AACACACCGC	TACTGCTAAA	300
GTTTGTAAT	TAAACGATGC	TGAAAAATGC	AAGGACTTAG	CAGAGTTTTA	TTTTAATGTA	360
AACGATCTTA	AAAATGCTTT	AGAATATTAC	TCTAAATCTT	GTAAGTTAAA	TAATGTTGAA	420
GGGTGTATGC	TGTCAGCAAC	TTTTTATAAC	GATATGATAA	AGGGTTTGAA	AAAAGATAAA	480
AAAGATCTAG	AATATTATTC	TAAAGCTTGC	GAGTTAAATA	ACGGTGGAGG	GTGTTCTAAA	540
TTAGGAGGGG	ATTATTTTTT	TGGTGAAGGC	GTAACAAAAG	ATTTCAAAAA	AGCTTTTGAA	600

SUBSTITUTE SHEET (RULE 26)

237

TATTCTGCCA AAGCTTGTGA GTTGAACGAT GCTAAAGGGT GTTACGCTCT AGCAGCGTTT	660
TATAATGAGG GTAAAGGCGT GGCAAAGGAT GAAAAGCAAA CGACAGAAAA CCTTGAAAAG	720
AGTTGCAAGC TAGGATTAAA AGAAGCATGC GATATTCTCA AAGAACAAAA ACAA	774

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223

GTGGCTCTCA CTTGGGGGGC TAGAGGGGGG GTGTATTGTT GTGGGGGGAT TATCCCACGA	60
TTCATTGATT ATTTTAAAC TTCGCCCTTT AGAGCGCGTT TTGAAACGAA AGGGCGCATG	120
GGAGCGTTTC TCGCTTCCAT CCCTGTGCAT GTCGTGATGA AAAAAACTCC CGGACTTGAT	180
GGGGCGGGCA TTGCGTTAGA AAATTATTTA CTGCATGATA GAATA	225

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224

ATGAAAGGTT TAACAATGAA AAAATTAGTT TTAGCATGC TTTTATGTTG TAAAAGCGTG	60
TTTGACAGAG GGGAAACTCC TTTGATTGTC AATGACCCAG AAACCCATGT AAGTCAAGCC	120
ACTATCATAG GCAAATGGT AGATAGTATC AAAAGATACG AAGAGATTAT TTCTAAGGCT	180
CAAGCTCAAG TCAATCAGTT ACAAAGATC AATAACATGA TAAATACGAC TAATTCTTTG	240
ATTAGTAGTA GTGCTATCAC TTTAGCCAAT CCTATGCAAG TTTTACAAAA CGCTCAGTAT	300
CAATAGAGA GCATTAGATA CAACTATGAG AATTAAAGC AAAGCATAGA AAATTGGAAC	360
GCACAAATTT TGTTAAGAAA CAAATACTTA CAGCAACAAT GCCCTGGGCT TAATGTCAAT	420
GCTCTTACTA ACAATAAGAT TGTCAATCTT AAAGATCTCA ATAACCTAAT CACCAAAAAAT	480

SUBSTITUTE SHEET (RULE 26)

238

GGCGAACAAA	CCCAAACCGC	AAGAGATGTG	CAAAATCTCA	TTCAGTCCAT	TAGTGGCAGT	540
GGCTATGGAA	ACATGCAATC	ACTTGCTGGG	GAATTGAGTG	GTAGAGCGTG	GGGGGAAATG	600
TTGTGTAAAA	TGGTAAACGA	TAGTAATTAT	GAAAGCGAGC	AAGCTCTTTT	AGCAACAGGC	660
AATAACCCAG	AAGAGCAAAA	ACGAAGATTT	TTGCTTAGAG	TAAAGAAAAA	GGTTAATGAT	720
AATAAGCAGT	TAAAAGATAA	ACTTGACCCA	TTTCTAAAAA	GACTTGATGT	CCTACAACT	780
GAGTTTGGTG	TAACTGACCC	TACAGCTAAC	CATAATAAGC	AAGGGATACA	TTATTGCACA	840
GAAAATAAAG	AGACAGGTAA	ATGCGACCCT	ATTAAAAATG	TATTTAGGAC	AACTCGCTTA	900
GATAACGGAAT	TAGAACAAGA	AATCCAAACG	CTCACACTTG	ATTTAATCAA	AGCCTCCAAT	960
AAAGACGCTC	AAAGCCAAGC	CTACGCAAAT	TTCAATCAAA	GGATTAAATT	ACTTACTCTA	1020
AAATATTTAA	AAGAAATTAC	CAATCAAATG	CTCTTTTTAA	ATCAAACAAT	GGCAATGCAA	1080
AGCGAGATTA	TGACAGATGA	TTATTTTAGG	CAAAATAATG	ATGGCTTTGG	GGAAAAAGAA	1140
AACCATATAG	ACGAACAATT	AACGCAAAAA	AGAATAAACG	AAAGAGAAAG	AGCTAGAATA	1200
TACTTTCAAA	ACCCTAATGT	TAAATTTGAC	CAATTTGGCT	TTCCCATTTT	TAGTATATGG	1260
GAT						1263

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225

ATGAGCGTGA	ATTTATTGGA	ATTGTTAAAA	CTCGCTGTGC	CTTTAGCGGT	TATTTTGAGC	60
GTTCAAGTGG	CGGTTATGAT	CCTTTATGTG	GTGCTTGTA	CCTTTAGGGT	ATGCGGGAAG	120
GATTATGATG	CGGCGGTGTT	GTGCGCGGGG	CATTGCGGTT	TGGGGCTTGG	AGCGACCCCA	180
ACGGCTATGG	TGAATATGCA	AACCATCACC	AACCACTATG	GGCCATCGCA	TGTGGCGTTT	240
ATCGTCGTGC	CTTTAGTGGG	AGCGTTTTTT	GTTGATATTA	TTAACGCTTT	AGCGATTAAA	300
GGCTTTTTGC	TTTTGCCTTT	TTTCCCTAGT				330

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

SUBSTITUTE SHEET (RULE 26)

239

(A) NAME/KEY: misc_feature
(B) LOCATION 1...336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226

ATGCAACTAA GCCCCTTACA AAGCGCGCTG TTATATTTCC GTTACTTTAT TTATCCGGAA	60
AAAAAAACAA GGAGCTTTGA TTTAAGCGAT TTAATTTTGA TTGTCATGGT TTTTITAGTC	120
CTAGCTTTGG GGCTGTTGAT GAGCGAAGAA ATTCTATCA GCTACAATGA AGCGAAAGAC	180
TTTTTTTATA GCGATGCGTG GTTTGTCAAA ATCGCTCAAA AAAGCGTAGC CATTITTAAGG	240
CCAAAACGAT TTGGCTTTAA GATTGCCTTT TTTGATCGCT CACGTCATCA ACATGTTTTT	300
ATTCTACCTC ATAGGGCGAA AGATTTTAAA AAAGCC	336

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227

GTGTATGCGC TCATGGTGGC GTTTTTTGCT TACATGAGTT ATTGCTTGGG GTATCAATTC	60
TCCAAAATTTCG TTTCTAAAAA CAACATTTC TCGCTCTCAT CGCTTTTATC AAGCTGTGTG	120
CGCGTGGTCT CTGTGCTAAT CTTGTCGCTC AGTAGCCTAG AGTTGCGTTA CTTCTCACCC	180
CTAACTATCA TAACCATGCA TTTTGCCCTA ACGCTTATCA TCCTCTTTTT CTTTTGTAT	240
AAGGCTAAGC CGTTTGATGA G	261

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1257 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228

SUBSTITUTE SHEET (RULE 26)

240

ATGAGGTCTT	GGATGAAGAA	AAAATACTTC	ACGCTTTTAT	TGCAAAGTAG	TGTGGTATTA	60
GCGGTTTTTA	TAGGGTGTTC	TTCTACCAGG	AATCATACTT	TTTCAGCCCT	TAGTAATCAA	120
GAAAATACAG	ACGATAAGCT	CCCAGTGGTC	CATTCCATTA	AAACGATTAA	CGATGTGAGT	180
TCAGTGGGCT	TTGAATGGTC	TAAAGTCGCT	GACACTTATG	ACATTGACGG	GTTTGTTTTG	240
TATCGTTTGA	AAAAAGACTC	CAAGCTTAAA	AGAATCGCCA	CCATTAAAAA	CCCTTATGCG	300
ACCCACTATT	ATGATGAGGG	GTTAGAAACA	GAGAGTTCCT	ACACTTACCA	ATTAGCCACC	360
TACAAGGGCG	ATAAAATTTC	CAAACCTTCA	GAACCCATT	TAGTAAAAAC	CTCCTTTATC	420
AATCCTGTAG	AAAGCGTGT	TGCAAGCCTT	GAATACCCTA	AAAGCGTGAA	AGTCTTTTGG	480
AGCCCGCACC	CAAATCCCAG	CGTTTCTAAA	TACATCATTC	AAAGGCAGAA	TAAAGACGGC	540
AAATTTTAA	ATGTGGGGGC	TGTAAAAAAC	CGCTTATTCG	TGGAGTTTTT	TGATAAAGAT	600
TTAGAAGATG	GGCAAAAATA	CCGCTACCAA	ATCATCGCCG	AAAATTTTCAT	GGGGGATAAA	660
TCCAGGCCTA	GCGTGATAGT	GGAGGGGAAA	ACCAAAGACT	TGCCCAAAGA	AATCGCTAAT	720
GTTAGAGTGA	GTCAAAACCT	CACACGACAA	ATTGAATTGA	GTTGGGATAA	ATCCCCAGAA	780
GAAGATGTGA	TAGCTTATCG	CATTTACGCT	TCCAATAACC	GCAACGATAA	ATACAAATTC	840
ATCGCTCAAA	CCACCAACAC	TTCTATGTG	GATAAGATAG	AAAAAGACAA	TCTCACTCGT	900
TATTATAAAG	TCGTCGCCGT	AGATAAAACG	CATCTTGAAG	GGGCGTTACC	CAAAGAGCCT	960
GCCATGGGTG	AGACCTCTGA	TAGGCCTGAA	GCCCTATCA	TACTAAAGG	GACTATTCAA	1020
GACTCTTCGG	CCTTGATCCA	ATGGGAAAAC	AACCCAAGCC	CTAAAATAGC	CACCTTATGCG	1080
GTGTATCGTT	TTGAAGCCAA	CTCCAAAACC	CCTTTGCGTT	TTGGGAATAT	CACACAAAAC	1140
CAGTTCGTGG	ATAAGGACAT	GAAAGTGGGC	GTGGCTTATC	GCTATCAGGT	GGTGAGCGTG	1200
GATAAGATG	GTTTAGAGTC	GCACCCAAGC	AAAGAAGTGC	GTTTGTTTTT	AGAGCGC	1257

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229

ATGCTTCCTA	CTAAAACACG	CATTAGAGAT	CCGAACAAGC	AAGAACTTAC	ACAACCAAAA	60
ATAAAAGGAT	TGAGTATGGG	AAAAATTTTA	GCTTCTTTGT	TGGGTGGCGG	AACAAATCTT	120
TTTACAGGTT	TATCCAGTGA	TTTGTTTTCT	ATGATATTAA	ATTTTTTGTT	CTTCCTGATG	180
TTAATGATGG	GACTTAATGA	AGCATTAGGG	AAAAAATTTA	ACTTGCCTAT	GGACAATATC	240
AAGAATTTTA	TGGCAGAAGT	GCTGAAGAAT	GGATTCGATA	GTATCAAAAA	CATGGGATCT	300
GCTTTGGTTG	GTAATGGTTT	TGGTAGCAGC	AAATCAGACA	AAACCACTAA	TAAAATGAGT	360
GTCCCAACAG	TAAGACTC					378

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

241

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...216
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:230

ATGGCGAACA TGATGATGGC AGCGGCCATG TTAGGGATTG ATTCTTGCCC GATTGAAGGG	60
TATGATCAAG AAAAAGTGGG GGCTTATTTA GAGGAAAAAG GCTATCTAAA CACGGCAGAA	120
TTTGGCGTGT CGGTAATGGC CAGTTTTGGT TATCGTAACC AAGAGATTAC CCCTAAAACC	180
CGCTGGAAGA CAGAAGTTAT TTATGAAGTG ATTGAA	216

(2) INFORMATION FOR SEQ ID NO:231:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...333
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:231

ATGGCCGGGC TTGTTTTGAT GGTGCTGCTC GCCAGTTATG AAAGCTTTGT TTCTAAATTA	60
GACAAGGTGG ATGCTAGCGA AATCACTTGG CTA AACACA CAGATTTTAA CGCTTTAAAA	120
TTAAAGGTTT CCCTCTCCAT TGTAGCCATT TCGGCGATTT TCTTGCTCAA ACGCTACATG	180
AGTTTAGAAG ACGTTTTATC CAGTATTCCT AAAGACACGC CCCTATCGCA TAACCCCTATT	240
TTTTGGCAAG TGGTGATCCA TTTGGTGTTT GTGTGTTTTCAG CGCTGTTAAC CGCTGTTACC	300
AATAACATCG CTTTTTCGCA GAAAGAAAGG CAT	333

(2) INFORMATION FOR SEQ ID NO:232:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

242

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232

ATGATTACGA TCGTTATTGC AAAAGCGGGG AATATAGTCA AAGYCGATAT TTTTACGCAC	60
ATTAGCGATA TTAAGATGGG GCTTATTAAA GGAGGTCAAT GGGGGGTTAT TGGTTTAGGC	120
AATATCGGTA AAAGAGTCGC CAAGCTCGCT CAAGCTTTTCG GGGCAAAGGT GGTGTATTTT	180
TCCCCTAAAG ATAAAAAGA AGAATACGAG CGCTTGAGTT TAGAGGAATT GCTTAAACA	240
AGCGGTATTA TCAGCATTTCA TGCCCCCTTA AATGAAAGCA CGCGCGATT AATCGCTCTG	300
AAAGAATTGC AAAGCTTAAA AGATGGGGCG ATTTTAATCA ATGTGGGGCG TGGGGGCATT	360
GTGAATGAAA AGGRTTTGGC TTTRRTTTTA GAAACCACAG ATTTGTATTA CGCGAGCGAT	420
GTGTTT	426

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 189 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233

GTGAATTTCA ACGTAAAAA TATTTCAATT GATAATTTGG TAGAAATCAA TAATCGTGTG	60
GGTTCTGGAG CCGGAGAGAA AGCCAGCTCT ACGGTTTGA CTTTGCAAGC TTCAGAAGGG	120
ATCACTAGYA GTAAAAATGC GGAAATTTCT CTTTATGATG GCGCCACGYC AATTTGGCTT	180
CAAACAGMG	189

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 930 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

243

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234

```

ATGCCAACGC TCATTCTGTC GCTTCTAAAA CATGCGATTT TAATGGGCAT GCTTTTAAAA      60
GAATGCCAAG AAAAGTTAAA GCGTTCCTTA AATTGAGTG  CTAATCATTG CGTCTTGAGC      120
GCGGGGTATG GGGCGAGTTC AGCGATTAAAG AAATTTC AAG AAATTTTAGG GGTGTGTATC      180
CCTTCAAAAA CGAAGAAAAA TTTAGAGCCG TATTTGAAAG ATATGGCTTT AAAGCGTGTG      240
ATTGTAGGGC CTTATGAGCA TCATTCTAAT GAAGTTAGCT GGCCTGAAGG CTTGTGTGAA      300
GTGGTGCGTA TCCCTTTAAA TGAACATGGT TTATTGGATT TAGAAATTTT AGAGCAAAC      360
TTAAAAA AAAA CCCCTAACAG CTGGTTTCT GTGAGCGCGG CTTCTAATGT AACGGGAATT      420
CTTACGCCTT TAAAGAAGT TTCATCATTG TGTAAAGGAAT ATAGGGCTAT TTTAGCTTTG      480
GATTTAGCGA ATTTTAGCGC GCATGCTAAC CCTAAAGATT GCGAATACCA AACCGGTTTT      540
TATGCGCCTC ATAAGCTTTT AGGGGGCGTT GGAGGGTGCG GTCTTTTAGG CATTTCTAAA      600
GATTTGATTG ACACGCAAAT YCCTYCGAGT TTTAGCGCAG GGGGCGTGAT TAAATACGCT      660
AATCGCACAC GGCATGAATT TATTGATGAA TTGCCTTTAA GAGAAGAATT TGGCACGCCA      720
GGATTGTTGC AATTTTACAG GAGCGCTCTA GCGTATCAAT TAAGAGATGA ATGCGGTTTG      780
GATTTTATCC ATAAGAAAGA AAACAACCTT TTAAGGGTGC TTGTGTATGG CTTAAAAGAC      840
TTGCCCCGTA TTAATATTTA TGGGAATTTA ACGGCGAGTC GTGTGGGGGT AGTGRC'TTTT      900
AATATTGGAG GGATTTCRCC CTATGATTTA

```

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235

```

GTGGCATGCA ACACCGCGAG CGCTCTGGCT TTAGAAGAGA TGCAAAAGTA TTCTAAAATC      60
CCTATTGTGG GCGTGATTGA GCCAAGCATT TTAGCGATCA AGCGGCAAGT GGAAGATAAA      120
AACGCCCTTA TTTAGTGCT AGGGACAAAA GCGACGATTC AATCCAACGC CTATGACAAC      180
GCCCTGAAAC AACAAGGCTA TTTGAACATT TCGCATTTAG CTA'CTTCTCT TTTTGTGCCT      240
TTGATTGAAG AAAGTATTTT AGAGGGCGAA TTGTTAGAAA CTTGCATGCA TTATTATTTT      300
ACTCCCTTAG AGATTTTACC CGAAGTGATC ATTTTAGGTT GCACGCATTT TCCCTTAATC      360
GCTCAAAAAA TTGAGGGCTA TTTTATGGGG CATTTTGCCC TTCCAACGCC CCCCTACTC      420
ATCCATTTCG GCGATGCTAT TGTAGAATAT TTGCAACAAA AATACGCCCT TAAAAACAAT      480
GCATGCACAT TCCCTAAAGT GGAATTTTCAT GCGAGCGGCG ATGTGATCTG GCTAGAAAGA      540
CAAGCTAAAG AATGGCTCAA ATTG

```

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

SUBSTITUTE SHEET (RULE 26)

244

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236

GTGTTGTGGG	TGCTATATTT	TTTAACCACT	TTATTTATTT	GCTCTTTGAT	TGTTTTGTGG	60
TCTAAAAAAT	CCATGCTCTT	TGTGGATAAC	GCTAATAAAA	TCCAAGGCTT	CCATCATGCA	120
AGAACCCAC	GAGCCGGGGG	GCTTGGGATC	TTTCTTTCTT	TTGCGTTGGC	TTGTTATCTT	180
GAACCTTTTG	AGATGCCTTT	TAAGGGGCCT	TTTGTTTTCT	TAGGGCTATC	GCTAGTGTTT	240
TTGAGCGGTT	TTTTAGAAGA	CATTAACCTT	TCATTAAGCC	CCAAAATACG	CCTTATTTTG	300
CAAGCTGTAG	GGGTCGTTTG	CATCATTTCA	TCAACGCCTT	TAGTGGTGAG	CGATTTTTCG	360
CCCCTTTTTA	GCTTGCCTTA	TTTCATCGCT	TTTTTATTCG	CTATTTTTTA	TGCTGGTGGG	420
TATCAG						426

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237

ATGGCGTGTA	AATTTTGCCC	TAAGATCAGA	AAAACAGATT	GGATTTTAT	TTTAATCGCC	60
GCTTTAGGCT	TTTATTCAGT	TAATAAGCTA	GGGTATGCGC	CCAAATTCAA	TACCCCCACT	120
CCAAAATCTT	CACGCCCTCT	TTCACGCCCT	ATTGAAAAGC	CTAACAATAT	GACTGAAGAA	180
GAAAGGAAAA	AGCGTTTTAT	AGAGTTGCAA	AAAGCATGCT	TACTTCATAA	AGACAAAAAG	240
GCATGCGAAG	AGGTTTTT					258

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 363 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

SUBSTITUTE SHEET (RULE 26)

245

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238

GTGGATTCCA TTTTAATTGA TGAAGCGAGA SCTCCTTTAA TCATTTTCAGG GCCTGTGGAT	60
AGGCGCATGG AAAATTACAA CAAGGCTGAT GAAGTCGCTA AAAGCATGCA AGTGGAAAGTG	120
GATTTACCA TAGACGAAAA AAACCGCGCG ATTTTAATCA CTGAAGAGGG GATTAAAAAA	180
GCCGAAAATC TCTTTGGCGT GGATAATTTA TACAAAATTG AAAACGCCGC CCTATCGCAC	240
CATTTAGACC AAGCCTTGAA AGCGAATTAC CTCCTTTTTA TTGRTAAAGA TTATATTGTA	300
GCCAATAATG AAGTGGTGAT TGTAGATTRA TTTACCGRCC GTTTGYTTGA AGGGGAGGCC	360
CTT	363

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239

ATGACGATCA CCACCCTATC TTTTATTTC ACAACGCCAG AAGTGTGTTGT CAATCAGGAT	60
TTCCCATGGC TTCTGGGGC TGGAAAGGTA GTGGTTAAAG ACTTGCGGTT ATTTGCTGGA	120
GGCTTGTTTG TGGCCGATT TGATCGAAAC GCTATTTGGA GGTAAAGGG TTTTGCT	177

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 426 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

246

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240

GTGTTTTCTG GCAATAAAAG GGCTATAAAT TATCGCACGA TTGTCAGCGC CTTGTGATT	60
CAAGTGGCTT TAGGGGCGTT GGCTTTATAT GTGCCTTTGG GCAGAGAAAT ACTGCAGGGT	120
TTAGCTAGCG GCATACAAAG CGTGATTGGT TACGGCTATG AGGGGGTACG CTTTTTATTT	180
GGCAATCTCG CTCCAAACGC TAAGGGCGAT CAAGGGATAG GAGGCTTTAT CTTGCGATC	240
AACGTTTTAG CGATCATTAT CTTTTTGCT AGCTTGATTT CACTTCTATA TTATTTAAAA	300
ATCATGCCCT TAGTAATCAA CCTCATCGGS GGGGCGTTGC AAAAATGCTT AGGCACTTCT	360
AAAGCAGAAA GCATGAGCGC AGCGGCTAAT AYTYTTGTGG CGCACACCGA AGACRCCCTT	420
AGTCAT	426

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241

ATGCTGGTGG GTATCAGTAA CGCTATTAAT ATCATTGACG GGTTTAACGG GCTTGCATCT	60
GGGATTTCGG CGATCGCGCT TTTAGTCATT CATTATATAG ACCSTAGCAG TTTGTCTTGT	120
TTGCTCGCTT ACATGGTGCT TGGGGTTTAT GGTGTTAAAW TTCCCTTCAG GAAAGATTTT	180
TTAGGWCAT CGGGGGGCG TATTTTTTGG GTTTGCTGWR CGGRATTTCT CTCTTGCATT	240

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 225 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

247

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242

ATGCTACATA AAAAATATCG TCCTAATGTT GCGGCCATTA TCATGTCGCC AGACTACCCT	60
AACACATGCG AAGTTTTTAT CGCTGAGCGC ATAGACATTG AAGGGGCGTG GCAGTTCCCC	120
CAAGGAGGCA TTGATGAGGG AGAGACCCCT TTAGAAGCAC TCTATAGAGA ATTACTAGAA	180
GAAATTGGCA CGAATGAAAT AGAGATTTTG GCGCAATACC CTAGA	225

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243

GTGATGCTAA TGGCAATTTT TACCCCTTAT ATTCTTATTT TGAAAATGAT GAAAAAGTCT	60
ATGAGTTTAT TCGCCAATAT GGGGTTGGAG CAAATTTTTT GCAACAGAGA CATTAAAGAT	120
TTAAATGATT TTGTTTTTGG TATAGAAGTG GGGCTTGATA GCAATGCGAG AAAAAATCGT	180
AGCAGAAAGG CTATGGAAAA TCATCTTATC GGTCTTTTGG TCCAAGCTCA ATTAAATTTT	240
AAAGAACAAG TAGATATTAG AGAATTGAG GATTTACGCC AGGCTTTTGG AAATGATACT	300
AAAAAATTG ATTTTGTTAT TTTTAGCAAA GAGAAAACCT ATTTCATAG AAGC	354

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...627

248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244

ATGATCCGTC	TAGCCGCGTT	TTTTTTAGCT	CTCGCTTGCG	CGATTACGCC	AAAAAGCCGC	60
CTTCTTTTAA	AAAATGTCTT	GCTCAACCCC	ACTCGCATAG	AAGCTTTTGA	GGTTTTGAAA	120
AAAATGGGCG	CTCATATAGA	ATATGTTATC	CAATCCAAAG	ATTTAGAAGT	TATTGGCGAT	180
ATTTACATAG	AGCATGCCCC	TTTAAAAGCG	ATCAGTATTG	ATCAGAATAT	CGCCAGCCTT	240
ATTGATGAAA	TCCCCGCTTT	AAGCATCGCT	ATGCTTTTTG	CAAAAGGCAA	AAGCATGGTG	300
AGAAACGCTA	AAGATTTACG	AGCCAAAGAA	AGCGATAGGA	TTAAAGCGGT	TGTTTCTAAT	360
TTCAAAGCTT	TAGGGATTGA	GTGCGAAGAA	TTTGAAGACG	GGTTTATAT	AGAGGGATTA	420
GGAGATGCCA	GTCAATTAAA	GCAGCATTTT	TCTAAGATTA	AACCCCTAT	TATCAAGAGT	480
TTCAATGATC	ACAGGATTGC	GATGAGTTTC	GCTGTTTTTA	CTTTAGCGTT	GCCTTTAGAA	540
ATTGATAATT	TAGAATGCGC	GAACATTTCT	TTCCCAACCT	TTCAGCTTTG	GCTCAATCTA	600
TTCAAAAAAA	GGAGTCTCAA	TGGAAAT				627

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245

GTGGGGAGTT	TGAAATTTTT	AAACGCTATG	GGGGTTGATT	TAAAGGTTAA	AGAGAGCGCT	60
AATATCATGG	TAGGCTTTGC	GAAAAATAAG	ACCTTATGCG	CGTTATTCAT	TTTAGAAGAG	120
CGTTTGAAAG	CTAACGCTAA	AGAAGTCATT	CAGGCTTTAC	AAAATCAAGG	CTTGGAATTA	180
GAAATTTTAA	GCGGGGATAA	TGAAAGCTCG	GTTAAGGAGT	GCGCG		225

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...363

SUBSTITUTE SHEET (RULE 26)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246

ATGGAGGCTT TAAACGCTTT GAACGCGCAA AGTGATGAGC AAATTTTATG CGAGGGTTAT	60
TTTGTGTGTG TGCAAATCTT AGAGCCTATG ATCCCGCACA CGGCATGGGA ATTGAGCGAG	120
AGGCTTTTAA AAAGAGAGAA TTTCAAGCCT ATAGAACTAG ATGAAAGCGC TTTGATAGAA	180
GACTTTATGA CTTTAGGGCT TACCATTAAT GGCAAAAGGC GCGCGGAATT GAAAGTCAAT	240
ATTAACGCTA GCAAAGAAGA GATTATTATT TTGGCTAAAA AAGAATTAGA GAAATATTTA	300
GAAAACGCGA GCGTTAAAAA AGAAATTTAT GTGCCTAATA AACTTGTTAA TTTTGTACC	360
GCA	363

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247

ATGAAAGAAA GTATTAAATA CTTGCTAGAA AGCGTGGGGC TAGTGCTTTT AATGAGCGTG	60
AATCCGGGCT TTGGCGGGCA GAAGTTTTTA GATCTAGTGC TAGAAAAGTG CTTGAAAGTT	120
AAAGAACTGA TCAAACGCTA CAACCCTAGC TGTCTTTTAG AAGTGGATGG GGGCGTGAAT	180
GATAAAAATA TCCTTGAACT CCAACAAGCG GCGGTGGATG TGGTGGTTTC AGGGAGTTAT	240
ATTTTTGAAT CCAAAGATYG TAAGCTGGCT ATTGAAGGCT TACAGAATGT CAGACAACCT	300
CTTGCA	306

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248

250

GTGCATGACG	GCGTGCCTGG	GTGGGTAGGC	TTCACTTTGA	TTGCGAGCAT	GTATCACATG	60
ACCCCTAGGC	TTTTCAAAAG	AGAGATCTAT	TCAGGAAGAC	TTGTGGATT	CCAATTTTGG	120
ATCATGACTT	TAGGGATTGT	GCTTTACTTT	TCGTCCATGT	GGATTGCAGG	GATCACGCAA	180
GGGATGATGT	GGAGGGATGT	GGATCAATAC	GGGAATCTCA	CTTACCAATT	CATTGACACG	240
GTTAAGGCGC	TAATCCCTTA	TTACAATATT	AGAGGCGTTG	GGGGTCTTAT	GTATTTTATT	300
GGATTATTAT	TTTTTGCTTA	CAATATCTTT	ATGACAATCA	CGGCAGGCAA	AAAATTAGAG	360
CGTGAGCCCA	ATTACGCCAC	SCCTATGGCA	RRA			393

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1323

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249

ATGATAACGC	TCTTTAGTTT	TGGAGCGTTC	GCTTACTATT	TCGTGTCTTC	TCAAATCAGT	60
CACGAAACT	ATCAAAACGA	AATGCGCCAT	TACCAGTTTG	TTACCACTAT	CAATGAAATT	120
TTAAATAACT	ACTCTGATTA	TAGAGCCATA	GAAGATTACC	TCTATAAAAT	TGGCTTTAGA	180
GAAACCACAA	TAGAAAATTT	AGAAAAGGTT	TTAGCCAAAA	GACGCCACCA	GTTGCACCAC	240
AGAAATATTT	GGTATGCTGA	AGTGTTTTAA	TTCAGCGATA	TGGTTTTTAT	CCTTTTAAAA	300
AAGGATGAGC	ATTTTGTGCT	TTATAAAGAT	TTGCAATTCG	TTTCTTATAG	GAATTATTTC	360
TTAGCCATTA	CGGTGGGTTT	ATTATTGATT	TTATTCCTCT	TTTTATTGT	TTTGCAGAGT	420
TTATTGCCTT	TAAGAGAGTT	AAGATCTCAA	GTGAAACGCT	TCGCTCAAGG	GGATAAAAGC	480
GTGAGTTGTA	AAAGCAAGCA	AAAAGATGAA	ATAGGGGATT	TGGCTAACGA	ATTTGACAAT	540
TGCATCCAAA	AAATCAATGC	GATGAATGAA	TCTCGGGTTT	TATTTTTGCG	CTCTATCATG	600
CATGAATTAC	GCACCCCTAT	CACCTAAGGC	AAGATACTAA	GCTCTATGCT	CAAAGAAGAG	660
CTGTCTTGCA	AACGCTTTTC	ATCTATATTT	GATCACTTGA	ACATGTTGAT	TGAGCAATTT	720
GCCCGCATG	AGCAGCTCGC	TTCCAAAAAT	TATGGGAGCA	ATAAAGAAAA	ATTTTTAATG	780
AGCGATTGTA	TAGATAAGAT	TGAAAAATG	CTTTTAATTG	ATGAAGATAA	AAAAAGCCCT	840
ATCCATGTAT	CCTCTTCAAA	TTACATCATT	GAAGCGGATT	TTGAATTGTT	TGCTATAGCG	900
TTAAAAACA	TGATAGACAA	TGCGATCAAA	TACAGCGATG	ACAAACAGGT	GTTTTTGGAT	960
TTCATAGGGA	ATAATTTAGT	GGTGCCAAT	AAAAGCAAAC	CTTTAAAAGA	AGATTTTGAA	1020
AAGTATTTGC	AACCTTACTT	TAAATCTTCT	AACCCAGGCC	AAGCCCATGG	GTTTGGGTTA	1080
GGCATGTATA	TCATTAAAAA	CGCTTTAGAG	GCTATGGGAT	TGAATTGAG	CTATCATTAT	1140
AGCAATGGAA	GAATCTGTTT	CACATCCAT	GATTGCGTTT	TTAATAGTTT	TTACGATTTA	1200
GAAGCGGATA	ATGAAGAGCT	ACCCCCCCCC	GAAAAATTGA	GAGAGGTGAA	GGAATGAAG	1260
GGAACAGAAA	AAGCCAATTG	TGGGTTTAAA	GAAAAACAAA	AAGAGAGAAC	ATGTTCAAAC	1320
GAT						1323

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

SUBSTITUTE SHEET (RULE 26)

251

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...381
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:250

```

GTGCTTCTCC TTTCTCGTAT GGGTATCGCT TTTGCCCACT CTATTTTTTG GTCCATCAGC      60
GCTTCTTTAG TCAATTCGTGT CGCGCCAAGA AACAAAAAAC AACAGGCCTT AGGGCTGTTA      120
GCGTTAGGGA GTTCGTTAGC GATGATTTTA GGGTTGCCGC TTGGGAGGAT CATTGGGCAA      180
ATTTTGGATT GCGATCCAC TTTTGGCGTG ATTGGGGGCG TTGCGACTCT TATAATGCTG      240
CTTATGTGGA AATTGCTCCC GCATCTACCG AGTAGAAACG CCGGCACGCT CGCAAGTGTT      300
CCTATATTAA TGAACGCCC GCTTTTAGTG GGGATTTATT TGCYTGTGAA TCATGGTTAT      360
TTCTGGGCAT TTCACCACTT A                                     381

```

(2) INFORMATION FOR SEQ ID NO:251:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251

```

ATGCGCATTG TCATAAGGTT ACTTTCATT AAAATGAACG CTTTTTTAAA ACTCGCGCTC      60
GCTTCTTTGA TGGGGGGGCT TTGGTATGCT TTCAATGGCG AAGGCTCTGA GATTGTCGCT      120
ATAGGGATTT TTGTGTTGAT CTGTTTGTG TTTTATATCC GCCCTGTGAG TTTCCAAGAC      180
CCAGAAAAAC GAGAAGAATA CATAGAACGG CTTAAAAAAA ACCATGAGAG GAAAATGATC      240
TTACAAGACA AGCAAAAAGA AGAGCAAATG CGCCTCTATC AAGCCAAAAA AGAGCGAGAG      300
AGCAGGCAAA AACAAGACCT TAAAGACAA ATGAAAAAAT ACTCA                               345

```

(2) INFORMATION FOR SEQ ID NO:252:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 258 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

252

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...258
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:252

GTGCGATCTT	GCAAACAGAT	TTTGATAAG	GGTTTAAAGC	CCTATTATAA	ACATTCTGTT	60
TGCTTAAAGC	CTTTTTTTAG	GTTTTGTTTT	CTCAAATTC	ATGCTTATCA	ACAGCGTTAT	120
AGAGCGTTTG	CTCTAACGCT	CTTTCCTTGT	AAGTTTTTTA	ACGCTTGTA	GATTTTTATT	180
CCCATAATTG	ATTTTAAAT	CGTTTTATC	CCTATTCTAA	AACACCAAGC	CAAGCTAAAA	240
AGAGTCTCTA	ATGCCTAT					258

(2) INFORMATION FOR SEQ ID NO:253:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 132 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...132
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:253

ATGTGTGGAA	TGGGGTTTAT	TGGCTTCAAA	ACAAACTTA	CTCAAACAAA	GGCATTATT	60
ATATTGATCC	CAATCTTTCA	GGACAGAGCG	GTCAAAGCGG	CAACACGCTC	AGCACCTATA	120
CAGCTAATTT	GT					132

(2) INFORMATION FOR SEQ ID NO:254:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1680 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

253

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1680

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254

```
ATGGGGGAATT TTAATAGCTA TGGCGATTTG GTGTTTAAACC TCAGTCATTG AGTTAGTCAT 60
GCTATTATCA ATACTCAAGG CACAGCGACG ATCATGGCCA ATAATAACCC TTTGATCCAA 120
TTCAACGCTT CTTCAAAAGA AGTGGGTACT TACACGCTGA TTGATAGCGC TAAAGCCATT 180
TATTACGGGT ATAACAACCA AATCACAGGA GGCAGTAGCC TGGATAATTA CCTTAAGCTT 240
TATGCGCTCA TTGATATTAA TGGCAAGCAC ATGGTGATGA CTGACAACGG CTTAACCTAT 300
AACGGGCAAG CCGTGAGCGT TAAAGATGGC GGTTTAGTTG TAGGCTTTAA GGACTCTCAA 360
AATCAATACA TTTACACTTC CATTCTTTAT AATAAAGTGA AAATCGCTGT TTCTAATGAT 420
CCTATCAATA ACCACAAGC CCCCACTTTA AAACAATATA TCGCTCAAAT TCAGGGCGTT 480
CAAAGCGTGG ATAGCATCRA TCAAGCTGGG GGAAATCAAG CGATTAAATG GCTCAATAAA 540
ATCTTTGAAA CTAAAGGAAG CCCTTTATTC GCTCCCTATT ATCTAGAGAG CCACTCCACA 600
AAAGATTTAA CCACGATCGC TGGAGATATT GCTAACACTT TAGAAGTCAT CGCTAACCCCT 660
AATTTTAAAA ATGACGCCAC TAATATTTTA CAGATCAACA CCTACACGCA GCAAATGAGT 720
CGTTTAGCCA AGCTCTCTGA CACTTCAACT TTCGCGCGTT CTGATTCTCT AGAACGCTTA 780
GAAGCCCTTA AAAACAAGCG ATTGCGTGAT GCGATCCCTA ACGCTATGGA TGTGATTTTA 840
AAATACTCTC AAAGGAATAG AGTTAAAAAT AATGTGTGGG CGACAGGAGT TGGAGGGGCT 900
AGTTTCATTA GTGGAGGTAC TGRAACTTTA TATGGTATCA ATGWAGGGTA TGATAGGTTT 960
ATTAAGGGCG TGATGTGGG AGGTTATGCC GCTTATGGGT ATAGCGGGTT CCATGCAAAC 1020
ATCACTCAAT CAGGCTCTAG CAATGTCAAT GTGGGCGTTT ATAGCCGAGC GTTTATCAAA 1080
AGAAGCGAGC TAACCATGAG CTTGAATGAG ACTTGGGGAT ACAATAAAAC TTTCATCAAC 1140
TCCTATGACC CCCTACTCTC AATCATCAAT CAGTCTTACA GATACGACAC TTGGACGACT 1200
GACGCTAAAA TCAATTATGG CTATGATTTC ATGTTTAAAG ATAAAAGCGT TATTTTTAAA 1260
CCCCAAGTAG GCTTAAGCTA TTATTACATT GGTTTGTCTG GTTTAAGGGG CATTATGGAT 1320
GATCCTATTT ACAACCAATT CAGAGCCAAT GCTGACCCTA ATAAAAAATC CGTTCTAACG 1380
ATCAATTTTG CCTTAGAAA TCGGCATTAT TTCAATAAAA ACTCTTATTA TTTTGTGATT 1440
GCGGATGTGG GCAGAGACTT ATTCATTAAT TCTATGGGGG ATAAAATGGT GCGTTTCATC 1500
GGTAATAACA CCCTAAGCTA TAGAGATGGT GGCAGATACA ACACCTTTGC TAGCATTATC 1560
ACAGGCGGGG AGATAAGATT GTTCAAAACC TTTTATGTGA ATGCGGGCAT AGGGGCTAGG 1620
TTTGGGCTTG ATTATAAGA TATTAATATT ACCGGAAATA TTGGTATGCW SYATRCTTTT 1680
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(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255

```
ATGGAGTCGA ATCAWTCAC CCCCATGGCA TTAATATCAT GCTCACCTAA CGCTAAAGGG 60
GCGGACATTA AAGGCTATAA CGGCTTAGTG GGGGAATTGA TTGAAAGGAA TTTCCAACGC 120
TATGGCGTGC CGTTACTGCT TTCTACGCTC ACTAACGGCC TATTGATTGG GATCACTTCG 180
GCTTTAAACA ACAGAGGCAA TAAAGAAGAG GTGACTAATT TCTTTGGGGA TTATCTTTTA 240
TTGCAATTGA TGAGGCAAAG CGGCATGGGG ATCAATCAAG TGGTCAATCA AATTTTAAAG 300
GACAAGAGCA AGATCGCCCC CATTGTGGTG ATTAGAGAGG GGAGTAGGGT CTTCAATTCG 360
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SUBSTITUTE SHEET (RULE 26)

254

CCCAATACTG ACATCTTCTT CCCTATACCC AGAGAGAATG AAGTCATCGC TGAGTTTGTG 420
AAG 423

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256

GTGAATTTTT ACCTTTCGCC CAAAGATTAC CACCACTACC ACGCCCCTTG CGATTAGAA 60
ATTTTAGAGG CTCGTTATTT TGCGGGGAAA TTACTACCAG TCAATAAGCC CTCATTACAC 120
AAAAAACAAA ATCTGTTTGT GGGCAATGAA AGG 153

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...699

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257

ATGGATATTT TAAAGCAGA GCATTAAAC AAACAGATTA AAAAAACCAA AATCGTTTCA 60
GATGTTTCTT TAGAAGTGAA AAGCGGCGAA GTGGTGGGCG TTTAGGGGCC TAATGGGGCG 120
GGTAAACCA CCACCTTTTA CATGATATGC GGGCTTTTAG AGCCTAGTGG GGGGAGCGTT 180
TATTTAAACG ATGTGGATT AGCTAAATAC CCCTTACACA AGCGTTCTAA CTTGGGCATA 240
GGCTACTTGC CCCAAGAATC CAGTATTTTT AAAGAATTGA GCGTGGAAGA GAATTTGGCC 300
CTAGCAGGGG AGAGCACTTT TAAAACTCT AAAGAGAGCG AAGAAAAAT GGAAAGCTTG 360
CTTGATGCTT TTAATATCCA AGCCATAAGA GAGCGCAAGG GCATGAGCTT GAGTGGGGGA 420
GAAAGAAGGC GCGTAGAAAT CGTAGGGCT TTAATGAAAA ACCCTAAATT CGTGCTGTTA 480
GATGAGCCTT TTGCGGGCGT GGATCCGATT GCGGTGATTG ACATTCAAAG AATCATTGAA 540
AGCTTGATTG GATTAAACAT TGGCGTGTG ATTACTGATC ACAATGTGCG AGAGACCTTG 600

SUBSTITUTE SHEET (RULE 26)

255

AGCGTGTGCC ATAGGGCGTA TGTGATCAAA AGCGGCACGC TTTTAGCGGC GGAACGCTA 660
 ATGAAATTTA TGAAACGCT TTGGTTCGTA AGTATTATT 699

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258

ATGAAAGAAA	TCGTTACAAT	AGAGAATGTG	TCTTTTAACT	ACCACAATCG	CGCTATTTTT	60
AAGGATTTTA	ATTTAAGCAT	TCAAGAAGGG	GATTTTTTAT	GCGTTTTAGG	GGAGAGCGGG	120
AGCGGTAAAA	GCACGCTTTT	AGGCTTGATT	TTAGGGCTTT	TAAAACCCAG	TCTGGGGAGC	180
GTTAAATCT	TTAATGAGAC	CCTTTCAAAC	AACGCTTTTT	TACGCCAAAA	AATAGGCTAT	240
ATCGCTCAGG	GCAATTCCTT	ATTCCCTCAT	TTAAACGCCT	TACAAAACAT	GACTTTTTGC	300
CTTAATTTAC	AAGGCATAAA	CAAACAAGCC	GCTCAAAAAG	AAGCCAAAGC	CTTAGCGTTA	360
AAAATGGGGT	TAGACGAGAG	CCTTATGGAT	AAATTCCCTA	ATGAATTGAG	TGGGGGGCAA	420
GCCAAAGAGT	GGGCATTATT	AGGGGGATTA	TCCACAGGCC	AGAACTCATT	TTAT	474

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259

ATGATTTTCC	CCGAGCGCTT	TCAAAACGCC	TTTTTAGGGT	TAAGCGAATT	GTTTTACTAC	60
GCTTCCAGCT	TGAGTTTTTA	TACGATTTTG	TCTTTATCGC	CTATTTTGTT	GTTCTGTTC	120
AGTCTTTTIG	TGCTCATTA	CTTGCAAGCG	CACAGCGGTG	AAATGGAAGC	CTTGATTTTC	180
CCTAACGCTC	CTAAATCAT	TGGCGCGATT	AAGGATTTTT	TAGAAAATTT	TAAAAAACA	240
GACATGACCT	TAGGCACGCT	TGAAGAGGTG	TCTATTGTGG	TGGCGTTGGT	GCTTTTTTGT	300

SUBSTITUTE SHEET (RULE 26)

256

GAAACTACC	GCTCCATCGC	GTCAAAAATT	TTTGACGCAA	AGCCCAGAGA	TTATGCGCAT	360
TTTAAGGGTA	AAGAAATCTT	TTTATTTTGG	GGGTTTGGCA	CGACTTTAGT	GTTTTTATTC	420
GCTTTGCCCTT	TGGTGGTGTT	TTTTGATATT	AAGATCCAAG	TGTTTTTTGA	AGATAAAGAT	480
TCAAGCTTGT	TGCATGTTTT	AAGATGGATA	GGCACTTACG	CGTTTTTTTT	GATCCTTTTT	540
ACCATTCCCA	CGAATAAGGT	GTTTAACTA	YYA			573

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260

ATGGTTTTGA	TGATTTTCAC	AAGCATCTTG	AAGATAGCGT	TAAAAGTTTT	ATCAGAGCGA	60
AAAAAAATC	GTTATGGTTT	TCCTAGAATC	TTTGATGTTG	CAGACATAGA	ACAAGAAGAG	120
AGGGAAGTCA	TTGAATGGCG	AGAAAAAAG	AAAGCGTCAA	AACAAAGCTA	TAAACAAAAC	180
CTTCAAATCA	ATAAAATCGC	TAACGATTTA	AAGCGTGATA	AGATAGTGGA	TAAAAGAACG	240
ATTTTAAGCG	TGATAGACGC	TGATATAGAG	CGTGGTTTTA	TCCCGCCTAA	AGATTTGTTA	300
AAACAATTAG	AAAAAATTAG	CGCTTCTCTT	TCTAAAGACA	TCGTAATAAC	GATAAAGCAA	360
GTAGAAAAAT	TAGAGCTTAA	CTATGCGCTA	ATAGACAATA	TCCAACATAA	CACGCTTGAT	420
GACACGCTTG	ATTTTACCTT	TATTGTTGGG	GATTCTTTGA	GCCTTCAGTC	GCTTTATGTT	480
ACCTTTAATC	TTGTGATTGA	TATTGATAGA	CCCATGAGCG	AGCAGTTTCT	CAACCWTATT	540
GGGAAATTGG	GGAGTTTGA	ATCTAGAGAG	CAAGCGTTAG	AGTGGGTGCG	ATTATCGCAA	600
ACTAAACTGA	TCAATTGAAAC	GCCTAAAGAA	GCCTTAAAAA	ATGCGGAATT	ATCACAAATT	660
GAAGAAATAT	TGACCGGCTG	TATTTTAAAT	GGCGCTTACC	GCCTTCAAAA	CGATCTTAAG	720
AAAGGGCGA						729

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...708

SUBSTITUTE SHEET (RULE 26)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261

GTGAGTGAGG	TCGCGAGCGT	GGGGGGCTTT	GTGAAGGATT	ATGAAGTAAC	GCTTCAAAAC	60
GATTCTTTGA	TCCGTTATAA	CTTGAGTTTA	GAACAAGTCG	CTAACGCGAT	TAAAAATTCC	120
AATAACGATA	CCGGTGGGGG	CGTTATTTTA	GAAAACGGGT	TTGAAAAAAT	TATAAGATCG	180
CATGGCTATA	TCCAATCTTT	AAACGATTTA	GAAGAAATTG	TGGTTAAAAA	AGAAGGGGCT	240
ATCCCTTTAA	AAATCAAAGA	TATAGCGAGC	GTTAGGCTAG	CGCCCAAACC	GCGCAGAGGG	300
GCGGCTAATC	TCAACGGCGA	TAAGGAAGTG	GTGGGCGGGA	TTGTTATGGT	GCGCTATCAC	360
GCTGACACTT	ATAAGGTGCT	TAAAGCCATT	AAAGAAAAAA	TCGCCACCTT	ACAAGCGAGT	420
AACCCGTGATG	TGAAAATCAC	CAGCGTGTAT	GACAGGAGCG	AAATGATTGA	AAAAGGCATT	480
GACAATTTGA	TTCACACGCT	CATAGAAGAA	AGCGTCATTG	TGCTAGTCAT	TATTGCGATT	540
TTCTTACTGC	ATTTCAAGAG	CGCTTTAGTG	GTGATTATCA	CTCTGCCTTT	AAGYGTGTGC	600
ATCAGTTTCT	TGCTCATGSG	TTATTTTCRAT	ATTGAAGCGA	GCATCATGAG	TTTGGGGGGC	660
ATTGCAATCG	CTATAGGGGC	GATGGTGAAT	GCGGCGATTG	TGATGGTG		708

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262

GTGGAAACTT	TTCTTAGAAT	TTTTGAAAAA	GATATTTTTA	ACACGCCCTA	TAAATTAGAA	60
GTCATTAAACG	CTACTGAGGG	GGGGGCTAGG	ATTAAAGGGA	CTAAAGAAAT	GCCCTTTAAA	120
GAAGTGTGCG	AAAAAWTAGA	CAAATCCAAG	CCAAAGCCTC	CTATCAATCT	TATTTATCCC	180
ACCCAATCAG	AACAGGCTAA	AAATTTAAAG	ATCGCCAAGA	AAAAATGCGA	AGAGATCATC	240
AAATACGCCA	ATGAGAAAAA	AACGCAAGTT	GAAGAAGCGT	TTTTAAAGGT	GGCAGAGTTT	300
TTAGAAAAAG	TGAAAAAGCT	TCATGAAAAA	AACAAATTAG	AAGAGTTGGA	TTTTGAAGAA	360
TTAGAAAAAT	TGAGCGCTGA	AATTGATAAC	GTTAAAGAGC	TTTTTGATGA	CAAACGATTC	420
AATTCGTATT	TTATGGATGC	GATACAATCT	TACATTTTCC	ACCAGGAATT	GCATATCGCT	480
GAAATCGTGT	GTAAAAAAAC	GAGTAATGAA	GACGGGATTA	AGGGC		525

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

258

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263

ATGAAAACGC	CTTGCAACGC	CTATTTTCTC	AAAACGCCAC	CCAAAAACAA	AAAAAGAAGA	60
GTTTATGTTA	ATTTAGCGGT	GTTTCTTTT	TTATGCTAG	CGAGCGCTTT	ATGGCTCATT	120
CCTAGAAGTG	CCATAGAAGR	AAAGCCCTTA	GTCGTGGCGA	CAAAACCTAG	CAGCGAGCAG	180
TATATTTTGG	GCGAAATTT	AAGCCTTTTG	TTAGAAAAAC	ACCATATCCC	TATCAAGCGA	240
GCGTTTGGCA	TTGGTGGGG	GACGATGAAT	ATCCATCCGG	CATTGATTAG	GGGCGATTTT	300
GATTTGTATG	TGGAATATAC	CGGCACCGCT	TGGGTGAACA	CGCTCAAAAA	CCCTTTGACT	360
CAAAAAGTGG	ATTTTGAAAC	GATTAAAAAG	CGTTATGAGA	AGGAATTTAA	TCTTTTGTGG	420
GTGGGACTTT	TGGGCTTTAA	TAACACCTAT	TCTTTAGCGA	TTTCTAAAGA	AGACGCTCAA	480
AAATACGCAA	TTGAAACTTT	CAGCGATTTA	GCCTTTCATA	GCCCGAATTT	TGATTTTGGA	540
GCGGAGYTTG	ATTTTITTTGA	AAGAGAGGAC	GCTTTTAAGG	GCTTAATCAA	AGCTTATCGC	600
TTTCATTTTA	GAAGTTTGCA	TGAAATGGAY	ATTAATTTGC	GTTATAAAAG	TTTGAATCC	660
CTCATAAGAT	YAACGCTT					678

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264

GTGATGGTTT	ATAAACTCCC	CAAACACCAG	CAAATAAGG	TCATGATTTT	AGGCTTGGGC	60
TTAGCGATGA	TCACTCGTAT	AGGGCTTTTA	GGGAGCTTGT	TTTTCATCAG	CCATTTGCAA	120
AAGCCTTTAT	TCGCTATAGC	GGGCATGAGC	TTTTCATGCG	GTGATGTGGT	GCTGCTTTTA	180
GGGGGGGCGT	TTTTGGCTTT	TAAGGCGTTA	GTGGAATTAA	AAAGAGCAGA	TCTATCC	237

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 630 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265

```

ATGTTTGTGG TTTTATAGA AGGTTTGGT TTAGCGATT CTTTGTGCGC GGCGGTGGGG      60
GCGCAATCCT TGTTTATTGT GGAAAGGGG ATGGCTAGGA ATTATGTGTT TTTGATTGTC      120
GCCTTGTGTT TTATGTGCGA TATTGTCTTA ATGAGCATGG GCGTGTGTTG CGTGGGGGCT      180
TATTTTCGCTA AAAACCTTTA TTTGAGCTTG TTTTGAATT TATTTGGGGC AGTTTTTACC      240
GGATTTTACG CTTTTTTGGC TTTAAAAACC CTTTTTCAA CCTTTAAAA AAAGCAAGTC      300
CAAACCCCTA AAAAATTATC CTTAAAAAAG ACCTTATTAT TCACCTTAGG CGTTACCTTA      360
CTCAATCCTC AAGTGATTAT GGAAATGGTG TTTTAAATG GCGCGAGCGC TATGTCCTTT      420
AACCTAGTGC AAAAATTCGT CTTTCTAGCT GGCACCTTAT CGGCTGCCTT TTCTTGGCTT      480
TTATTGTTAT GCACCATGTC CTTACGCTAT GGCTCTAAAC TTTTGAACAA CCAAAAAATC      540
TTTATGGGCG TGAATCTCTT TGTAACCGCT ATCATGGGAA CGCTCAGCGT TACTTTATTG      600
AGGGATTTTT TAGCGTTATT GAGCAAAACC                                     630

```

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 888 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266

```

GTGAAGCCAA AGAGCATGAA AGAGAAGCTA AGAGGCGCTA TGGTGAATAT CTTAAGGATA      60
AAAATGATTG AAATAAGCGA ATGGTTGCAA AAAGTAGACG ATGCCTTAGA TAAAGTTGTT      120
GCTAAAAAAG AGCCAGAGAG TTTTCTCAA CCGATCATTT CACCAATAGA GGAATACCAA      180
AAGAGTGTC AAGCAATTCA AGCGCAATTC ACAGACGCGC CGAAGTTCAA TGAAGAGGGT      240
GCTTACCCTC AATTTTAAAG CTGTGGTTTA TTGCAAGTTA GGGGCAAAAA TGGTGCTAAC      300
ATGGAATTTT TATTGCCTAA AGTTTATCCT TTCCCCCTA AAAGCTTGTA TATAGAGCAT      360
GAAAAAGACG GGCAGTTTTT GAGAGAAATG CTCATGCGCT TACTCTCCAG CGCGCCTTTA      420
GTGCAATTGG AAGTGATCTT AATTGATGCG TTGAGCTTGG GGGGCATTTT CAATCTGGCC      480
AGAAGGCTTT TAGATAAAAA CAATGACTTT ATTTACCAGC AAAGGATTTT GACCGAAAGC      540
AAGGAAATAG AAGAAGCCCT AAAGCATTTG CATGAATATT TAAAGGTTAA TTTGCAAGAA      600
AAATTAGCCG GTTTTAGAGA TTTTGTGCAT TATAATGAAA ACGCCAAAGA CTCCTTGCCT      660
TTAAAAGCGC TTTTTTAAG CGGGGTGGAT GCTTTGAGTA AAGACGCGCT TTATTATCTA      720
GAAAAGATCA TCGGTTTTGG CTCTAAAAAT GGGGTTTTGA GCTTTGTCAA TTTGGAGAGC      780
GAAAAAACA ATCAATCCGC AGAAGATTTG AAACGCTATG CGGAGTTTTT TAAAGACAGG      840
ACAAGTTTTG AGTGSTTAAA ATACCTTAAT GTAGAAATCA TCACCGAT                                     888

```

(2) INFORMATION FOR SEQ ID NO:267:

260

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 282 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...282
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:267

```

GTGCTTATAA GCGTGATGAT AGGCCAAAAT CAAGTCTTAG GCTTTATAGG GACTAATTTT      60
AAGCAAGAAT TAGTCGTGGA TTTCATTGTC CCAAGCGCTG AAATCAACAT AGGCRRTCAA      120
GTGYTAACGA GCGGGCTAGA TGGGATTTT GGAGCGGGGG TGTGTGTGGG TGAAGTTTCA      180
AGCGTTGAAG ATCATTACAC TTATAAAAGC GCGGTGTGTA AAAACGCTTT TTTAAGCGAA      240
GCCAAACTTT TAAGGCATGT GTTTTAAAGC GGTGTGAAAA AC                          282

```

(2) INFORMATION FOR SEQ ID NO:268:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 249 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...249
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:268

```

ATGGAAGCGC AATTACGATT TACGCTGTTT GGAGGGCAAG GCGTGTGTT AGCGGGAGAG      60
ATTTTAGCTG AGGCTAAGAT CGTGAGGCTT GCTATGGCA CTAAGACTTC CACCTACACT      120
TCGCAAGTGC GTGGAGGTCC CACTAAAGTG GATATTTTGT TAGATAAAGA TGAAATTATT      180
TTCCCTTATG CTAAGAGAGG CGAGATTGAT TTCATGCTTT CAGTCGCTCA AATCAGCTAC      240
AACCAGTTT

```

(2) INFORMATION FOR SEQ ID NO:269:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 609 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

SUBSTITUTE SHEET (RULE 26)

261

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...609
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:269

```

ATGCAAGCTT GGGTGGATAA GCCGCTATTG TTAGAGCCAG ATAGTAACGC CCAATACGCC      60
GCTGTCAATTG AAATTGATGT GGCAGAAATC ACGGAGCCTA TTTTGGCATG CCCTAATGAC      120
CCTGATGACG TCGCTACTTT GAGCGAAGTT TTAGCGGATA CGACCGGCAA AAGACCCAC      180
GCTATGATG AAGTGTTTAT TGGCTCTTGC ATGACGAATA TTGGGCATT CAGAGCCTTT      240
GGTGAAATCG TTAAAAACGC CCTCCCAGT CAAGCACGCC TTTGGGTAGT GCCACCCAGT      300
AAAATGGACG AACAAGAGCT TATTAATGAG GGCTATTATG CGATTTTGG GGCTGCCGGG      360
GCAAGGACTG AAGTACCAGG CTGTAGCTTG TGCATGGGCA ATCAAGCGAG GGTAGGGAT      420
AATGCGGTCG TTTTCTTAC TTCCACACGG AATTTTGATA ATCGTATGGG TAGAGGGGCT      480
AAAGTGTTAT TGGGCAGTGC GGAGCTTGGG GCGGCGTCCG CTTTACTAGG GAGGATCCCC      540
ACTAAGAAG AATACATGAA TTTAGTGAGT GAAAGCTAG AGAGCCAAAA AGACAAGATC      600
TATCGCTMC                                     609

```

(2) INFORMATION FOR SEQ ID NO:270:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 660 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...660
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:270

```

GTGGGCAATG CCGGGGTGGC TTTAGCGGGT TTGATGAGCG ATGAAATTTA TTTGTGCGCT      60
TTAGATTGCG CTTATATCAA AGGGTTTAAA AAGCACGCTC AAAATTCCTA TTATGGAGAT      120
GAAAAAGAGA TTGACACCTC ATCTTTAATC AGCGTAGAGG GTAATGTTGA AGGTTATGAA      180
ACTTTTAGCG ACTCGCTTTT TTTGCTCTCT AAAGAAAGGA TTGAAGAAGC CCTTCATTAT      240
TACCAGCCTA AAAAAGTCTA TAATTTAAGC TATGGGGCGA AAATCAAGCA CGCGGTTAGC      300
CTCAATCACT CTCAAGTGAA ATTGAAACAA ATCAACAAAC AAGACGCTAT CGTTCGCATT      360
AAAAGCATGT TTAGCCCTAG AAGTAATCAT GCTAAGGATT TAAAAAATT ACAAAAAAT      420
CTGATTGCGT TTAAAGAGGA TTTTTCACG CATTTAAACA CGCCTTGTA AACCAGCAA      480
GAAGCATTTG AATGGGTGGA TAGCTTGAGT GGATTTTGCC AAACAGCCAG CGCTAAAACC      540
CCCACTATAG GCATTTTATT TGAAGGGAGT GTCGCCATA TCTTACAAAG CGTTCTAATC      600
GTTTCATTGC ATCTTAAAGA AAATGAGCTG ACGCTTTTAT CAAATTCTCT CAAAACGCCT      660

```

SUBSTITUTE SHEET (RULE 26)

262

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 744 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271

```

ATGCAAAAAA GTATATTCAA AATAACTCTG TGTGTTGTTT TCCTCTTTT AAGGAATGCT      60
GTTGGTTTAG ACGATAAAAA AGCAGCTCCT AAAAGCGTTC AAAATACCCC TAAAAATTTA      120
CCCCCTATCC AGTTAAGGCT CGATCAAGCC TATGAAGACC TTATCAAAAT GTTAGACAAT      180
ATGGGAAAAA GCACGCAGTA TGAGTTCCCT AAAATTAAAG AAATCCTAGA ACAAAGCGAA      240
GAGGAATGGC TAGGAGTCGC CCATGAAGAA TGTGTGGCGT TAGTCATGTT AATAAGCCCT      300
AAGGCTTCTA TTGAAAACAG CCCGATTAT AAGAATTGCT ATGAAGCTTA TGTGAAACAA      360
AGAATCCATG ATTTATATGA TTTTATATA GAGGGCAAAA AAGTGAAAAG AAAAATCAAG      420
AAAGCCCATG AGCATGAAAT GGCCCTCAAC AAATCCCAAC CCTTAAAAAA GGAACCGCCT      480
AAAAGCGAGA ATAAAAAGGG CTTAACAAAA CCTAGCTTGA AAGACGCAA GATCCCTAAA      540
GGGTATTACT TGCAAAATTGG GGCTTTTTTA AATTGCCCCA GTAAGGATT TTTGCAAACG      600
CTCAAACTT TCCTTCACCA AATGGAGGAA AAAGACTCCC TCACGCATTA TTTGATTGGC      660
CCTTATAAAA CCAAAGAAGA AGCCCTAAAA CAGCTTGAAA ATGCGGCTAA AAGCTTTAAA      720
AATAAGCCTG CGTTGGTAGA GAAG                                     744

```

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272

```

ATGCAAGAAA TCTTAATCCC TTTAAAAGAA AAAAGCTATA AAGTGTTTT GGGGGAAGTG      60
CCTGAAATAA AATTGAAACA AAAAGCGCTC ATCATTAGCG ATAGCATCGT GGCCGGGTTG      120
CATTTGCCCT ATTTGTTAGA GCGCTTGAAC GCCTTAGAAG TCAGAGTGTG CGTGATAGAG      180
TCCGGGGAAA AATACAAAAA TTTTCATTCA TTAGAGCGGA TTTTAAACAA CGCCTTTGAA      240

```

SUBSTITUTE SHEET (RULE 26)

263

ATGCAATTAA ACCGCCATTG TTTAATGATA GCCCTTGGTG GGGGAGTGAT AAGCGATATG	300
GTGGGGTTTG CGAGCAGTAT TTATTTTCAGG GGGATTGATT TTATTAATAT TCCCTACGAC	360
TTTACTCGCT CAAGTGGATG CGAGCGTGGG GGGGAAAACA GGGATCAACA CGCCTTATGG	420
CAAGAACCTA ATCGGATCGT TCCACCAGCC	450

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273

ATGCGAATAC TTCATTATGG AGGTGAGCTC CCATGCGATT GTCCAAAACG CATCGCTGGG	60
CTTGATTTTCG CTCTTAAAT TCTACCAAT ATCACAAGCG ATCATTTAGA TTTCATCAA	120
AATATAGAAA ATTACAGGGA CGCTAAAAAC AGCTTTTTTA AAGATGAGGG CTTAAAGTC	180
ATCAACAGAG ATGAAACAAA CGCCCTTTTT AACCCCATTA ACGCGCGCAC TTACGCACTG	240
GATAAAAAAG CGCATTTGAA TGTTCAGGCC TTTTCGCTCA ACCCTTCCAT TAGCGCGTCT	300
TTATGCTACC AACACGATTT AAGAGATCCC AATCTTAAAG AAACCGCCCT GATCCATTCC	360
CCCCTTTTAG GCGGTTACAA CCTTTATAAT ATTTAGCGG GCGTTTTAGG GGTTAAATTG	420
CTCACTCAAT TGCCTTTAGA AACGATCGCA CCGTTATTGG AAAACTTTTA TGGGGTTAAG	480
GGGCGTTTGG AAATTGTACA TTCTAAACCT TTAGTGGTCG TGGATTTTGC CCACACAACA	540
GACGGCATGC AACAAGTTTT T	561

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274

GTGAGCATTAA AAGAAGAGAG CCAAACCTTA GCCGATATTA CTTTCAAAA TTATTTTCAGG	60
--	----

264

ATGTTTTCTA	AACTTTCAGG	CATGACAGGC	ACGGCTCAAA	CCGAAGCCAC	AGAATTTTTA	120
GAAATCTACA	ATTTAGAAGT	GGTGTCCATC	CCTACTAATC	TAGCGATCAA	GCGAAAAGAT	180
TTGAACGATC	TGATCTATAA	GAGTGAAAAA	GAAAAATTG	ACGCTGTGAT	CCTTAAAAAT	240
AAAGAATTAC	ACGATAAGGG	TCAGCCCGTT	TTAGTCGGCA	CGGCTAGCAT	TGAAAAGAGT	300
GAAACCTTGC	ACGCTTTACT	CAAAAAAGAG	CGCATCCCTC	ACACCGTTT	AAACGCCAAG	360
CAACACACTA	AAGAAGCTGA	AATCATCAAA	GACGCCGGGC	TTAAAGGGGC	GGTTACGATT	420
GCGACCAACA	TGGCAGGCAG	GGGCGTTGAT	ATTAAGCTCA	CTGATGAAAT	TAAAGAAGCT	480
GGGGGGCTGT	ATATCATTTG	CACTGAAAGG	CATGAGAGCC	GTAGGATTGA	CAATCAATTA	540
AGGGGGCGAA	GCGGGCGTCA	AGGCGATCCG	GGAGTGAGTC	AGTTTTATTT	GAGC	594

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275

GTGGTGGCTG	ATGAGGTGAG	AAAGCTCGCT	GAAAAAACCC	AAAAAGCCAC	TAAAGAAATC	60
GCTGTCGTGG	TTAAAAGCAT	GCAACAAGAA	GCGAACGATA	TTCAAACCAA	CACCCACGAT	120
ATTAATTCTA	TTGTAGGCTC	TATTAAGGGT	GATGTGGAAG	AGCTTAAATC	CACCGTAAAA	180
AATAACATGA	TTGTCGCGCA	AGCCGCAAAA	TACACCATCT	ACAATATCAA	TAACCGGGTG	240
TTTTGCGGTY	TGGCTAAACT	CGATCATGTG	GTCTTTAAAA	ACAATCTTTA	TGGCATGGTG	300
CSTTTGGTCT	CAATTCCTTT	GACATTACCA	GCCCATAAGA	GTTSCCGTTT	AGGCAATGG	360
TATTATGAGG	GTGCGGGTAA	AGAAAACCTT	GCTAACACTT	CAGGCTATAG	AGCTTTAGAA	420
AGCCACCATG	CGAGCGTGCA	TGCTGAAGCT	AATGATTGG	TTAAAGCCGT	TCAAGAAGAT	480
CACGTCACCG	ATTCAAAATA	CCTAGAACAT	AAAGTGCAAT	TAATGGAAGA	TAGCGCTAAG	540
CATGTCAAAG	AAAATATTGA	TAAGATGTTT	TATGAAAAAC	AAGATGAACT	CAATAAAATC	600
ATTGAAAAAA	TTCAAAAAGG	CGAA				624

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

SUBSTITUTE SHEET (RULE 26)

265

(A) NAME/KEY: misc_feature
(B) LOCATION 1...603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276

```

ATGAATACAT CAAAAAATT AGGTAACCCC TTGCTTTTTT TGCATGATAA TAAAATTTTG      60
TTGTTTGTCG TAGGGGTGAG CATGGGCGGG TGGGCCACTT CTAAATCTA TCAATTTGAA      120
AGCGCTTTAG AGCCGATTCA TTTAAGTTT GCGCGAAAAC TCTCTTTAAG CCCTTTTTTA      180
AATTTGAGCC ATTTAGTAAG GAATAAGCCT TTAAACACCA CTGATGGCGG GTTTATGCTA      240
CCACTCTATC ACGAATTAGC CACCCAATAC CCCTTGTTGT TGAAATTTGA CCAACAAAAT      300
AACCCAAGAG AGCTTTTAAG GCCTAATACC TTAAACCACC AGCTCCAACC AAGCTTAACC      360
CCCTTTAAAG ACTGCGCTGT CATGGCGTTT AGAAACCATT CTTTTAAAGA TAGCCTCATG      420
CTAGAAACCT GTAAAACCCC CACTGATTGG CAAAACCCCA TTTCTACAAA TCTTAAAAAC      480
TTAGATGATT CTTTAAATTT ACTCAATTTA AATGGAATAT TGTATTGAT CCACAACCCT      540
AGCGATTAT CACTGCGTCG TAAAGAACTT TGGCTTTCTA AATTAGAAA CCYYCAACTC      600
RTT                                                                    603

```

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 381 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277

```

ATGAGTATTC AACATTTCCG TGTGCGCCTT ATTCCCTTTT TTGCGGCATT TTGCCTTCCT      60
GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG CTGAAGATCA GTTGGGTGCA      120
CGAGTGGGTT ACATCGAACT GGATCTCAAC AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC      180
GAAGAACGTT TTCCAATGAT GAGCACTTTT AAAGTTCTGC TATGTGGCGC GGTATTATCC      240
CGTATTGACG CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG      300
GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT AAGAGAATTA      360
YGCWGGTGGT GCCATAACCA T                                                                    381

```

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

SUBSTITUTE SHEET (RULE 26)

266

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278

GTGAACGTGG	GCGTGCCTTT	TAGCTATCAA	GTGAGCGCGA	CCTTTCAAAA	CTCAGGCCTT	60
TCTAGTTTGC	TAGAACTTT	AAAAAGAGT	TTTTAGAAA	AGCCCTTAAT	TGAGAGCAGC	120
GCGAATAAAA	TCGCGGATAT	TTTTTCTAAA	GCGGTGTTGT	TTTTCAGCCTT	TGTGAGCTTT	180
TTATTGTGGC	AATTGTGTTT	GGGGGTAAT	TTGAAAAAS	GCTTTAATGG	TGTGTAT	237

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279

ATGCTAATGG	TTAATGGCTA	TCAAATCACG	ATGCATAAGG	GTTATAAGGT	AGGGTTTTTTT	60
ACAAGCGGTT	ACAACCCTGA	TTTCGCTCAA	ACCATTCAAA	ATAGAAGCTA	TTTGATGAGC	120
TCTTATGAGT	TATCGTTTTT	AAGAAAT				147

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280

SUBSTITUTE SHEET (RULE 26)

267

ATGGTGCAAT	TTCAAAACAC	GCTTATAAAA	TTCCATGCCC	TATCCTTTAA	AAACGCAAAT	60
TTAATTTATA	ATGCAAAATT	AAACAAAACA	TGCTATAAAG	AAAATTCAAA	TACTATCATT	120
TTAAGGATTA	AAATGCTCAC	CCAAGAAGAT	GTCTTAAACG	CGTTAAAAAC	GATCATCTAC	180
CCTAATTTTG	AAAAGGATAT	TGTCAGCTTT	GGTTTTGTTA	AAAACATCAC	CTTGCAATGAC	240
AACCAATTAG	GGCTTTTAAT	AGAAATCCCC	TCAAGCTCTG	AGGAAACGAG	TGCGATTTTA	300
AGGGAAAATA	TCTCCAAAGC	GATGCAAGAA	AAAGGCGTGA	AAGCTTTGAA	TTTGGATATT	360
AAAACCCCCG	CTAAACCGCA	AGCTCCAAAG	CCCACCACTA	AAAATCTGGC	TAAAAACATC	420
AAGCATGTGG	TCATGATAAG	CTCAGGCAAG	GGCGGTGTGG	GTAAAAGCAC	CACCAGCGTG	480
AATTTAAGCA	TCGCTTTAGC	GAATTTAAAC	CAAAAAGTGG	GGCTACTAGA	CGCTGATGTG	540
TATGGCCCTA	ATATCCCTAG	AATGATGGGC	TTGCAAAAACG	CTGATGTGAT	CATGGATCCT	600
AGCGGTAAAA	AACTCATTCC	TTTAAAAGCT	TTTGGCGTTT	CTGTGATGAG	CATGGGGCTT	660
TTGTATGATG	AGGGGCAGAG	TCTCATTTGG	AGAGGACCCA	TGCTCATGCG	AGCGATTGAG	720
CAGATGCTAA	GCGATATTAT	TTGGGGGGAT	TTAGACGTGC	TGGTGGTGGA	TATGCCCCCA	780
AGGAACAGGC	GATGCGCAGC	TCACGCAGCC	CAAGCCGTGC	CACTCAGCGC	AGGAATCACC	840
GTTACTACGC	CTCAAATCGT	GAGTTTAGAT	GACGCTAAAC	GGAGTTTGGA	CATGTTTAAG	900
AAACTACACA	TTCTATTGTC	GGGCATTGTA	GAAAATATGG	GGAGTTTTGT	GTGCGAGCAT	960
TGCAAGAAAG	AGAGCGAGAT	TTTTGGCTCA	AATTCCATGA	GTGGATTATT	AGAGGCTTAT	1020
AACACGCAGA	TTTAGCCCAA	GCTCCCTTTA	GAGCCTAAAG	TGCGTCTAGG	GGGGGATAAG	1080
GGTGAACCGA	TTGTGATTTC	TCATCCCCACT	AGCGTGAGTG	CTAAAATTTT	TGAAAAAATG	1140
GCAAAGGATT	TGAGTGCTTT	TTTAGACAAG	GTGGAAGGG	AAAAACTAGC	CGATAATAAG	1200
GACATCCAGC	CCACACAAAC	GCATGCTTAT	TCGCAT			1236

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281

ATGGGTGTGG	TGATTGGCGA	GACCACAGAG	ATTGGAGATG	ATGTTACCAT	TTATCATGGC	60
GTAACCTCTG	GGGGTACGGG	CAAGTTTAAG	GGCAAACGCC	ACCCTACTTT	AGGCAACCGA	120
GTGGTAGTTG	GGGCAGGGGC	TAAGGTCTTG	GGCGCGATTT	GCGTGGGCGA	TGATGTGAGG	180
ATTGGGGCTA	ATGCGGTGGT	GCTTTCAGAT	TTACCCACGG	GTTCTACGGC	TGTAGGTGCT	240
AAAGCCAAAA	CCATCACAAA	GGATCGT				267

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

SUBSTITUTE SHEET (RULE 26)

268

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282

ATGCTATCTT	TTATAAGCGC	GTTTGATAAA	AGGGGCGTTT	CAATACGCCT	TCTAACAGCC	60
TTGTTACTGC	TTTTTAGTTT	GGGTTTGGCT	AAAGATTTAG	AAATCCAAAC	TTTTGTGGCT	120
AAATACCTTT	CTAAAAATCA	AAAAATACAA	GCCCTACAGG	AGCAAATTGA	CGCTTTAGAT	180
TCTCAAGAAA	AAGTCGTTAG	CAAAATGGGAT	AACCCTATTT	TGTATTTAGG	CTATAACAAC	240
GCTAACGTGA	GCGATTTTTT	CAGGCTGGAT	AGCACCTTAA	TGCAAAACAT	GAGCTTGGGT	300
TTGTCTCAAA	AAGTGGATTT	AAATGGTAAA	AAACTCACGC	AGTCTAAAAT	GATCAATTTA	360
GAAAAACAAA	AAAAAATATT	AGAGCTTAAA	AAAACCAAGC	AGCAATTGGT	GATTAATTTA	420
ATGATAAACG	GCATTGAAAA	CTATAAAAAC	CAACAAGAAA	TAGAGCTTTT	AAACACAGCG	480
ATTAAAAATT	TAGAAAACAC	CCTCTATCAA	GCCAAACCATT	CCAGTTCGCC	CGATTTAATA	540
GYGATYGYCA	AGTTRGAAAW	TTTAAAAATC	GCCAWT			576

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 348 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283

GTGCCGGCTG	TTGGGGGGGC	TTTGATTGGG	ATYCYTAG	YGATTTATGA	GCTTTATCAT	60
GGGYATGTGA	ATGAGGYTAT	TTTTAYYGT	TTGTATTCCA	TTTTGTTAAT	TGGTGTGTTG	120
ATTGATAGCG	TGATCAAGCC	AATTTTAATC	GTTTTTATCA	AAAAAAGAAT	CTTTAAAACC	180
ACCCTTAAAA	TCAATGAAAT	ATTGATTTTC	TTTTCTATGA	TTGCTGGGAT	TTCTCAATTT	240
GGTTTTTGGG	GGATTATCGT	AGGGCCTACC	ATCAGGCGCT	TTTTTATCGC	GTTACTGCGA	300
TTGTATGAAA	ATTACTTTAT	TCAAAGGAG	CAAAAACAT	GCGAATGT		348

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 489 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

SUBSTITUTE SHEET (RULE 26)

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284

GTGGTTGTCA TTATTTTAGT GGTGTTATC ATTCAAAACA GCTCTTCTTT AAAAGAAGAG	60
AGAGAGCAAG AACGCGCTAT TAAGCCCGAC ACCAAAAATA ATTCTTTCAA TGAAACTAAT	120
CCTACAGAAG AAAAAAGTT AGAGCCAACG CCTAAATTAG AAGAAAAACA CAAAGAACAA	180
GACAAGCAAG GCAAAGAAGC GATCAAAGAA AATCCTAATA CCATTACAT TATCCCTAAA	240
CGAGATATTT GGGTAGAAGT GATTGATTGA GATGAGAAAA AAAACTCTTT TCAAAAGGTT	300
TTTAAAAAAA GTTATCCTTT AGAGGCTAAA AACCACCGCT TGTGTTACG CTTTGGGCAT	360
GGGCATCTTA TTCTTAAAA CAACCATCAA GAACAAGATT ATAACGACAG CAAAAC TAGG	420
CGGTTTTTAT ACGAGCCAAA TAAAGGTTTA ACGCTCATCA ATGAGGCCCA ATACAAAGCG	480
CTCCAGCAA	489

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285

ATGGATGAAA TCTATCAAAT CGCTAAAAAT AAAACCCTAA TCGTTATCGC CCACCGCTTA	60
AGCACGATTG AACGCTGTGA AGTCATCATT GACATGAGCC AACACAAAGA CAATCTCGGC	120

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

SUBSTITUTE SHEET (RULE 26)

270

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286

```
GTGGCGGGCA GCTTTATTAT TGCTCTTTTT AGCGTTTITAG CGGATCAATT TGTGAGCGTG      60
TTTCAGCATG AAAACGCCTT GCAACGCCTA TTTTCTCAAA ACGCCACCCA AAAACAAAAA      120
AAGAAGAGTT TATGT                                     135
```

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 354 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287

```
ATGGTAGCTT TAAGCAACGC TCTTTCAGG GTTTTGGTT CTGTGGCTGG CTATAAATTC      60
CCTTCTTTTA TCCAAAAAAG CATCAACGCT CTTTATGTTA AGATCTTTAA AATTGATTTG      120
AGCGAGTTTG AGCCTTTAGA AAATTATAAG AGTTTGAACG CTCTTTTCAT GCGCTCTTTA      180
AAAAAAGAAC GCCCCTTTGA CAAAGCCCCT ATATTTGCAT TGCGCCTTGC GATGGCTTTA      240
ATCACTGAAT GCGCTTTTTT AGACAACGAT AGCGCTTTAC AAATTAAAGG CATGCCCTAT      300
AAAGCGCATG AATTAGTGGG CGAAATCAAC CCCTTAAGCC CTCTTTTTTC TATG          354
```

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 600 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...600**SUBSTITUTE SHEET (RULE 26)**

271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288

ATGGCAGTGT	TAAAAAAGAT	GATAGGTTTG	GTGGCGGTTT	TAAGCGTTTT	ATTAGCCAGA	60
GACAACCCTT	TTGAGCCTGA	AATCAATTCC	AAGAATTTGC	AAGGGGGCTT	TAGCGGGATC	120
TATGATGACT	ACCTCAAAGA	AATCCATGTG	GATTTGCCCA	CGAGCGCTAG	GATCTTAAAA	180
AAAATCACGC	TCACTTACCA	AGATATTGAT	GGCTCTATCC	ATTCTAAAGT	CGTGGGTATT	240
GATAAAAGCA	TTGATTGGCA	CTACCCCTTA	AAACTTTCCC	AACACACCCT	TAATCAAGAC	300
GCCTTTGAAA	AACGCTACCA	GATCCAAGAT	TTTGATTTT	TAATGGCAAA	CAACACGATG	360
ATTTTGC GTT	CCCCCTATAA	AATTTTGC GC	TCTTTTGTGT	TAGTCAATCC	TTATAGAATC	420
GTGTTAGACA	CGCAAAAAGG	CCCTTTGGAT	ATTTATCAAA	ACATGGATTT	AAACCAGAAG	480
TTTTTTTCTC	ACATTAAAGT	CGGCACGCAC	AAAGATTATT	ACCGCATCAC	GCTCATTTTA	540
GACGGGAAAT	ACCGCTATCT	TTTGAAGAA	AAAAACGGGG	CGTATGAATT	AAAAC TGAAA	600

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289

ATGGGCGGAT	TCACAAGCAT	ATGGCATTGG	GTCATTGTTT	TATTAGTGAT	TGTGTTGTTA	60
TTTGGGGCTA	AAAAGATCCC	AGAATTGGCT	AAAGGTTTAG	GCAGTGGGAT	TAAGAATTTT	120
AAAAAAGCCG	TGAAAGACGA	TGAAGAAGAG	GCTAAAAACG	AGCTAAAAAC	CCTAGACGCT	180
CAAGCAACAC	AAACC AAAGT	GCATGAAACT	AGCGAAATTA	AAAGCAAACA	AGAAAGT	237

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290

SUBSTITUTE SHEET (RULE 26)

272

GTGCGTTTGA	ATGCGGCGGT	TGTGGTGGAT	GGCAAGTATA	AAATCGCGCT	CGAAGACGGG	60
GCAAACGCTT	TAGAATACGA	GCCTTTAAGC	GATGAATSGS	TTAAAAAAT	CAACGYCCTA	120
GTCAAACAAG	CCATTGGTGA	TAACCAAAAT	AGAGGCGATG	ACGTGGCGGT	GAGTAATTTT	180
GAGTTTAACC	CTATGGTGCC	TATGATTGAC	AACGCCACCT	TGAGTGAAAA	AATCATCTAT	240
AAAACCCAAA	AAATTTTAGG	TTTATTTATG	TTTTTAATCA	AGGTATATTT	GGTGTTTATA	300
GTGTTATTCA	TTTTCTATAA	AAAAGTGATC	GTGCCTTTCA	GCGAACGCAT	GCTGGAAGTG	360
GTGCCTGATG	AAGATAAGGA	AGTGAAATCC	ATGTTTGAAG	AAATGAACGA	AGAAGAAGAT	420
GAGTTGAACA	AACTCGGCGA	TTTGAGGAAA	AAAGTAGAAG	ATCAATTAGG	GCTTAATGCA	480
AGCTTTAGCG	AAGAAGAAGT	AAGATATGAA	ATTATTTTAG	AAAAGATTAG	AGGAACCCCTT	540
AAAGAGCGTC	CTGATGAAAT	CGCCACGCTC	TTTAAACTCT	TAATCAAAGA	TGAAATCTCT	600
TCAGACAGCG	CGAAAGGT					618

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291

GTGTGTTTTA	TATTGCCTTT	TGTTTTAGGG	GTTTTAGGCA	CGCAAATCTT	TAAACAAGAG	60
ACCCCAAGAC	AGCTCCCTAT	CGTGGTGGTG	GATTTGGATA	AGACCACTAC	AAGCCATCAA	120
GTGGCGTTTG	AATTAGGCGC	AACGAGTGCG	GTTGAAATCA	AATACCAAGT	GACTAGCCTT	180
TCAGAAGCTA	AACGCTTTTT	AAACTCCGCT	GAAGTGTATG	GGGCGTTAAT	TTTGCCTAAG	240
GATTTGGAGA	GAAAAATCAA	AATGGGGCGA	AAAGTGSAT	TTGCCCTTTT	ATTA	294

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...591

SUBSTITUTE SHEET (RULE 26)

273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292

ATGAAAGGCT	TATGGCTTGT	AATCTCTTTA	GTTTTTGTG	GTTTTTGTG	GGCTAATGAA	60
TCTTATGTTT	TTAACAATTC	TAAGGGGCGT	TTAACAGAAA	AAAGCGTTGC	GTTTATAGAG	120
GGCGTTTCTA	AAGAGCTTTA	TCTTAAAACC	GGCGTGCCTT	TTGCGATTGA	TATGACGGAT	180
TTTGAAAAAA	ATCCTATCGC	TCTAGCGAAT	AAAAAAGAGC	GCCAAAGCTA	TCAAGAGGGC	240
TTTTTAAAGC	AGCTCAAACC	CCCTTTTGTG	GTATTCTTTT	TCTACCATGA	CGCTCAAAAA	300
ATAGAATTAG	TGGCTAACCC	TAAAGATTTG	CTAGACACTG	ATAAAATCTT	TTTTGAAAAA	360
ATCGCTCCCT	TACTCCCCAC	AAACGCTAAA	GAATACACGC	CCCAAAGAAT	TTCAGCCATG	420
CTCATTAACG	GCTATTCCGT	CGCAGTAGAT	GCTTTAGCGG	AAAAATATCA	TGTGAATATC	480
ACGCAAAATT	TTAGCGCTCC	TAAGGGAGTA	ACTTTGTAA	AGGTGGTTAT	TTATATTTTG	540
TTATTGACGC	TTTTGGGCGC	GTTTTTGGGG	CTTTATTTT	TTAAAAATC	T	591

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293

ATGTGTTCTA	AAAAAATAAG	AAATCTCATT	TTATGCTTTG	GTTTTATTTT	AAGCTTGTGC	60
GCTGAAGAAA	ATATCACCAA	AGAAAACATG	ACTGAAACGA	ACACGACTGA	AGAAAACACC	120
CCTAAAGACG	CTCCCATCT	TTTGGAAGAA	AAACGCGCCC	AAACTCTAGA	GCTTAAAGAA	180
GAAAATGAAG	TGGCAAAAAA	GATT				204

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294

SUBSTITUTE SHEET (RULE 26)

274

GTGCTAAAGA	CATTATCCAT	ACGATTAGTC	ATACTTTTAA	ATTGCTCCCT	AGCGACAAAC	60
GCTTGCACTG	GGGTGCAAAA	ATTGCGCGAT	GAAAGCCACC	GGTATGCGAT	AAACTTCCAT	120
AGATCCACTA	AACTTAAAAA	CATGAAACAA	ATCGCTCTTT	TAAAAGAAAA	GGGCATAGGA	180
GAAGCCAGCG	TGAAAAAATT	GTTGGATTAT	TTTGGGAGTT	TTGAAGCGAT	AGAAAAAGCG	240
AGCGATCAGG	AAAAAACGCG	CGTTTAAAAA	AAACGAAAAA			279

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295

GTGGGCATTA	TTAGGGGGAT	TATCCACAGG	CCAGAACTCA	TTTTATTAGA	TGAGCCTTTT	60
AGCGCTTTAG	ATACTTTGAA	TCGTAAGAAT	TTACAGGATC	TCATCAAAGA	AATACACCAA	120
AATTCTTGCG	CTACTTTTCAT	TATGGTAACG	CATGATGAAA	ACGAGGCGCA	AAAGTTAGCC	180
ACAAAAACCC	TAGAAATCAA	AGCCCTTAAA	CAAGAGCAG			219

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296

GTGATTTTAA	TCGCTACCGC	TAATAATATT	GACAGGATCC	CAGCTCCTTT	AAGAGACAGA	60
ATGGAATTAA	TCAGCGTGTC	CAGCTACACG	CCTAGCGAAA	AAGAAGAGAT	CGCTAAAAAC	120
TACCTCATCC	CCCAAGAATT	AGAAAAGCAC	GCCTTAAAGC	CTAGCGAAGT	GGATATTAGC	180
CATGAATGTT	TGAAACTCAT	TATTGAAAAA	TACACCAGAG	AAGCGGGCGT	TAGGGATTAA	240
CGAAGACAGA	TCGCAACGAT	TATGCGTAAA	GCGGCTTTAA	AATACCTAGA	AGATAACCCG	300

SUBSTITUTE SHEET (RULE 26)

275

CACAAAAAAG	GGCGGACCAA	AAAAAGCGAA	GACAAAGATA	AAAAAGGCGG	AAATGAAGAA	360
AACGAAAAAA	GAGGTGAGAG	TAAAGATTTT	TGCGTCTCTA	TCACGCCTGA	TAACTTAAA	420
GAGTATTTAG	AACGCATGGT	GTTTGAAATT	GRCCCATAG	ATGAAGAAAA	TAAAATCGGT	480
ATCGTCAATG	GCTTGGCATG	GACTCCAGTG	GGCGGTGATG	TGCTTAAAT	TGAAGCGGT	540
AAGATTAGAG	GCAAGGGGGA	ATTGAAACTC	ACCGGGAGTT	TGGGCGACGT	GATGAAAGAA	600
TCCGCCATTA	TGCGCTTTTC	TGTTGTCAAA	GTCTTGTTGG	ATAACGAAAC	CTTAAAAGTG	660
CCTAAATCC	CTAGCGAGAC	CGATGCAGAG	AATWAGAAAA	AGAAAAAGT	GCTGAAAGTT	720
TWWAACGCTT	ACGATTGCA	CTTGCATGTC	CCTAAGGGGC	TACGCCTAAA	GACGGCCCGA	780
GCGCTGGGAT	CGCTATGGCG	AGCG				804

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297

ATGGGGTGTT	CGTTTATCTT	TAAAAAAGTT	AGGGTTTATT	CTAAAAATGTT	GGTTGCTTTG	60
GGGCTTTTCAA	GCGTGTGAT	CGGTTGCGCG	ATGAATCCAA	GCGCTGAGAC	AAAAAAACCA	120
AATGACGCCA	AAAACCAACA	ACCAGTTCAA	ACTCATGAAA	GAATGACAAC	AAGTTCTGAA	180
CATGTTACGC	CACTAGATTT	TAATTACCCG	GTGCATATTG	TTCAAGCCCC	ACAAAACCAT	240
CATGTTGTAG	GTATTTTAAT	GCCACGCATT	CAAGTGAGCG	ATAATCTAAA	ACCCTATATT	300
GATAAGTTTC	AAGACGCTTT	AATTAATCAA	ATCCAAACTA	TTTTTGAAAA	AAGAGGCTAT	360
CAAGTGTTGC	GTTTTCAGA	TGAAAAAGCT	TTGAATGTGC	AAGATAAGAA	AAAGATTTTT	420
TCCGTTTTGG	ATTTGAAAGG	GTGGGTAGGA	ATCTTAGAAG	ATTTGAAAAT	GAATTTAAAA	480
GATTCCCAT	GTCCCAT					498

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...432

SUBSTITUTE SHEET (RULE 26)

276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298

ATGGATAGAA AACTCTTAAG ATTATACCAG CCCTTAAACG CTTATTCTTA CAATAGCGAT	60
TCGCTTTTTT TATACGATTT TTCACGCCCT TTTATCAAAA ATAGCGGCGC GATTTTAGAC	120
ATAGGCTCAG GGTGTGGGGT TCTAGGCTTG CTCTGCGCTA GAGACAACCC GCTAGCGAGC	180
GTTTCATTTAG TGGAAAAGGA TAGCAAAATG GCGTTTTGCT CCCAAAAAAA CGCCCTTAAA	240
TTCCCTAACG CTCAAGTGTT TGAGAGCGAT TTTTAGATT TTAACCCTCC GATTTGTAT	300
GATGCGATTG TGTGCAACCC TCCTTTTAT GCTTAGGAT CTATTAAATC TCAAATTAAA	360
GGGCATGCGA GGCACCAGAG CGAATTAGAC TTCGCTTCTT TGGTGGCTAA AGTGAAAAAA	420
TGCCTGAAAC CC	432

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299

ATGTTGAGTG CGTTGGTGAT GCTGCCTTTT ATGGAGGTTT TTTATTATTT CAATTTTCCG	60
TTGTGGCTCA ATCTTTTCTT AGGGCAAACC ATTGGAGCGG TGATTTTMTT CAAGTTGGAT	120
AAGTTGATTT TTTCTAAAAA A	141

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300

ATGAATACTA TTATAAGATA TGCGAGTTTA TGGGGCTTGT GTATTACTCT AACTCTAGCG	60
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SUBSTITUTE SHEET (RULE 26)

277

CAAAACCCCT	CTAAAACCCC	TGATGAAATC	AAGCAAATCC	TTAACAATTA	TAGCCATAAG	120
AATTTAAAGC	TCATTGATYC	GCCGACAAGT	TCTTTARRAG	CGACACCGGG	TTTTTWCCC	180
TCGCCTAAAG	AAACAGCGAC	CACGATCAAT	CAAGAGATCG	CTAAATACCA	TGAAAAAAGC	240
GATAAAGCCG	CTTTGGGGCT	TTATGAATTG	CTAAAGGGGG	CTACCACCAA	TCTCAGTTTG	300
CAAGCGCAAG	AACTCAGTGT	CAAGCAAGCG	ATGGAAGAAC	CACACCATCG	CCAAAGCGAT	360
GTTTTTGCCCT	ACTTTGAACG	CGAGTTA				387

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301

ATGGTTTTGT	TTCTATCCAT	TTTTAAAAAA	AGCTTTAATG	ATTTTTTAAG	CGCTAGAATG	60
CTTTTAATCA	ATCTTGGCCC	TATCCTTTTG	AGTTTGGCGT	TTTTTGGAGC	TATCTTTTAT	120
TACAATGGCG	GGAGTATTGT	GAATTATGTC	CAAACCTTTAT	TACCGCAATC	TTTGAATGAT	180
TACGCTCATT	CTCAAGGCTT	TTTTGCCGGT	GTGTTCCGAT	GGGTTTTTAA	AGCGTTAGTG	240
TATTTTCTTA	TTTTTTGGAT	CGTAATTCTT	TTGAGTTTAG	TCATCAATAT	TTTTGCGTCT	300
ATTTTTTACA	CCCCTTTAGT	GGTCTCTTAT	TTGCACCAAA	AATATTATCC	CCATGTCGTT	360
TTAGAAGAAAT	TTGGCTCTAT	CCTTTTTTCT	ATTAAATATT	TTTTAAAATC	GCTCACTTTT	420
ATGCTTTTAT	TCTTAGCGGT	TTTAACGCCC	CTTTATTTCA	TTCCCTTTAT	AGGGGTCTTT	480
GGGGTCTTTT	TTTCTATAGT	CCCGCATTTT	CYCTTTTTC	AAAACACCAT	GAGTTTGGAT	540
ATAGCCAGCA	TGATTTTCAA	CCATCAAAGC	TATCAAAATT	TACTCAAACA	GCACCGATTG	600
AAGCATTATC	GTTTTTCGTT	TTTTTGCTAT	CTTTTTTCCT	TGATTCCTTT	TTTTAATTTT	660
TTTGCCACCT	TGTTGCAAAC	CCTAAYGCTA	ACGCACTACY	TTTTTATCTT	TAAAGAGAAA	720
GAATGC						726

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

278

(B) LOCATION 1...378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302

ATGCAATACG CTAACGCTTA TCAAGCCTAC CAGCATAACC GAGTGAGTGT GGAATCCCCG	60
GCAAAACTCA TTGAAATGCT TTATGAAGGG ATTTTAAGAT TTTCTTCGCA AGCCAAACGC	120
TGTATTGAGA ATGAAGACAT TGAAAAGAAG ATCTATTATA TTAATAGGGT TACGGATATT	180
TTACGGGAGT TGTTGAATAT TTTAGACTAT GAAAAAGGGG GGRAAGTGGC GGTGTATCTT	240
ACAGGCTTAT ACACCCATCA AATCAAAGTT TTAACGCAAG CCAATGTGGA AAATGACGCG	300
AGTAAGATTG ATTTGGTGTT GAATGTGGCT AGGGGGTTGT TAGAGGCATG GAGGGAAATC	360
CATTTCAGATG AACTCGCC	378

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303

ATGATGTTTG ATAACACGCT TATCAATTTA TTTGAGACAG CGCCTCTTTT AACYTCGCTT	60
TTAGCTGGGA TTTTAACTTT TTTAAGCCCT TCGGTGTTGC CTTTGATCCC GCGGTATATG	120
TCTTATATTT CGCAAAATTC TTTAGAGGAT ATTAAAGATG GTAAGGCTAA AAGGGTTTCG	180
GTTTTTTTAA AATCCTTGAT GTTTGTGGTG GGGTTTTTCG TCGTGTTTTT GGGCGTGGGC	240
ATGTCTATGG CCAAGCTTAT CCATAGCTTT TCGTTTTTCT GGGTGAATTA TATCGCTGGG	300
GGGATTGTGA TCCTTTTGGG TTGCAATTTT TTAGGCGTGT TTCGTTTTGC ATTTTGTAT	360
AAAACCCAAA GCGTTGTTT AGCGAGCAA TCTAACAGCA TGCAGCGCTT TACCCCTTTC	420
TTTTTGGCA	429

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

279

(B) LOCATION 1...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304

GTGCTGGTGG TGGGCAAACC CAACGAAAGC TATGCAGATA CCCACGCCCG CATTGAGCAT	60
TTTATCAAGC TTGTAGATTT TAAGGGCGAA ATCGTTTTTA TCAATGAAGA TAATTCTAGC	120
GTAGAAGCTT ATGAAAATTT AGAGCATTTG GGTAAGAAAA ATAAGCGGAT CGCTACCAAA	180
GATGGCCGGT TAGACTCTTT GAGCGCTTGT AGGATTTTAG AGCGCTATTG CCAGCAGGTT	240
TTAAAAAAGG GC	252

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305

ATGCGGATAT TAATTCTCAA AAACAAGCCA CCAACGCTAC GATCAAAGGC TTGACGCGC	60
TCTTGGGGTA TCAATTTTTC TTGAAAAAAC ACTTGGGCTT ACGCCTTTAT GGGGTTTTTT	120
GACTACGCTC ATGCCAATTC TATTAAGCTT AAAAACCCCTA ACTATAATAG CGAAGCGGCG	180
CAAGTGGCTA GTCAAATTCT TGGGAAACAA GAAATCAATC GTTTAACAAA CATTGCCGAT	240
CCCAGAACTT TTGAGCCGAA CATGCTCACT TATGGGGGGG CTATGGACGT GATGGTTAAT	300
GTCATCAATA ACGGCATCAT GAGTTTGGGG GCTTTTGGCG GGATACAATT GGCCGGCAAT	360
TCATGGCTTA TGGCGASACC GAGCTTTGAG GGCATTTTAG GGGAAACAAGC CCTTGTGAGC	420
AGAAAGCCAC TTCTTTCCAA TTTTATTCA ATGTGGGGGC TCGCM	465

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...513

SUBSTITUTE SHEET (RULE 26)

280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306

ATGAATGTCA	AAAAAAGGA	AAAGCCACAA	AGTGGAAGA	TTGATAGGGT	GGATTGTTTG	60
GAGAACTTG	GGAAAGAAA	CACTACTTTT	TTAAGCAGTA	TAGCTATGGG	GAGCATTTGGT	120
CAATTAGCGA	TCCCCATTCC	TGGAGTTGGA	GTGCTCATTG	GGGGCTTTGT	GGGTGGGGTG	180
ATGAGTAAAA	CTTTTATGA	TGTCTCGCTA	ACGATTTTCA	AAGAGGCTAA	ATTAGCGCGT	240
CAAAGGCGTA	TTGAGATTGA	AAAAGAATGC	CGTGAGAGTA	TCAGACAGTT	AGAGATGTAT	300
CAAAATCAAT	TTAATGAAGT	GTTTGAGCGG	TATTTTCATG	GGAATAAAA	ATTCTTTAAT	360
GAAAGTTTTG	ATGAGCTGGR	GAGGGCGCTT	TGTGCGGGCG	ATGCGGATTT	GGCTATAGCA	420
GTCAATAACA	AGATCCAAGA	GGGGATGGGT	CAAGAGTTGC	TGTTTGACAA	TAAGCAAGAG	480
TGCTGGGAAT	TTATCACTAG	CCGTAAAGAG	GGT			513

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307

ATGTGGCCGT	RAAAGCTTTT	TCTAAAACCC	CTAAAAGAAA	CGAGCCTTGC	CCTTGTGGGA	60
GTGGCAAAAA	ATATAAGAT	TGTTGCGCTA	AAAGCGGGCC	TAAAAGGGC	TTATTTGCCA	120
AATAGATCCT	TAATCTTTTT	CCTTATCAAG	CGTTATTTGC	GTTTTGATAA	AAGCCAGCCT	180
TTCATTAGTA	TCACTGCTTT	GTTAGCCTTT	TTTGGCGTGG	CGGTTGGCGT	GATGGTTTTA	240
ATTGTGGCTA	TGGCGATCAT	GAACGGCATG	AGTAAGGAAT	TTGAAAAAAA	GCTTTTTTGT	300
ATGAACCTAC	CCTTAACGCT	CTATACCACA	AGCCCTTATG	GGATCAGCGA	AGAAGTGGTT	360
CAAGCTTTAG	AAAAAAAGTT	CCCTAATTGT	CCTTTTTTCAG	YCCCTATTGT	CAAACCCAAA	420
GCC						423

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

281

(B) LOCATION 1...210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308

ATGGTATCGT	TGCTTGGCGC	GCTTAAACGC	ACCCCTTGCA	CTAATCGCTT	TTATCTTAAA	60
GCACTACTAT	TTGCTATATT	CTATCATGCA	GTAATAAATT	TTCTAACGCA	ATGCCCCGCC	120
CATCAAGTCC	GGGAGTTTTT	TTCATCACGA	CATGCACAGG	GATGGAAGCG	AGAAACGCTC	180
CCATGCGCCC	TTTCGTTTCA	AAACGCGCTC				210

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309

GTGCATCAIT	TGYAACGGCT	TTTAGACTCA	GGCTCTGAAA	GGTGTATAGG	CTGTGGGCTG	60
TGCGAAAAGA	TTTGCACGAG	CAACTGCATA	AGGATCATCA	CGCATAAGGG	CGAAGACAAC	120
CGCAAAAAGA	TCGATTCTTA	CACGATCAAT	TTGGGGCGTT	GCATTATTG	CGGGTTGTGT	180
GCGGAAGTTT	GCCCAGAATT	GCCGATCGTT	ATGGGGAATC	GGTTTGAAAA	CGCCAGCACC	240
CAACGCTCCC	AATACGGCTC	TAAAAGCGAG	TTTCTAACGA	GCGAACAAGA	CGCTAAAAAC	300
TGCTCGCATG	CCGAATTTTT	AGGCTTTGGT	GCGGTAAGCC	CTAATTATAA	CGAACGCATG	360
CAAGCCACCC	CTTTAGATTA	TGTCCAAGAA	CCTTCAAAAG	AAGAATCCAA	AGAAGACTTT	420
YCCACAAGCC	CAGAAAGCCA	TAAGGGAGAT	GAAAATGTT			459

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310

SUBSTITUTE SHEET (RULE 26)

282

ATGGCTATTT	GGGGGTGGTG	TTTTTTATTT	TTATCGTCCT	TGATGTGGGG	TTCAAGCATG	60
CATGAGTTGG	TTTTAAGATC	CCAAGCTTTA	GGGTTTGAAA	CGCGCTTAGT	CCAGTGCGAT	120
TTATCGTTTT	CTTATGAAAG	GTTTATTCT	AAAACCAAAC	GCTCTTTAGC	GGTGTTAGAA	180
GAATTGATT	GGTTAAATTC	TGGCTTTGAT	TTTTCACGCT	TGAACGTTGA	AAATGACACT	240
CTGGAATTAC	TCAAAGCGCT	GTATTTTAAA	TTAGAAAAAT	TAGAGAGCCT	GCTTTTAAAA	300
GAAAAATTAC	TTGAATTGGA	GCAAAAGGAT	CGCATCATCG	CTTTAGGGCA	TGGGCTAGTT	360
TGCCTAAAAA	AACAAAGCCT	GATAGCGCCT	CAAACCTACT	ATGGGCGTTG	CGTGTTAGAG	420
GGGAAATCC	TAGCCTTTTT	TGGCGTGGCA	AGGGATAAAG	ATTTTTTGA	AATCACTCGC	480
ATGCACGCCT	TAGACATTAA	GCGTTATGAT	TCCTTCATTG	TTGATAGCGA	AAGAAAAGGC	540
TTGAAATTA						549

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311

ATGCCGGA	AAATTCTAACT	ACAACCTGCT	AAGTTAGGGA	AAAATTTTGA	CCCTGTGGAT	60
CATCTAACA	GGAATTTTTT	CTTTCTCTC	ATTCTGTCTG	TATTGTTACA	CTGGTTGATT	120
TATTTTTTAT	TTGAACACAG	AGAAGATTTT	TTTCCTTCAA	AACCCAAGCT	CGTTAAATTA	180
AATCCTGAAA	ATTATTGGT	Y				201

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312

SUBSTITUTE SHEET (RULE 26)

283

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GTGTTTTTAG TTCAATCGTG GGCTTTGAGC TTGAAAATAG ACAGCCTGTT TTCTCTTTTT 60
AGCGTGGGTA AAATCCCTAG CGGATCTAAA GATCCCTTTG CGTTAAGGCG TTGAGTTTT 120
GGGCTATTGA AAATCATCGC GCATTACGGG TTAGAATTTG ATTTGAAAGC GGATTTAAAA 180
AACCTCTTTG AAAAAGTGGG CGTTTATCAA AGCTTTGATT TAGAGTTTTT AGAAAAGTTT 240
TTACTGGAGC GCTTTCATAA TTTAATAGAT TGTAACTCT CTATTATAAG AAGTGTGTTA 300
AACACCAACG AGCGAGACAT TGTAAAAATC ATTCAAAAAG TCAAAGCCTT AAAACGCTTT 360
TTAGACAATC CTAAGAACGC TCAAAAAAAA GAGTTGCTTT TTAGCGCTTT CAAACGATTA 420
GCTAATATCA ATAAAGACAG AAACCCTAAC GAATCAAGCG GGTTTTCTAC GAGTCTTTTC 480
AAAGAATTAC AAGAGCATGC CCTTTTGGAA GCGTTCAAC 519

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(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313

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ATGAGTCTTG CTCCAAGCGT TATGGCGGGC TTCTTGTTTT GTGCCGGCTC TTGCTCGCTT 60
CGCTTCCCTA ATTATTCTAA AATCATTTCC ATAGATGTGG ATACGGTGTT TTAGGCGGAT 120
GTTGCAAGCG CTTATTTTGC GCTGGATAAT GAACCCACTA AATTGCTTGG CATGGTGAGA 180
GACACTTTTT CCCACCTTCC TTTTGAAGCC TTTTGTGATT TTTGCGAACG CACATGCAAG 240
AATTTTAAAA TTGATCTTTT GCGCTTTAGC CAAAACGAAT TAAAACGCAT CCATCAGGGC 300
TTTAACATGG GCTTTTTTGGT GGCGAATTTA GATTATATGGC GCGAAAATGG GTTTGAAAAA 360
ATCGCTTTAG AGTTTTTGAA AACTAGGGGA AAGGATCTTT TCTACCCTGA GCAGTGTTTA 420
ATCAATATGG TGTTTTTAGA GCGTATTTTA GAATGCGCTA TTCATTATAA TGCTATTCT 480
GATTTTTTCA AAGAGCACTA CCCTAAAAGT ATCATCATGC TCCATTTCAT CAAATACAAG 540
CCGTGGCGTT CTGTCACTTC TTTGAACGGG CGTTTGATTT GCTATGAAGC TGAAGCGAGT 600
TTTTGGCTCG CCAACCTTTT TTGCACCCCT TTTAAAAACG ATTTTTTTAA AGAACGCCTT 660
GAAATGGCTA AAGACCAACA AATGCAATCT TTTAAAACCC ACATCCGATC AAAAACGATT 720
AGGGATTATT TTTATTTTAG GATAAAAAAT ATTTTGAAAA AAGTTTTCGA ACTCTCT 777

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(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

284

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314

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GTGATGTGTT GCAGCGCGGC GGGGTTGAGC CATTTTTTTG GGTGTTCTAT GTCTTTGGGG      60
GCGTTCATTG TGGGCATGGC GATTTCTAAA TCGCGCTATA AAATCAATGT CCAAGAAGAA      120
TTCGCGCAAT TAAAAAACCT CTTTTTGGCC CTTTTTTTCA TTACGATAGG GATGCAGATT      180
AATGTGAGTT TCTTCATGGA GAAATTCCTT GTCGTCATCT TTTTACTCAT TTTAGTGATG      240
AGTTTTAAGA CTTTTATCAT TTATGCGCTA TTGCGTTTTT TTAGAGACGC TAAAACCGCC      300
ATCAAAACCG CTCTTCTTTT GGCGCAAATT GGGGAGTTTT CTTTCGTGAT CTTTTTAAAT      360
TCAGGCTCGC ACCAGCTCTT TAATTTGCAA GAAAAAAAAG GGATTCCTTG TTTTTTACAC      420
CAAAAAATA TCTTAAATAT TGCTCAAAAT GACATCCACC AGCTCCTTAT TCTCATGGTG      480
GTCTTTTCTA TGTTAGCAAC CCCTTTTATT TTAAATACC TAGAATCTAT CGCTCAATTT      540
ATTTTGCACC AAAAGAGCCA AGAAAACGAG CCGCTAAAA AA                               582

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(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315

```

ATGTTCTATC TTATCAATAC AGGAGTGCCT CATTTAGTGG GATTGTGAA AAATAAAGGG      60
TTATTAAATT CTCTTAACAC ACTGGAATTA AGGGCTTTAA GGCATGAATT TAACGCTAAT      120
ATTAACATCG CTTTTATAGA AAATAAAGAG ACGATTTTTT TACAACTTA TGAGAGAGGG      180
GTTGAAGATT TCACGCTAGC TTGCGGGACA GGCATGGCAG CGGTTTTTAT CGCCGCGCGC      240
CTTTTTCATA ACACCCCTAA AAAAGCCACT CTCATCCCTA AAAGCAACGA ATTTTATAGAG      300
CTTCTTTTAA AAAATGATGG AATTTTTTAT AAAGGAGTCG CGGTTATAT CGGCATGAGC      360
GTTTTAGGCA TGGGTGTTTT TAAAAATGGG TGTTTT                               396

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(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

285

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316

ATGATTAAAG CGATTGATAT TTCTCATGST TTTGAAAARC CTCTTTRTRA TGGCGTGAAT	60
TTGCGCATTA AACCCAAAGA AAGCYTGGYG ATTTTAGGCG TGAGCGGGAG CGGTAAAGC	120
ACGCTTYTAA GCCATTGGC CACCATGCTA AAACCGGATA GCGGAACAGT CAGTTTGTTA	180
GAACACCAAG ATATTATGC CCTAAATCC AAAAAGCTTT TGGAAATGCG GCGCTTAAAA	240
GTGGGCATCG TTTTCAATC GCATTACCTT TTTAAGGGTT TTAGCGCTTT AGAAACTTG	300
CAAGTCGCTT CAATCCTAGC CAAGCAAGAA ATAAATCATT CCCTTTTAGA ACAATTAGGC	360
ATAGCCCACA CCCTAAAACA AGGCGTGGGC GAATTGAGCG GCGGCCAGCA ACAACGCTTA	420
AGCATCGCCA GAGTGCTTTC TAAAAAACCC CAAATCATT TCGCTGATGA ACCCACC GG	480
AATTTAGACA CCACTAGCGC TAATCAAGTC ATCAGCATGC TGCAAAATTA CATTACAGAA	540
AACGAAGGGG CGTTAGTCTT AGCCACGCAT GATGAGCATT TAGCCTTCAC TTGCTCTCAA	600
GTCTATCGCC TAGAAAAAGA ATCTTTGATT AAGGAAAAA	639

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317

ATGCTTGATA AACGCATTAA AACGCTTTTA CTTTTTTTGT GTCTTAATAT GGTGTGTTT	60
AGCGTGAGTT TTACCAATAA GCCTCATTG TGTTTTTGGT TTTAGTGTT AGGTTGTTAT	120
TTAGTTTATG AGTGGCAAAA GAAACAAAAA AAAGATTTTC AAAGCGCTAA AAGTTTGAAA	180
TTTGACAGCG TTAGCGAATT AGAAAAGGAT TTTGAACATG GAAGTAAC	228

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 207 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

286

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318

ATGAAAACAA TTAAAAATGG TATTATGATC GGCACACTCG GTGCGTTGTT ATTGAGCGGT	60
TGTTCTAGCT TTGATGCTCA GCGTTTCGCT TGTCTCCCTA AAGACCATTG TTCAAAAGAC	120
GCTTCTACCA AAAAAGAAGC GCAATACATT CCTAAGGGCT TTTTGACCC TTATTCTTCT	180
AACTTAAACC ATTGGGATTG TACATTG	207

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 570 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319

ATGGAGCTTA TTTTAGGCTC TCAATCCAGC GCTAGGGCGA ATCTTTTAAA AGAGCATGGG	60
ATTAAGTTTG AACAAAAAGC GCTCTATTTT GATGAAGAAA GCCTAAAAAC CACAGACCCT	120
AGGGAGTTTG TCTATTGGC GTGCAAGGGG AAATTAGAAA AAGCTAAAGA GTTACTTGCG	180
AATAATTGCG CTATCGTGGT GGCTGATAGC GTGGTGAGCG TGGGTAATCG CATGCAACGA	240
AAAGCTAAAA ACAAGCGAGA AGCCCTTGAA TTTTAAAAAC GCCAAAATGG CAATGAAATA	300
GAGGTTTTAA CTGCTCTGCG ATTGATTTCT CCTGTGTTGG AATGGCTGGA TCTATCGGTT	360
TTTAGAGCGC GTTTAAAGGC GTTTGATTGC AGCGAAATAG AAAAATATTT AGAGAGCGGT	420
TTATGGCAAG GAAGTGCGGG CTGTGTGCGT TTAGAGGACT TTCATAAGCC TTATATTAAA	480
AGCTCAAGCA AGAATTTAAG CGTGGGGTTG GGGCTGAATG TGGAAAGGCTT GTTAGGGGCA	540
CTAAAATTAG GGGTTAACT TTCATTATTA	570

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 405 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

SUBSTITUTE SHEET (RULE 26)

287

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320

ATGCTTATTT TAGGACACCC TTAAATCCCT AGCGCTCGTT TTGTTTTTCAT TAAAAACACC	60
GATGCTATTTC ATTCCAGCGC CAATAACGAT ATAGTGTGTT TTGAAGCAAA CCCAAAAAAT	120
TTGGAATTAG CCCAATATTG CTGTGAAAAAT GCGCTCCATT TTAGCGTGAT CTTTTTATCG	180
CACAAGATAG AGACGGACAC CTTTTTTTTT TCAACGCTT TCAAACCGCT CTATTGTATT	240
TTTAAGGATA TTAAGCAAGC CATACTCGCC CAACAACACG CCACTAATTA CTGTGTAGAT	300
AGCAAAATCT TGTCTTCTAT GGATTTTAAAC GATACAGAGT CATGGGAGAT TTGCGCTAAA	360
AATCAAAATAG ATGGTGTCTAT TTCTAAAGAT TCACTCCTTT TGAAA	405

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321

ATGAAAAAAA GATTGAATAT AGGGCTTGTTG GGTTTAGGGT GCGTGGGGAG CACGTCGCT	60
AAAATCTTAC AAGAAAATCA AGAAATCATT AAAGACAGAG CCGGCGTGGA AATTAAAATT	120
AAAAAAGCGG TGGTGCGAGA CGTGAAAAAA CACAAGGGCT ATGCTTTTGA AATCAGTGAT	180
GATTTAGAAA GCGTGATAGA AGATAAAGGG ATTGATATTG TCGTGAGGCT TATGGGTGGG	240
GTGGAAGCGC CTTATCTTTT AGCTAAAAAA ACTTTAGCCA AACAAAARGC CTTGCTTACA	300
GCCATAAAG CCATGTTAGC GTACCACCGC TATGAATTAG AACAAATCGC TAAAAACACC	360
CCCATAGGCT TTGAAGCGAG CGTGTGTGGG GGTATCCCA TTATCAAGGC TTTAAAAGAC	420
GGCTTGAGCG CTAATCACAT CCTTTCTTTT AAAGGGATTT TAAACGGCAC GAGCAATTAC	480
ATTTTAAGCC AGATGTTTAA AAATCAAGCG AGCTTTAAGG ACGCTTTGAA AGACGCGCAG	540
CATTTAGGCT ATGCGGAATT GAACCCTGAA TTTGACATTA AGGGCATTGA TCGGCGGCAC	600
AAATTATGA TTTAGCGTC TTTAGCGTAT GGCATTGATG CGAAATTAGA AGAAATCTTG	660
ATTGAAGGCA TTGAAAAGAT AGAGCCAGAT GACATGGAAT TTGCAAAAGA GTTTGGTTAT	720
AGCATCAAAC TTTTAGGCAT CGCTAAAAAA CACCAGGGAT TGCAT	765

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

288

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322

ATGCAAGAAA	AACGACTTAA	AGCCATTCAA	AACAAAATCG	CTTCTTGGAT	CAAGGAAATT	60
GAAAGCGGCT	TTATAGATGC	ATTGTTTTCT	AAGATTGGCC	CTTCAAAGAT	GCTGCGCTCC	120
AAACTCATGC	TCGCTTTGTT	AGACGAAAAA	ACAGACGCTA	TTTTATTAGA	TAAAGCGCTC	180
AATTTGTGTG	CGATTGTGGA	AATGATACAG	ACCGCTTCTT	TATTGCATGA	TGATGTGATT	240
GACAAGGCGA	CCATGCGCCG	AAAGCTCCCT	AGCATTAAACG	CTCTTTTGGG	GAATTTTAAC	300
GCCGTGATGC	TTGGGGATGT	GTTTTATTCT	AAAGCCTTTT	TTGAGTTGTC	TAAATGGGCG	360
GAATCCATCG	CTCAAGCCCT	CTCTAATGCG	GTTTTAAGGC	TCTCTAGGGG	CGAGATTGAA	420
GACGTGTTTG	TGGGGGAATG	TTTTAATAGC	GACAAACAAA	AATACTGGCG	TATTTTAGAA	480
GACAAGACCG	CCCATTTCAT	AGAAGCGAGC	TTAAAAAGCA	TGGCGATTCT	TTTAAATAAA	540
GACGCCAAAA	TGTATGCGGA	TTTTGGGTTG	CATTTTGGCA	TGGCGTTTCA	AATCATTGAT	600
GATTTGTTAG	ACATCACTCA	AGACGCCAAC	ACTCTAGGTA	AGCCCAATTT	TAGCGATTTT	660
AAAGAGGGCA	AGACCACTCT	ACCCTACTTG	CTTTTATATG	AAAAATTGAA	TCAGCATGAA	720
CAGGGCTTT						729

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 756 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323

ATGTTAGGGA	AAAAAACGGA	AGAACTCTTG	ATTGATGAAA	ATTTGGTTGG	GGGTGTGATA	60
GCCCTTGATA	GATTGGCAAA	ACTCAATAAG	GCCAATAGGA	CTTTCAAAAG	GGCTTTTTAT	120
CTCTCTATGG	TGCTCAATGT	CGCCGCTGTA	ACGAGTATTG	TGATGATGAT	GCCTTTGAAG	180
AAAACAGATA	TATTTGTTTA	TGGCATTGAT	CGATACACAG	GAGAATTTAA	AATCGTCAAA	240
CGCTCCGATG	CTAGGCAAAT	CGTCAATTCT	GAAGCCGTTG	TGGATAGTGC	AACTTCAAAA	300
TTTGCTCAT	TGCTGTTTGG	TTATAGCAAA	AATTCTTTGA	GGGATCGCAA	GGATCAACTA	360
ATGCAGTATT	GCGATGTGAG	TTTCCAAACC	CAAGCAATGA	GAATGTTCAA	TGAAAATATC	420
AGACAATTCC	TAGATAAAGT	CCGAGCAGAA	GCTATCATT	GCTCCAACAT	ACAAAGAGAA	480
AAAGTCAAAA	ATAGTCCCTT	AACGAGATTA	ACATTTTTC	TTACCATCAA	AATCAGCCT	540
GATACAATGG	AAAATTATGA	ATATATCACT	AAAAACAAG	TAATATTTTA	TTATGATTTT	600
GCTAGAGGTA	ACTCTTCTCA	AGAAAATCTT	ATCATCAACC	CTTTTGGCTT	CAAAGTGT	660
GACATTCAAA	TCACGGATTT	ACAAAACGAA	CAGACAGTAA	GCGAAATTTT	GAGAAAGATT	720
AAAGAAGTGG	AATCAAAAAA	TAAGGCATTA	AATAAA			756

SUBSTITUTE SHEET (RULE 26)

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324

ATGAGAGCGA	TCGCTATTGT	TTTAGCCAGA	AGTTCCAGTA	AAAGGATTAA	GAATAAAAAAT	60
ATGATTGATT	TTTCAATAA	ACCCATGCTC	GCTTACCCTA	TTGAAACAGC	ACTAAATTCC	120
AAGCTCTTTG	AAAAAGTGT	TATCTCTAGC	GATAGCATGG	AGTATGTCAA	TTTAGCCAAA	180
AATTATGGGG	CGAGTTTTTT	GAATTTACGC	CCTAAAAATT	TAGCAGACGA	CAGGGCCACG	240
ACTTTAGAAG	TGATGGCCTA	TCACATGAAA	GAATTAGAAT	TAAAAGATGA	AGACATTGCG	300
TGTTGTTTGT	ATGGCGTTTC	AGTATTTTTA	CAAGAAAAGC	ATTTACAAAA	CGCTTTTGAA	360
ACTTTAAAC	AAAATCAAAA	TACGGATTAT	GTTTTACAT	GCTCTCCCTT	TAGCGCTTCG	420
CCTATCGTTC	TTTAGCCTT	GAAAACGGCG	TTCAAATGGC	TTTTAAAGAG	CATTCAAACA	480
CGCGCACGCA	AGATC					495

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325

ATGAGTAATC	AAGCGAGCCA	TTTGATAAT	TTTATGAACG	CTAAAAATCC	CAAAAGTTTT	60
TTTGATAATA	AGGGGAATAC	CAAATTCATC	GCTATCACAA	GCGGTAAGGG	GGGCGTGGGG	120
AAATCCAACA	TTAGCGCTAA	TTTAGCTTAC	TCTTTATACA	AGAAAGGTTA	TAAGGTAGGG	180
GTATTGATG	CGRATATTGG	TTTAGCGAAT	TTAGATGTCA	TTTTTGGGGT	GA AAACCCAY	240
AAAAATATCT	TGCATGYCTT	AAAAGGCGAA	GYCAAATTGY	AAGAAATCAT	TGCGAGATT	300
GAACCCGGGC	TTTGCTTAAT	CCCTGGGGAT	AGCGGCGAAG	AAATTTTAAA	ATACATCAGC	360
GSSGCGGAAG	YTTTCGATT	ATTCTTAGAT	GAAGAGGGGG	TTCTAAGCGC	TTTAATTTAT	420

290

ATTTTAATTA ATACATTTTC TAAAAATTG GGTCCACTAT CTCAACTTT TCTTAATTTT 480
CAGTCATTTT TTTTATTTT TATCAATCT CCC 513

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326

ATGCAGCATT TAGTCTTAAT CGGTTTATG GGGAGCGGTA AAAGCTCTCT AGCACAAGAA 60
TTGGGGCTGG CTTTGAAATT AGAAGTGCTG GATACGGATA TGATCATTAG CGAGAGGGTG 120
GGCTTGAGCG TGAGAGGGAT TTTTGAAGAG CTTGGCGAAG ACAATTCAG GATGTTTGAA 180
AAAATT 186

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327

ATGAGCATT AAGAAAATTT AGAGCAAGTT AGAAACGAAT TTAAGCGGA TGAAAAGCTT 60
TTAGAAGGAG CGTTTAGATT AGAAAAGTTT TTCAAACGCT ACAAGTGGGT GTTGTGTTT 120
ATCGTGGTGG CTTTATCGC TTATTAGGG GATACAAAAT TACAAGATTA TAAGCATGAG 180
CAAAACGAG AGCGGATCAC TCAAATTTAT AATGAAGTGC TAGAGAGTCC TAATAATATA 240
GCCTTGCAAA AAAGATTGAA AGAAGTCGCC CCAGAGTTGT ATGACTTGTA TCAGTTCGCC 300
AGAGCGAGTG AGAGGAACGA TGCAAACGAG TTTAAAGGC TTTCGCAATC TTCTAATGAA 360
ATCGTTAAAG CGTTCGCCAA ATATTCTTAC GCATCGCTCT CTAGAGATAA AAACCTGCTT 420
GAAAAAAGCC CCATTCTTAA AGAAATGAGC GCTTTACAAG AAGTGAACCT GTTGATGAA 480
GAAAATTCTA AAGACGCAAT CAAAAAGCG CATCAAAGTT TATCAACTAT CCCTCTAAGT 540

SUBSTITUTE SHEET (RULE 26)

291

TCTTCACTCT ATGCTATAAT CTCTGTTTAA AACATTATG GAATGTTAGA AGATATTCAG 600
 CAAAACCTT CCAAACCAAC CAATCTAAAG AAAGAAACCA TTCAAGGAAC GCAT 654

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328

GTGCATTTC AATCAGGTTGT TCTCCCAAAA GGCCTGGGCG CGATTTTAGT CGCACCAAAA 60
 GGGCCCGGGA GCGCTTTAAG AGAAGAATAC CTTAAAAATA GGGGTTTATA CCATCTAATC 120
 GCCATAGAGC AAGAAAGCTC AATTCATAAC GCTAAAGCGG TGGCTTTAAG CTATGCTAAA 180
 GCGATGGGTG GGGGAGAAAT GGGGTTTATA GAAACGAGTT TTAAAGAAGA ATGCGAGAGC 240
 GATTTATTCG GCGAGCAAGC GGTCTTGTGC GGGGGGTTAG AAGTCGATCG TAAGAATGGG 300
 GTT 303

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329

ATGAAAAAT TTTTCTCTCA ATCTTTGTTA GCTCTTATTA TCTCTATGAA TGCGGTATCT 60
 GGCATGGATG GTAATGGCGT TTTTCTAGGG GCGGGTTATT TGCAAGGACA GCGCAAATG 120
 CATGCGGATA TTAATCTCTA AAAACAAGCC ACCAACGCTA CGATCAAAGG CTTTGACGCG 180
 CTCTTGGGGT ATCAATTTTT CTTTGAAAAA CACTTTGGCT TACGCCTTAA TGGGGTTTTT 240

(2) INFORMATION FOR SEQ ID NO:330:

SUBSTITUTE SHEET (RULE 26)

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330

ATGCTAAAAA	AGATTTTTTA	TGGTTTTATC	GTGTTATTTT	TGATTATCGT	AGGGTTGTTG	60
GCCGTTCTTG	TCGCTCAAGT	TTGGGTAACT	ACGGATAAGG	ATATTGCTAA	AATTAAAGAT	120
TATCGCCCCA	GTGTCGCTTC	ACAGATTTTA	GACAGAAAAG	GGCGTTTGAT	CGCTAATATT	180
TATGATAAGG	AATTTGTTTT	TTATGCGCGT	TTTGAAGAAA	TCCCCCACG	ATTGTTGAA	240
AGCCTTCTAG	CGGTAGAAGA	CACCCTCTTT	TTTGAGCATG	GGGGGATCAA	TTTAGACGCT	300
GTCATGCGCG	CTATGATTAA	AAACGCTAAA	AGTGGTCGTT	ACACTGAAGG	GGGTAGCACT	360
CTAACCCAAAC	AACCTCGTTAA	AAACATGGTG	CTCACACGGG	AAAAAACCCCT	AACCAGAAAA	420
CTCAAAGAAG	CTATCATCTC	CATACGCATT	GAAAAAGTCT	TAAGCAAAGA	AGAAATTTTA	480
GAGCGTTATT	TGAACCAAAC	TTTTTTTGGG	CATGGGTATT	ATGGCGTGAA	AACCGCAAGT	540
TTAGGGTATT	TTAAAAAACC	CCTTGACAAA	CTCACGCTTA	AAGAAATCAC	CATGTTAGTC	600
GCCTTACCTA	GGGCTCCAAG	TTTTTATGAC	CCTACCAAAA	ATTTAGAATT	TTCACCTCTT	660
AGGGCTAATG	ATATTTTAAG	GCGGTGTAT	TCTTTAGGCY	GGATTTCTTC	TAACGAGCTC	720
AAATCCGCTC	TCAATGAAGT	GCCAATCGTC	TATAACCAAA	CTTCCACGCA	AAATATCGCT	780
CCCTATGTCG	TGGATGAAGT	GTTGAAGCAA	TTGGATCAAT	TAGACGGGTT	AAAAACTCAA	840
GGCTATACCA	TAAAACTCAC	GATAGATTTG	GATTACCAAC	GCTTAGCGTT	GGAGTCTTTG	900
CGTTTTGGGC	ATCAAAAAAT	CCTAGAAAAA	ATCGCTAAAG	AGAAGCCAAA	AACTAACGCT	960
TCTAATGATA	AAGATGAAGA	CAACTTAAAC	GCCAGCATGA	TAGTTACAGA	AACGAGCACC	1020
GGTAAGATT	TAGCCTTAGT	GGGGGGGATT	GATTATAAAA	AAAGCGCTTT	CAATCGCGCC	1080
ACGCAAGCCA	AACGGCAGTT	TGGGAGCGCR	ATCAAGCCTT	TTGTGTATCA	AATCGCTTTT	1140
GATAATGGCT	ATTCCACCAC	TTCCAAAATC	CCTGATACCG	CGCGAAATTT	TGAAAATGGC	1200
AATTATAGTA	AAAACAGCGT	GCAAACACCAC	GCATGGCACC	CTAGCAATTA	TRCTCGCAAA	1260
TTTTTAGGGC	TTGTAACCTT	GCAAGAAGCC	TTGAGCCATT	CGTTAAATCT	GGCTACGATT	1320
AATTTAGCGA	TCGCTTGGCT	A				1341

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

293

(A) NAME/KEY: misc_feature
(B) LOCATION 1...654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331

ATGAACGATA	CAACAGAGCA	CCATGGATCC	AATCCGCTAA	ACGCCCCACC	ACCTAGCAAC	60
TCACAGAGCA	ACGATCTCTT	AAATTTGCTA	GACTCGTTAT	ATCCTAAAGG	GAGTTTAGGG	120
GAACAAAGAT	TTCACGAAGC	TTTAAAGAAT	CAAGAAGAGT	TGAAAAATAT	CCTAATAGAA	180
ATAGAAAAGC	TACCGCAAGA	AAAAAGGTAT	GAACCTCTGA	TGCAGATAGG	ACAAGCCAAA	240
CAGAGAATAA	TGGAAGCATA	CGCTCATTCA	TTCTTAGGAT	ATATAGGGGG	ACTAGAGCAT	300
CTGTTAGGAT	TGTGTATGGG	TGGGATATTT	GTTTGTGTTG	CAATCTATTT	TGTATTTTAA	360
AGAACTAGCA	AAAACACAGA	GCTAGTGGAA	AGTCTAAAAA	CAAAATTAAA	ACTTCAGTAT	420
TTTTACTATG	CCTTTGGTGT	GGGTGCGGTT	TTGTTTTTTG	GATTAGAAAC	AATTAGATCG	480
ATTTATGAAC	TATATATCTT	AGGAATTGGT	AGCACTAACG	ACAAGGTGCT	CTTTGTTTTG	540
AAAAACATTT	GCTTCATAGG	TATGGGCTAT	TTGATTATAA	AAGTTATTAA	AGTTATTGGT	600
ATAAAAAATT	TTATCAATGG	TCTTTTCGCT	TCAAAGAAAC	AAGCGCGTGC	AGAA	654

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332

ATGATGGATA	AGGTGGGTTT	TAAATCTCAA	GGCATCTTTG	TGATGGACGC	TAGCAAGAGG	60
GATGGGCGTT	TGAACGCGTA	TTTTGGAGGC	TTGGGTAAAA	ACAAGCGGGT	GGTGTGTTT	120
GACACTTTGA	TCTCTAAAGT	TGGGACAGAA	SGGCTTTTAG	CCATTTTAGG	GCATGAGTTA	180
GGGCATTTTA	AAAATAAGGA	TTGTGTGAAA	AATTAGGGA	TTATGGGAGG	CTTGCTCGCT	240
CTTGTTTTTG	CTTTGATCGC	TCATTTGCCG	CCGTTGGTTT	TTGAAGGCTT	TAATGTCCTC	300
CAAACGCCAG	CGAGTTTGAT	CACGATTCTA	CTCTTGTTTT	TGCCGGTGTT	TTCCCTTTTAC	360
GCCATGCCTT	TGATTGGGTT	TTTTAGCCGC	AAGAACGAAT	ACAATGCGGA	CAAGTTTGGG	420
GCGAGTTTAA	GCTCTAAAGA	GACTTTAGCC	AAAGCGTTAG	TGTCCATTGT	GAATGAAAT	480
AAAGCGTTCC	CCTATTCGCA	CCCTTTTAT	GTTTTCTTGC	ATTTACGCA	CCCGCCGCTA	540
TTAGAACGCC	TAAAGCTTT	GGATTATGAA	ATTGAA			576

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 603 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

SUBSTITUTE SHEET (RULE 26)

294

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333

ATGAATATTT	ATCAAAAAA	CTTGCAAGCT	CTTTTCAAAA	AAGACCTCT	TTTGTTCGCA	60
AAGCTCAAAG	CCATTAAAGA	AAACAAAAA	TACGAAGTG	TTTTAGGGAA	TGATAGCGCG	120
AATTTCAACC	TCTTAGATAA	AGAAACAAAC	ACGCCCTTAT	TTGAAAAAAG	CCCGCTAGAT	180
TCAAGCTTAG	AGCTATATAA	AAATAGCGAA	ATTCACATGC	TCTATCCTTA	TTTGTATTAT	240
TTTGGCTTGG	GTAATGGGGT	GTTTTATCGC	TTGCTTTTAG	GCAATGAAAA	TTTAAAACGC	300
TTGGTGGTCA	TTGAGCCTGA	AATAGAGGTG	ATTTTCATTG	TGCTGAATCT	TTTGGATTTT	360
TCCACTGAGA	TTTTAGAAAA	TCGTTTGATT	TTATTGCATG	CAAGTTTTTG	CAATTACAAC	420
ATGATTGCTT	CATTATTTGA	TATGGATAAA	AAGTCTCGTT	TATACGCAAG	AATGTATGAT	480
TTAAACTTTT	TTAACGCTTA	TTATGAACGA	TACTCTCATC	AAATGATAGA	AATCAACCAG	540
CATTTACGCG	GCGCTTTAGA	GCATGGCGCT	ATTAGCGTAG	GCAATGACGC	TAAAGCGCAC	600
TCA						603

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 390 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334

ATGAAAAAGA	TTATTCTTGC	ATGCCTTGTG	GCTTTTGTGG	GTGCCAATTT	AAGCGCAGAG	60
CCTAAGTGGT	ATAGCAAGGC	CTATAACAAA	ACAAACGCCC	AAAAAGGCTA	TCTTTATGGG	120
AGTGGTTTCA	CCACTTCTAA	AGAGGCTTCT	AAACAAAAAG	CGTTAGCGGA	TTTAGTGGCG	180
TCTATTAGCG	TGGTGGTCAA	TTACAAAATC	CACATTCAAA	AAAGTCGTGT	GGATAATAAG	240
TTAAAATCCA	GCGATTACAA	AACGATCAAC	TTAAAAACCG	ATGACTTGGA	ATTGAATAAT	300
GTAGAAATTG	TCAATCAAGA	AGCGCAAAAA	GGGATCTACT	ACACCAGAGT	GAGGAATCAA	360
TCAAAACTTG	TTTTTGCAGG	GTTTAAGGGA				390

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 432 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

295

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...432
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:335

```

ATGAAATCC AAACAATTTT AACACTTGTC CTTACAATAA TAATGGTAAT ACAAAAAATG      60
ATTGTTGGCA AAATTTTCACC CCACAAAACC GCAGAAGAAT TCACYAATT AATGTTGAAC      120
ATGATCGCTG TTTTAGACTC CCAATCTTGG GCGGATGCGA TCTTAAACGC TCCTTTTGAG      180
TTCACTAACA GCCCAACAGA TTGCGATAAT GATCCTTCAA AATGCGTAAA TCCTGGGACA      240
AACGGGCTTG TCAATTCTAA AGTCGATCAA AAATATGTGT TAAACAAACA AGACATTGTC      300
AATAAATTTA AAAACAAAGC RGATCTTGAT GTAATTGTTT TAAAGGATTC AGGGGTTGTA      360
GGGTTTGSCA ATGGATATGG CAATGATGGT GAATATGGCA CATTAGGGGT AGWAGCCTAT      420
GCTTTAGGAT CC                                     432

```

(2) INFORMATION FOR SEQ ID NO:336:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 927 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...927
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:336

```

GTGGTAATAA GGTTAGTCCT AAACATGCTA ACATGTCAAA TTAGCTATAT AAGGATAAGT      60
TATCTTGCTC CTGTTAGCGA TTTTGTGATT TGCAAGGAAA GATTTATGGA TGAAATTAAA      120
ACGCTGTTAG TGGATTTTTT CCCGCAGGCA AAGCATTTTG GGATAATCTT AATCAAGGCT      180
ATTGTTGTCT TTTGTATAGG TTTTATTTT TCGTTTTTCT TACGGAACAA AACCATGAAA      240
CTCTTATCCA AAAAGGATGA GATTTTGCGC AATTTTGTCG CGCAGGTTAC TTTTATCTTA      300
ATCCTTATCA TTA CTACAAT CATCGCGCTC AGCACGCTAG GCGTCCAAAC CACCTCTATT      360
ATCACTGTTT TAGGAACGGT GGGGATTGCG GTGCGGTTGG CTTTAAAAGA TTATCTTTCA      420
AGCATTGCTG GAGGGATAAT CCTTATTATT TTACACCTTT TCAAAAAAGG AGACATCATT      480
GAAATCTCTG GCCTAGAGGG CAAAGTAGAA GCGCTTAATT TTTTAAATAC TTCTTTACGC      540
TTGCATGACG GCGGCTTGCC GGTTTTGCCT AATAGAAGTG TCGCTAATTC TAATATTATC      600
AATAGCAATA AACTGCGGTG TCGGCGCATT GAATGGGTCT GTGGGGTAGG GTATGGGAGC      660
GATATTGAAC TGGTGCAATA GACTATAAAA GATGTTATTG ACGGGATGGA AAAAATTGAT      720
AAAAACATGC CCACCTTCAT TGGAAACACG GATTTTGAC AAAGTTCGCT GAACTTCACC      780
ATTAGGGTTT GGGCAAAGAT TGAAGACGGG ATCTTTAATG TGAGGAGCGA ACTCATTGAA      840
CGCATCAAAA ACGCCTTGGA CGCTAATCGT ATTGAAATCC CTTTCAACAA GCTAGATATT      900
TCTATCAACA AACAGACTC TTCTAAG                                     927

```

SUBSTITUTE SHEET (RULE 26)

296

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337

```

ATGAAAACT TTTCCCCACT CTATTGTCTT AAAARGCTCA AAAAACGCCA TTTAATCGCT      60
CTGAGTCTGC CCTTGCTTTC TTATGCGAAT GGCTTTAAAA TCCAAGAGCA AAGCTTGAAT      120
GGCACGGCTT TAGGCTCGGC GTATGTCGCT GGGGCTAGGG GTGCTGACGC TTCTTTTAC      180
AACCCGGCTA ACATGGGCTT TACTAACGAT TGGGGCGAAA ACAGAAGCGA ATTTGAAATG      240
ACCACCACCG TGATCAATAT CCCGACCTTT AGCTTTAAAG TCCCTACGAC CAATCAAGRC      300
TTATATTTCG TAACAAGTTT AGAAATTGAT AAAAGCCAAC AAAATATTTT AGGCATCATC      360
AACACTATAG GGTTAGGCAA TATCCTTAAA GCGCTTGGCA ATACGGCCGC TACCAATGGC      420
TTATCACAAG CTATCAATCG TGTTCAGGG CTTATGAACT TAACCAATCA AAAAGTCGTA      480
ACCCTCGCTT C                                     491

```

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338

```

ATGTGTTTAG CGATCCCCTC TAAAGTCATA GCCATTAACG ATAATGTGGC ACTCTTAGAG      60
ACTTTGGGCG TTCAAAGAGA AGCGAGCTTG GATTTAATGG GCGAGTCCGT TAAAGTGGGC      120
GATTATGTGC TACTACACAT CGGCTATGTG ATGAGTAAAG AT                                     162

```

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

297

- (A) LENGTH: 606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339

```

ATGAAATATT TATGGCTTTT TTAAATATAC GCTATAGGGC TTTTTCGAAC AGATAAAACG      60
CTAGATATTA TTAAACCAT TCAAAACTT CCTAAGATTG AAGTGCCTA CTCCATAGAT      120
AACGATGCCA ATTACGCTTT AAAATTGCAT GAAGTCTTAG CGAACGATTT AAAGACTAGC      180
CAGCATTTTG ATGTTTCTCA AAACAAAGAG CAAGGTGCTA TCAATTACGC AGAACTCAAG      240
GATAAAAAAG TCCATCTTGT AGCGCTTGTT AGCGTGCGCG TAGAAAACGG CAATAAAATT      300
TCACGATTAA AACTTTATGA TGTGGATACA GGAACGCTCA AAAAGACTTT TGAATACCCC      360
ATGTGAAGTT TAGATCTATA CCCTTTTGCA GCGCACAACA TGGCCATTGT GGTGAATGAT      420
TATTTAAAG CCCCTTCTAT CGCTTGGATG AAGCGCCTGA TTGTTTTTTC TAAATACATT      480
GGACCAGGAA TCACAAACAT CGCACTAGCG AATTATACGA TGCCTTATCA AAAAGAAATC      540
ATCAAAAAACA ACCGACTCAA TATTTTCCCC AAATGGGCGA ACGCTGAGCA AACGGAGTTT      600
TATTAC

```

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340

```

GTGGTGAGCG GGGTGGTGAT CATATTGTG TTTTGTGTC CGATTCTAAC CTTACAGGGG      60
TTAGAGGGCA AGATGTTTAG GCCTTTAGCG CAAAGCATTG TGTATGCGCT TTTAGGCACT      120
TTAGTTCTAT CCATCACTAT CATTCCTGTA GTGAGCTCTC TTGTCCTAAA AGCCACGCCC      180
CATAGCGAAA CCTTTTAAAC GAGGTTTTTA AACAGAATCT ACGCCCTTTT ATTGGAATTT      240
TTTGTGCATA ACCCTAAAAA AGTGATTTTA GGAGCGTTTG TTTTCTTAAT CGCAAGCCTT      300
TCTTTATTCC CTTTTGTGGG GAAGAATTTT ATGCCTGCTT TAGATGAGGG CGATGTGGTT      360
TTGAGCGTGG AAACCACCCC CTCTATTTCC TTAGATCAAT CTAAAGATCT CATGTTAAAC      420
ATTGAAAGCG CGATTAAAAA GCATGTCAA GAAGTTAAAA GCATTGTGCG GCGCACAGGG      480
AGCGATGAAT TGGGGCTGGA TTTAGGGGGT TTGAATCAA CCGATACTTT TATTTCTTTT      540

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SUBSTITUTE SHEET (RULE 26)

298

ATCCCTAAAA AAGAATGGAG CGTTAAAACC AAAGATGAAT TGTTAGAAA AAATCATGGA 600
TTCTTTAAAA GACTT 615

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341

GTGGGATATA TCCCTARGGA AAAGATGTGA GGCATTAGCG CGATCGCTAA ACTCATTGAA 60
ATTTATAGCA AACGCCTGCA AATCCAAGAA AGGCTGACCA CTCAAATTGC AGAAACTTTT 120
GATGAAATCA TAGAGCCAAG GGGCGTGATC GTGTTTGTG AAGCCAAGCC ACTTGTGCAT 180
GAGCATGCAA GGGGTGCAAA AGCAAAATGC GATCAT 216

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342

GTGGCTCTTG TGTTTGATAG TTTGATAGAG AACAAGAAG 39

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

SUBSTITUTE SHEET (RULE 26)

299

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343

ATGAAAAAA	TTGGTTTGAG	CTTGTGTTTG	GTTTGTGAGT	TGGGTTTTTT	AAAAGCCCAT	60
GAAGTGAGCG	CTGAAGAGAT	TGCGGATATT	TTCTACAAAC	TCAACGCCAA	AGAGCCTAAA	120
ATGAAATCA	ACCACACGAA	GGGGTTTTCG	GCTAAAGGCG	TGTTCTCTCC	TAACCCGCAA	180
GCAAGAGAGG	ATTTAGAGGT	GCCACTACTC	AATGAAAAAG	AAATCCCTGC	GTCTGTAAGG	240
TATTCTTTAG	GGGGCGTGGT	CGATTGGACG	ATAAAGCAA	GGTTAGGGGA	ATGGCGT	297

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 300 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344

GTGATCAAAC	CTCATAGCGT	GGGATTGGTA	AGGATTGGGA	TTTGTGTTGTC	TTTAGAAGTG	60
GGGTATGAAC	TGCAGGTACG	CACCCGTAGC	GGCTTGGCTT	TGAATCATCA	GGTGATGGTG	120
TTAAATTYCC	CTGGCACGGT	GGATAATGAT	TATAGGGGCG	AAATTAAGGT	CATTTTAGCG	180
AATTTGAGCG	ATAAAGATTT	TAAAGTTCAA	GTAGGGGATA	GGATCGCTCA	AGGGGTGGTT	240
CAAAAACTT	ATAAAGCCGA	ATTTATAGAA	TGCGAACAA	TAGATGAAAC	CTTCAAGGGG	300

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 765 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

SUBSTITUTE SHEET (RULE 26)

300

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345

```

ATGGAATCA TTTTATTAAT TGTTGCGGCG GTTGTGTTGT TTTATTTTTA CAACACCCTC      60
AAAGAATATT TGA AAAACCC CCTAAACCCT AAAACCAAAA CCGAAGAATA CGACTTGAAA      120
AATGACCCTT ATTGCTGGT GCAATCTAGC CCCCTAGACA AATTCAAGCA AACCCAAATA      180
GGCGCGTATA TGCGTCTTTT AAAATTTTTT GACATTCAAA AAAACGCCTT GGATAACGCT      240
TTAAGAACGC TTTTATATCCA TGAATGGAG CAGCCCTTAA ACAGCGAACA GCAAAATTTA      300
GCCAAAGAGC TTCTCAATGA GCCSGTGGAT AAAAAAGAAA ATTTTGAATC CTTATGCCAA      360
GAAATCGCCG ACCACACGCA TGGAGAATAC ACCAAGCGCC TGAAATTAGT GGAATTCTTT      420
ATGCTATTAG CCTATGCTGA TGGGATTTTG GACAGCAAAG AAAAAGAATT GTTTTGTAGT      480
GTGGGGCGCT TTTTGCAGAT AGACAATCAA GATTTTAACG AGCTTTATGA CAATTTTGAA      540
CACTTCAATT CAATAGAAAT CCCTATGTCT TTAGAAGAAG CAAAAAATCT TTTTGAAATC      600
CAAAACCACA CCACCATGCA AGATTTAGAA AAAAAAGCTT TGGATTAAAG CGCCCCCTAT      660
TACCATAAAA TGAATGACAA CAAACGCTAC AGCGAACAAG ATTTTATCTC TTTGAAAAAA      720
ATCGCCCTCG CTTCCCAACT TTTAGAAAAT GATTTAAAAG ACTCA                      765

```

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 318 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346

```

ATGGAAGTAG AGCATGGCAA GATTGAAACC ACTTTAAGCT TGGGGGCGTC TCATTTGGAA      60
GTCATTAAAA TGATGCTTTT AGAGAGCCTG CCTTCTTTAG TGAATAATAT CACCATCACT      120
TTAATTCTTC TAATAGGCTA TTCGGCTAWG GCGGAGCGT TAGGGGCTGG GGGATTGGGG      180
GATTTAGCCA TTAGGATTGG CTATCAAAGT TATAGGGGCG ATGTGCTTTT TTATGCGGTG      240
GTCGTGATCA TCGTTTTAGT GCAATCATT CAAAGCGCGG GGGATTATGT GGTGAACGCG      300
TTGAGAAAGA ATAAGTAT

```

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1581 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

SUBSTITUTE SHEET (RULE 26)

301

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347

ATGAACGAAA	TTGACAAATC	CGTTGATATC	GGATTCTTAC	GGATTCTGGA	TGTTATTAAA	60
AAAGTTAAAA	CCCCAAAGGG	TGGTATTGAG	GTTTTAAGGA	CTTTAATTGA	TTTCACGCCC	120
AAAATTGAAA	ACGCCCTAAA	TTTAGCGACC	AAAAGCCATA	AGGGGCAATA	CAGAAAGAGC	180
GGTGAGCCTT	ATATTGTCCA	TCCTATTTGC	GTGGCGAGCG	TGGTGGCGTT	TTGTGGGGGC	240
GATGAGGCGA	TGGTGTGCGC	CGCGCTTTTG	CATGATGTGG	TAGAAGACAC	GCCTTGTGAG	300
ATTGAAACGA	TTGAGCGAGA	ATTTGGGCAA	GATGTGGCTA	ATTTAGTGGA	TGCGCTCACC	360
AAAATCACTG	AAATCAGGAA	AGAAGAGTTA	GGCGTGAGTT	CTCAAGATCC	CAGAATGGTG	420
GTTTCAGCCC	TCACTTTTAG	AAAGATCCTT	ATTAGCGCGA	TACAAGATCC	AAGAGCCTTA	480
GTGGTAAAGA	TTAGCGACAG	GTTGCACAAC	ATGCTCACCT	TAGACGCCTT	GCCTCATGAC	540
AAGCAGGTGC	GTATTTCTAA	AGAAACTCTA	GCGGTGTATG	CCCCCATAGC	GAGTCGATTG	600
GGCATGTCTT	CAATCAAAAA	CGAATTAGAA	GACAAGAGCT	TTTATTATAT	TTATCCAGAA	660
GAGTATAAAA	ATATTAAAGG	GTATTTGCAC	AAAAACAAAC	AGTCTTTACT	CTTAAAACTC	720
AACGCTTTTG	CGAGCAAGTT	AGAAAAAAG	CTTTTGTACA	GCGGGTTTAG	CCATTCGGAT	780
TTTAACTCG	TTACAAGGGT	GAAACGCCCT	TATTCTATTT	ATCTTAAGAT	GCAACGAAAA	840
GGGGCGGTTA	ATATTGATGA	AATTTTGGAC	TTGTTAGCCA	TTAGGATTTT	ATTGAAAAAC	900
CCGATTGATT	GCTACAAGGT	TTTAGGGATT	ATTCAATTGA	ATTTCAAACC	CATTGTTTCT	960
CGTTTTAAAG	ATTACATCGC	TTGCCCAAAA	GAAATGGCT	ATAAGACAAT	ACACACGACG	1020
ATTTTGTATG	AATCTTCTGT	TTATGAAGTG	CAGATCCGCA	CTTTTGATAT	GCACATGGGG	1080
GCGGAGTATG	GTAATTCAGC	CCATTGGAAG	TATAAAGCCG	GGGGCGTGGA	TCATGAAGAA	1140
CATCATGAGG	GCATGCGGTG	GTTGCAAAAT	TTTAAATACC	ATGACAGCGA	TTGAAAAAAC	1200
GACCCTAAGG	AATTTTACGA	ACTCGCTAAG	AACGATTTGT	ATCGTGAAGA	TATTGTCGTT	1260
TTTTCGCCCC	ATGGGGACAC	TTACACTTTA	CCGGTGGGCG	CGATCGCTTT	AGATTTTCGCT	1320
TACATGGTGC	ATAGTGATTT	GGGCGATAAA	GCCACGGACG	CTTATATCAA	TAGTAAAAAA	1380
GCCTTACTCA	ATCAAGAATT	AAGGAGTGGG	GATGTGGTTA	AAATCATTA	AGGCGATAAA	1440
GTAATACCTC	GTTTCATTTG	GATGGATCAG	CTTAAAACTT	CTAAGGCTAA	AAACCATTTG	1500
CGCATCCAAA	GAAGAAACCG	CTTGAAAGAA	ATTGACACTA	AGAGCATGAT	CAATATCTTA	1560
GCGACTTTTT	TTTGGGCGCT	C				1581

(2) INFORMATION FOR SEQ ID NO:348:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 372 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...372

SUBSTITUTE SHEET (RULE 26)

302

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348

GTGGTGGTGG TTGAGAATAT AAAAGACGCT GTGCCTTTAG CGCAAAGCCT RATARAGGGG	60
GGTATTCCAA TCATAGAAGT AACTTTGCGA TCAAACTGTG CTTTAGAGGC CATAGAGCTT	120
ATCGCTAAGA ATGTGCCAAA AATGCGCGTG GGTGCTGGCA CGATACTCAA TCTCACTCAA	180
TTAGAGCAGG CTCAAAATAG GGGGGCAGAG TTTTGTGATTA GCCCGGGTCT TACGATAAAG	240
CTTTTAGAAC ACGCAAAGAA AAAAGACATG CCTTTAATAC CTGGGGTTTC TAGCAGCAGT	300
GAAGTCATGC AAGCTTTAGA ATTGGGTTAT AACGCTTTGA AATTTTTCCTT GCGGAGTAT	360
TGCGGGGGCC GT	372

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349

GTGGAAAAAA TCAAACCCTA TGCCCTAAA GATAGCCCTT TAATAGACTA TTCTAGCCTA	60
GTTAGAAACG TCCAATCCAC TTAAAAAGGC ACTTCTTTTG AAACGCTTAT CAATGGCGTT	120
TGGGAAAGCT TTGAAACGAA GGTTTTAGGG GAGTTTAACG CCTATAATAT CGCTTCAGCG	180
ATTTTAACCG CTAAGCATTT AGGCTTAGAG ACAGAAAGGA TCAAACGGCT TGTTTTTGAG	240
CTTAAGCCTA TTAACCATCG TTTGCAACTG TTGGAAGCGA ATCAAAAAAT CATTATAGAC	300
GATASCTTTA ATGGAATTT AAAGGGCATG	330

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1791 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350

SUBSTITUTE SHEET (RULE 26)

303

ATGTCTAATC	AAGAATACAC	CTTCCAAACT	GAAATCAACC	AGCTTTTGGG	TTTGATGATC	60
CACTCTTTGT	ATTCTAATAA	AGAGATTTTT	TTAAGGGAGT	TGATTTCTAA	CGCGAGCGAC	120
GCTTTGGATA	AGCTGAATTA	TTTGATGCTA	ACCGATGAGA	AATTTAAAGG	GCTGAATACC	180
ACGCCTAGCA	TCCATTTGAG	TTTTGATAGC	CAAAAAAAAAA	CCTTAACGAT	TAAAGACAAT	240
GGTATAGGCA	TGGATAAAAG	CGATCTCATC	GAGCATTTAG	GCACGATCGC	TAAATCAGGC	300
ACGAAGAGTT	TTTTAAGCGC	TTTGAGTGGG	GATAAGAAAA	AAGATAGCGC	CTTAATTGGC	360
CAATTTGGCG	TGGGCTTTTA	TTCGGCGTTC	ATGGTAGCGA	GTAAGATTGT	CGTTCAAACC	420
AAAAAAGTTA	CCAGTCATCA	AGCTTATGCA	TGGGTGAGCG	ATGGTAAGGG	CAAGTTTGAA	480
ATCAGCGAAT	GCGTCAAAGA	GGAGCAAGGC	ACAGAAATCA	CCCTCTTTTT	AAAAGAAGAA	540
GATTCTCATT	TTGCGAGCCG	TTGGGAGATT	GATAGCGTTG	TTAAAAAGTA	TTCTGAGCAT	600
ATCCCTTTCC	CTATTTTTTT	AACTTACACC	GATACGAAAT	TTGAGGGCGA	AGGGGATAAT	660
AAAAAAGAAG	TTAAAGAAGA	AAAATGCGAT	CAGATCAATC	AAGCGAGCGC	TTTATGGAAA	720
ATGAATAAGA	GCGAATTGAA	AGAAAAGGAT	TACAAAGACT	TTTACCAATC	GTTTGC GCAT	780
GATAACAGCG	AGCCTTTGAG	CTATATCCAT	AATAAAGTGG	AAGGCTCTTT	AGAATACACG	840
ACGCTTTTTT	ATATCCCTAG	CAAAGCGCCC	TTTGATTGTG	TTAGGGTGGG	TTATAAAGC	900
GGGGTCAAAC	TTTATGTTAA	ACGGGTGTTT	ATCACTGATG	ATGACAAAGA	ATTGTTGCCG	960
TCTTATTTGA	GGTTTGTTAA	AGGCGTGATT	GACAGCGAAG	ATTTGCCCTT	GAACGTGAGT	1020
CGTGAAATCT	TACAGCAGAA	TAAGATTTTA	GCCAATATCC	GTTCCGGCTT	AGTGAAAAAG	1080
ATTTTAAGCG	AGATTGAAAG	GCTGAGCAAG	GATAACAAGA	ATTACCATAA	ATTCTATGAG	1140
CCTTTTGGGA	AAGTGTAAAA	AGAAGGCTTG	TATGGGGATT	TTGAAAACAA	AGAAAAACTT	1200
TTAGAAATGT	TGAGATTCTA	TTCTAAAGAC	AAAGGAGAAT	GGATTTCTTT	AAAAGAATAC	1260
AAAGAAAATT	TAAAAGAAAA	TCAAAAAAGC	ATTTACTACC	TTTTAGGCGA	AAATTTAGAC	1320
TTATTAAAAAG	CGTCCCCCCT	TTAGAAAAAA	TACGCTCAAA	AAGGCTATGA	TGTTTTGTTA	1380
TTGAGCGATG	AAATTGATGC	GTTTGTGATG	CCAGGCGTGA	ATGAATACGA	TAAAACGCCC	1440
TTTAGAGACG	CTAGCCATAG	TGAGAGTTTG	AAAGAGCTTG	GTTTGGCAGA	AATCCATGAT	1500
GAGGTAAAAG	ATCAGTTTAA	AGATTTAATC	AAAGCGTTTG	AAGAAAATCT	TAAAGATGAG	1560
ATTAAGGGCG	TAGAGCTTTC	TGGTCATCTC	ACTTCAGCGG	TGGCTTTAAT	AGGCGATGAA	1620
CCAAATGCCA	TGATGGCTAA	TTGGATGCCG	CAAATGGGGC	AAAGCGTGCC	TGAAAGCAAG	1680
AAAACCTTTAG	AATTAACACC	TAACCATGCG	ATTTTGCAAA	AACTCTTAAA	ATGCCAAGAT	1740
AAAGAGCAGT	TGAGCGCTTT	TATCTGGTTG	CTTTATGATG	GGCGAAGCTT	T	1791

(2) INFORMATION FOR SEQ ID NO:351:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 468 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...468
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:351

GTGAATTTAG	GGGCTTACTA	CACGCCCCCT	TATTTAGTGG	ATTGCGCTTA	CAAGCTTTTA	60
AAAAAGCATG	TTGGTATTGA	AAACTACACG	CTTTTAGACA	CCGCATGTGG	TAATAAAGAG	120
TTTTTAAAGC	TCCACCACCC	TAAAAAAATA	GGAGCGGATA	TTGACCCTAA	GTGTGATGCT	180
TTAATAATAA	ACGCTCTAGC	CAATCCTAAA	AGAGAAAAAT	ATGGCATTAG	CCAAGATGAA	240
CCTTTAATCA	TCGTGGGCAA	TCCCCCCTAT	AACGATAGAA	CTTCCTTTAT	CAAACAAGAT	300
ATTAAAAATA	AAGATTTCAT	TTTTGAGATA	GACAACGATT	TGAAATCCCG	AGATTTAGGG	360
ATAAGTTTTT	TAAAATCTTT	TGCAATTTTA	AAGCCGGCGT	TTATTTGCGT	GCTACACCCT	420
TTATCTTATC	TCATCAAAGA	AGCTAATTTT	AAGCAATTTA	AAGCTATT		468

SUBSTITUTE SHEET (RULE 26)

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352

ATGAAAAGCA	TTTGCTCTT	TATAATTTTT	GTAAGTTGTC	AGTTAGAAGG	CAAAAATTT	60
TCACAAGATA	ATTTTAAGGT	GGATTATAAC	TACTATTTGC	GCAAACAGGA	TTTGCACATC	120
ATTAAACGC	AAAACGATT	GTCCAATGCC	TGGTATCTCC	CTCCACAAA	AGCCCCCAA	180
GAACATTCTT	GGGTGGATT	TGCTAAAAA	TATTTAAACA	TGATGGATTA	TCTAGGCACT	240
TATTTTTCG	CTTTTATCA	TAGTTTCACC	CCCATTTTC	AATGGTACCA	CCCTAATATC	300
AACCCCTACY	AACGCAATGA	GTTAAGTTC	CAATCAGTT	TTAGAGTGCC	TGTATTTAGG	360
CATATTCTTT	GGACTAAAGG	CACGCTTTAT	CTGGYTTATA	CCCAAATAA	CTGGTTTCAA	420
ATTTATAATG	ACCCTCAATC	CGCCCCCATG	CGAATGATTA	AATTCATGC	C	471

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353

ATGGGCTTGA	TGGCGGTGTC	GCAAGGCTTA	CCAAACACCA	CTAGCAAGTT	TGGTATTGAA	60
TTTGACTCTT	TAGCTGATGT	GGTCGCTTTT	GGAGTCGCCC	CAAGCCTTAT	TACTTACTTT	120
TATGTGGGGT	ATAACTTTGG	GCGTATAGGC	ATGGCGGTGA	GCGCGTTGTT	TGTGATTTTT	180
GGAGCGATAC	GATTAGCGCG	ATTCAATATC	AGCACCAACA	CAAGCGATCC	CTATTCTTTC	240
ATCGGTATCC	CCATTCCTGC	GGCGGCGGTA	TTGGTGGTGC	TTTGGCGTGT	ATTAGATAAT	300
AAATACCATT	TCTTAGAAGG	CAATACCGAA	AAGTTATTTT	TAGGCTTTAT	TGTCTTTATTA	360
GGGGTGCTTA	TGGTGAGCAA	TATCCGCTAC	CCTAATTTTA	AAAAAGTCAA	GTGGAATCTC	420
AAGCTTTTCA	TCTTAGTGTT	GATCTTTTTA	TCGTTAGTGT	TTGTGCGCCC	TTTAGAGGCT	480

SUBSTITUTE SHEET (RULE 26)

305

TTGAGCGTGT TTATGGGGTT GTATTTGATC TATGGCATCA TTCGGTGGAT CTTTTTAATG 540
GTAAAAATTA CTTTTAATAA AAATAAAAGC GCA 573

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354

ATGATAGGAG TTTACCCCAA TTATTCCAAA AAGCAACTAA AACGCCCCCTT AGTCATATTT 60
GTAAGTAGGG AGTTAGCGCT GGCTAATGGT ATTCTTACAG ACGCCTATGA CATTGAAGCA 120
AATCTTTACA TGAATGCTCG TATCGTTATG AARAATAATA AAAGGAAACA TTATGAGCAG 180
CGGGTTAATT TACATTTTCRT TAGAAGTCTT GGTARCGTGT TTGATCACCG CTCTAATCAT 240
GTATTATGTG ATGAAAAAGA TCTATTACGC 270

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355

GTGAAAATAA CCATAATGAT TAAAGATTTT AACCACTATT GTAGAAAAAT AACGAGAGGG 60
TTTGTAATAA TTCCACCAA AAAACAAGGA GCAAAAAAGA TGAAAAAAGC GGGTTTTCTT 120
TTTTTGCGCG CGATGGCTAT CATGTTGTG AGTTTAAACG CCAAAGATCC GAATGTGTTG 180
CGTAAGATTG TTTTGTAGAA ATGTTGCGCT AATTATGAGA AAAATCAAAA TCCTTCACCA 240
TGCATAGAAG TCAAACCCGA CGCCGGCTAT GTGGTTTAA AAGATATTAA CGGTCCGTTG 300
CAATATTTGT TGATGCCAAC GACTCACATT AGTGGCATTG AAAACCCTTT GTTGCTTGAT 360
CCTTCTACGC CTAACTTTTT TTACTIONGTC TGGCAAGCGC GCGATTTTAT GAGTAAAAAA 420
TACGGAAAAC CCATTCCTGA TTATGCGATC TCTTTGACGA TCAATTCTAA AAAAGGGCGA 480

SUBSTITUTE SHEET (RULE 26)

306

TCGCAAAACC	ATTTTCACAT	CCATATTTCT	TGCATTAGCC	TTGATGTGCG	CAAACAGCTG	540
GATAATAATC	TAAAAAATAT	CAACAGCCGT	TGGTCGCCAT	TATCAGGTGG	CTTGAACGGG	600
CATAAATATT	TGGCGCGTCG	GGTAACAGAG	AGCGAATTAG	CGCAAAAAAG	CCCGTTTGTG	660
ATGCTTGCTA	AAGAAGTGCC	TAACGCGCAC	AAACGCATGG	GAGACTATGG	CTTGGCGGTG	720
GTGCAACAGA	GCGATAACTC	CTTTGTCTTG	TTAGCGACAC	AATTTAACCC	ATTGACTTTA	780
AATCGCGCTT	CAGCCGAAGA	GATTCAAGAT	CATGAATGCG	CGATTTTGCG	T	831

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356

GTGCTAACGA	GTGGGGACAT	GATCACTTGT	CCGTATTGCG	GGCGTATTTT	RTACGCTGAG	60
ACTACGCATG	AAAGTAACGC	TCAACCTCCA	AAAGAAAGCC	AACCAAAAGA	AAGCCAAGAA	120
GAAAGCCAAG	AAGAAAGCCA	AGAAGAAAGC	CAAGAAGCCG	TCCGTTTGAT	TGTT	174

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357

ATGAAATTGA	ATGACCCTTT	CACAAGCCCT	AATAAAGCCA	AAAAAGAATT	ATCGCCAAAA	60
GGCTTTAGGG	GGGGGTTAGA	GTCTGAAATT	TTATTAGGCT	TTGTCTTGCA	AAAAGAAAGG	120
GTTTTTTTGC	ACACGCATGA	GCATTTGGAA	TTAAGCCACG	AAGAAGAAAC	ACGCTTTTTT	180
GAATTGGTAG	GAAAGCGTTT	GAATGACTGC	CCCATAGAGT	ATTTATTAGG	AAGCTGTGAT	240
TTTTATGGGC	GCTCTTTTTT	CGTGAATGAG	CATGTTTTAA	TCCCACGGCC	TGAAACCGAG	300
ATTTAGTCC	AAAAAGCCCT	TAATATTATT	TCTCAATACC	ATTTAAAAGA	AATAGGCGAA	360

SUBSTITUTE SHEET (RULE 26)

307

ATCGGCATAG	GGAGCGGATG	CGTGTCCGTG	AGTTTGGCTT	TAGAAAACCC	TAATCTCTCT	420
ATTTATGCGA	GCGATATTTT	ACCAAAAGCT	TTAGAAGTGG	CGTTAAAAAA	TATTGAACGC	480
TTTTGTCTAA	AAGAGCGTGT	TTTTTTAAAA	CAAACGCGCC	TTTGGGATCA	TATGCCAACG	540
ATAGAAATGC	TTGTCTCTAA	CCCGCCCTAT	ATCGCTAGAA	ATTATCCTTT	GGAAAAATCC	600
GTTCTCAAAG	AACCGCACGA	AGCCCTTTTT	GGGGGGGTTA	AAGGCGATGA	AATCTTAAAA	660
GAAATCGTTT	TTTTAGCCGC	TAAATTAAAA	ATCCCTTTTT	TGGTTTGTGA	AATGGGGTAT	720
GACCAGTTAA	AGAGCTTGAA	AGAATGCTTG	GAGTTTTGCG	GTTATGATGC	AGAGTTTAC	780
AAGGATTTGA	GCGGCTTTGA	TAGAGGGTTT	GTGGGCGTTT	TAAAAAGTTT	TTTAAGA	837

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358

ATGATTTCTT	TCATTGGGTT	TGAATGCTCC	GCATTAAAAG	TTTTTTTAAAC	TTTGGTTAC	60
ATAGTTTTTA	AAAGYTGGA	CTATAGCGCT	ATAAGACTAA	TGTTTATA		108

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359

GTGATCCAGT	CTCACCCCTAA	ACAAACTCTA	ATTGAAGATG	AAAATTATTT	TTATGCTAAC	60
AAGGGTCTTT	ATAAAACCAA	CAAAGAAGCC	TTTTTAAGGG	TTTATAAAAT	CCCAGAGAGC	120
ATGCCCATAG	AAAAACGAGA	AAGTTTAAGC	AAGTTTCTA	AAATCTTTTT	AGCGTTGCTT	180
TTTTTCATTT	CTAGCATGCT	TTTTGGGATC	TTTTGGCGTT	TGCCCCAACG	ATTGGACACT	240
AAAATGAGTT	TAGAGAGCGC	GCACAAAAAC	GAATTAGAAA	ATGCATTCCA	ACGATACGAT	300

SUBSTITUTE SHEET (RULE 26)

308

GCGCTAGGGG TCGCTTTTGA AGACATTGCA GGGGTGAATG AAGTCAAAGA AGAATTACTA 360
 GAAGTGATRG ATTWTTTWAA AAAACCC 387

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360

ATGTTTGTAG TTAAATGGT GTTAGGCTTT TTGATCCTTT TAAGCCCTTT GTGCGCTACT 60
 GGATGGGATA TTTCACAAAC AGACATTATA GAGCGTTCCT TAAATTCCTT CTGTTTGTG 120
 GGGATTTTGT GGTATTTTTT GGCTAAAAGA TTGCGTTCAT TTTTGATTTC CAAAAGCCTT 180
 GAAATCTCCA AACGCTTAGA AGAGATTCAA GCCCAACTTA AAGTGAGTAA AGAACATAAG 240
 AAAAACTCC TTAAAGAATT AGAGCAAGCC AAAGAAAAAG CTGAATTGAT TATTTCTGAT 300
 GCGAATAAAG AAGCCCTACA CGATCAGCA AAAATACGAA TTACAAACCA AAATGGATGT 360
 GGAAAATTTG ATCAAAAATT C 381

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 885 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361

ATGAGGTTT TAGAGTGGAA ATATTGGTTA AATACTGATA AGTGGGATAC GCCCACCAC 60
 AAACCGCCTC AAACCTTTTAA AATACAAATT TTAAAGATAC AAATAGGTAT AATCAATAAC 120
 TTCAATCATT TAATCAAAGG GAGTTCATG AAAAAGCCTT TCAAAGCCTT TGCCTTGTTA 180
 ATCGTATTTT TCTCAAACGC TCTATTAGCG CAGGATTTAA AAATCGCTGC TGCTGCTAAT 240
 CTCACGCGCG CTTTAAAAGC CTTTGTAA GAATTTCAA AAGAACACCC AAAAGACGCT 300
 ATTAACATTA GCTTTAATTC TTCAGGCAAA CTCTACGCTC AAATCGCTCA AAACGCCCT 360

SUBSTITUTE SHEET (RULE 26)

309

TTTGATTAT	TCATTTTCAGC	GGATATTGCT	AGACCCAAAA	AACTTTATGA	TGAAAAAATA	420
ACCCCTTTTA	AAGAAGAAGT	CTATGCTAAA	GGCGTGTGG	TTTTATGGAG	TGAAAATCTA	480
AAAATGGATT	CTTTAGAAAT	TCTTAAAGAC	CCTAAAATTA	AACGTATCGC	TATGGCTAAT	540
CCTAAACTAG	CCCCTTATGG	AAAAGCCAGC	ATGGAAGTCT	TGGATCGTTT	AAAACCTCACT	600
CCTAGTCTTA	AATCTAAAAT	CATTTATGGC	GCTTCTATTT	CTCAAGCCCA	TCAATTCATC	660
GCCACCAAAA	ACGCTCAAAT	AGGCTTTGGA	GCGTTATCTT	TGATCGATAA	AAAAGACAAA	720
AACCTCTCTT	ATTTTCATCAT	TGATAAAACC	CTTTATAACC	CTATTGAACA	AGCCTTAATC	780
ATCACTAAAA	ATGGGGCTAA	TAACCCTTTA	GCCAAAGTTT	TAAAGATTTT	TTTATTCAGC	840
CCTAAAGCTA	GAGCTATCTT	TAAAGAATAC	GGCTATATTG	TGGAT		885

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362

GTGGCTTTAT	TAGAGCCAAG	CGTGATGTAT	CTTACCGAAA	AGTATCAATA	CTCTCGTTTT	60
AAGGTTACTT	GGGTCTTGT	AGCGTTAATC	TTGTGTTAG	GCGTGGTGT	GATTTTCTCG	120
CTCCATAAGG	ATTATAAAGA	CTATCTCACT	TTCTTTGAAA	AAAGTCTTTT	TGATTGGTTG	180
GATTTTGCA	CAAGCACCAT	TATCATSCCT	TAGGCGGGA	TGRCAACCTT	TATTTTATG	240
GGCTGGGTTT	TGAAAAAGA	AAAATTGCGT	CTTTTGAGCG	CGCACTTTT	AGGCCCTAAA	300
TTGTTTGCAA	CTTGGTATT	CTTGCTTAAA	TACATCACCC	CTTTAATTGT	GTTTTCCATT	360
TGGTTGAGCA	AGATTTAT					378

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363

SUBSTITUTE SHEET (RULE 26)

310

GTGGGGCTTA	TGAAAATAAG	ATTTATGGGG	CGGAGTGTTC	TTGTGGGGGA	TTTGGAACGC	60
ATTGAAGAAG	TGGCTAGATT	TGAAGAATTT	TGGCTTTTAG	GGGGGCAAAA	AGCGATCAAA	120
GAGCCTAGAA	GATTGGTTTT	AGAAATCGCT	TTAAACACCC	AGCTCAACAA	GCTTTTAAAA	180
CGCGTTCAAA	AGCATTTCAG	AGAAGACGAA	TTAGGAATTT	TTAAACAAAT	GCATGACAAA	240
AAAATTCAAA	GCGTCGCCAC	CAATCCATA	GGGCGTTTGT	TTGATATAGT	GGCGTTTAGT	300
TTGGGCGTGG	TGGGAACGAT	TAGTTTGAAG	GCCGAGAGCG	GGCAGGTTTT	AGAAAATCTA	360
GCCCTACAAA	GCGATGAGAT	CGCTTTTAC	CCTTTTGAAA	TCAAAAACAG	CGTGGTGCCT	420
TTGAAGGAAT	TTTATCAAGC	GTTTGAAAAG	GATTTGGGCG	TTTTAGAACC	CAAACGCATC	480
GCTAAGAAAT	TTTTTAACAG	CTTAGTAGAA	ATCATTACCG	CTTTGATTGC	GCCTTTTAAA	540
GGGCATGTCG	TGGTGTGCAG	TGGGGGCGTG	TTTTGCAACC	AATTGTGTGT	CGAACAATTA	600
GCCAAGCGAT	TGAAAAAGCT	TCAAAGGGAG	TATTTTTCCT	ACAAGCATT	CCCCCCTAAT	660
GACAGYAGTA	TCCCTGTCGG	TCAAGCCTTA	ATGGCGTATT	TCAACCCTAC	AATCATCAAA	720
AAAGGA						726

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364

GTGAGCGATT	CTAACGCTTT	AAAGGAAGTG	TTTTTAAACA	TCAGCGCTAA	AGAAGATCAT	60
TGCGACGTTT	TGATCAATTC	CGCCGTTTAT	GGGGTGTTCG	GGAGCGTGGA	AGACACGCCC	120
ATTGAAGAGG	TTAAAAAGCA	ATTTAGCGTG	AATTTTTCG	CCCTTTGTGA	AGTGGTGCAA	180
CTTGTTTTCG	CCTTATTAAA	AAACAAGCCT	TATTCTAAGA	TTTTCAATCT	TTCTTCCATA	240
GCGGGGCGTG	TGAGCATGCT	CTTTTTAGGC	CATTACAGCG	CGAGTAAGCA	TGCCTTAGAG	300
GCTTATAGCG	ATGCCTTGCG	TTTAGAGCTT	AAGCCCTTTA	ACGTTCAAGT	GTGTTTGATT	360
GAGCCAGGCC	CGGTGAAAAG	CAATTGGGAA	AAAACCGCTT	TTGAAAATGA	TGAGCGGAAA	420
GATAGCGTTT	ATGCTTTTGA	AGTGAATGCG	GCT			453

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

311

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365

```

GTGATAGTGG CGTGGCTTTT TAGGTTTAAA AGCATTGCGT TTTCTATTTT AATCACTCTG      60
TTGGTTATTT TAGTGGATAT TTGGGTGTAT AGCGATGTGC GCCAGTTTTT ATTGGACACT      120
TCTAGCTCTT TTATTTGGCT TTTAATCGCT TTACTAATCA AGTGGGGCGT GATTGTTATA      180
AGTGCGCGCA AATGCTACCA ATTCAGCCAA AAAATGTTTG CGTTAATCCA AAGAAAAAGG      240
CAAATCAGAG AGAATTTAAA AAACCGCTCC AATCGCAAAG ATGCTAAAAA TTTTGAAAAA      300
CTCTCTAACA TCGCTGAAGA AATCATTTC AAAAAACAAG AAGAGTCCCA CCACAAAGAA      360
GATTCTAATG ATGAAAACCA CAAAGACAAG CTTTCTAACA TTACCGAAGA AATGATTCTC      420
AAAAACAAG AGGAACTGAA AGCTAGAAAG GATAAGGGGG AT                               462

```

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...537

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366

```

ATGAACTACC CTAATCTACC TAACAGCGCT TTAGRGATAA GCGAACAGCC AGAAGTGAAA      60
GAAATCACTA ACGAGCTTTT AAAGCAATTA CAAAACGCTT TAAGGAGCAA CGCGCATTTT      120
AGCGAGCAAG TGAATTAAG CCTTAAATGC ATCGTTAGGA TTTTAGAAGT GCTTTTGAGT      180
TTGGATTTTT TTAAGAATGC GAATGAGATT GATAGCAGTT TAAGAAATTC CATTGAGTGG      240
CTGACTAACG CCGGCGAGAG CTTGAAATTA AAAATGAAAG AATACGAGCG CTTTTTTAGC      300
GAGTTTAATA CGAGCATGCA TGCCAACGAG CAGGAAGTAA CCAATACCTT AAACGCTAAC      360
GCCGAGAACA TTAAAAGCGR AATTAAAARG CTAGAAAATC AATTGATAGA AACCACGACA      420
AGACTTTTAA CGAGCTATCA AATCTTTTAA AACCAAGCCA GAGATAACGC TAACAACCAA      480
ATCACAAAAA ACAAACCCR AAGCCTTGAA GCGATTACAC AAGCTAAAAA CAACAGC          537

```

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

312

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367

GTGTTTGCCA CTGACAGCAG TAGCTTTTCT ATGGGGCTTA CCATGGCGAG TGCTTATGAY	60
CCCATTTCAG GATCGCAAAA ACCCATTTGTG GGGCAAGCCC TTTTATTGTT AGCGATTTTA	120
ATTTATTGG ATTATCGTT CCACCATCAA ATCATTTTAT TTGTGGATCA CAGCTTAAAA	180
GCCGTCCCTT TAGGGCGATT TGTCTTTGAG CCAGAATTAG CTAAAAACAT TGTCAAAGCC	240
TTTTCACACT TGTGTGTCAT AGGGTTTCT ATGGCGTTCC CTATTTTATG CTTGGTGTTA	300
TTGAGCGATA TTAATTTTGG CATGATCATG AAAACCCACC CTCAATTCAA CCTGCTCGCT	360
ATCGGGTTTC CGGTTAAAAAT TGCATCGGG TTTGTGGGCA TTATTTTAAT CGCTTCGGCT	420
ATCATGGGCG GTTTTAAAGA AGAAATCAGC CTGGCCTTTA GCGTTATTTRG TAAAACTTTT	480

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 282 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368

ATGTATGGCG TGAAGAGAT TAAAGATAAA ATTGACAAGC AACTCCACAA TAACGATCAT	60
TTGTTTGAAG GGCTTTTGG GAAAAAGAA GATTGAAAA AATTGGTGAG CATGTTTGGG	120
CAGTTGCGTT TCCAAAAGCG CTGGAGCCAA ACCCAAGAG TGCCACAAAC CAGTGTCTA	180
GGGCATACTT TATGCGTGGC GATTATGGGG TATTATTGA GTTTTGA CTTT GAAAGCTTGT	240
AAAAGCATGC GGATCAATCA TTTTGTGGG GGGCTTTTTC CA	282

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 438 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

313

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369

```

ATGACTTTAG ATGACTTATT AGGGGGGAGT TTGGACCCGC ATTGTTTTTG CAAACCCCTTA      60
ATCAAAAACCA AAAAAGACCA AGAAAGGCTC TTATCCCTTG CTTTAAAAGC CCACCCTAAA      120
ATCTCTTTTG GAWWGGACAG TGCCCCGCAT TTCATTCTA AAAAGCATAG CGCTAACATC      180
CCGGCGGGCA TCTTTTCTGC CCCTATTTTG TTGCCTGCGT TGTGCGAACT TTTTGAAAAA      240
CACAACGCTT TAGAAAATTT GCAAGCCTTT ATCAGTGATA ACGCTAAAAA AATCTACGCG      300
CTAGACAAAT TACCCAGTAA AAAAGCGCAT TTGTCTAAAA AACCCTTTAT AGTCCCTACG      360
CACACGCTTT GCTTGAATGA AAAAATCGCT ATCTTAAGAG GGGGCGAAAC GCTATCTTGG      420
AACCTTCAAG AAATCGCC                                     438

```

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370

```

ATGGGCGTTT TGGGCATGTT CGCTTTTTTT TCATGGGTTT TTTTATTCAA GCACAATCTC      60
AGCCATAAAA TCCGCTTATA CCATGAAAAA AAGGATTTTG ACAAATTGCT CAAACAAATC      120
CTATCCCAAG ACACCCAAAA GACTTTTTTA AAAACAAAAT TTAAAAGCGA TCTCGCTAAA      180
AACCTCTCTC AAATCTTAGC CCGCTATGAT TTAAAAGCTG ATTTAAACAC GCCAAATAGC      240
GGGTGCGAAA AAGTGGATAA CCTTTTTTAA CATTACCACA ATATAGAAAA TAACACCCTT      300
GAGCCTAAAG ATCACGCTAA ACATTCCCTA GCTTATGAGC ATGCTTATTT TTCTAAACGC      360
TTGAAGGCTT TCATTCTATA CGATTTGAAA AACGCCTTTG AAGTTTAAAC AAACGCGCAA      420
ATCCCTTTGG AATTACGCCG CTACGCTTAT AGAAATCGCC CAAAAGGCA GCAAAAAAGA      480
GGTTTAAAG GCTGTGAATG CGATGCAAGA GGATTGGA                                     519

```

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

314

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...579
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:371

```

GTGAGTGTTC CTGCAACGAG TGCGAATTTA GGCCCCGGTT TTGATTGCTT GGGTTTGAGT      60
TTGAATTTAC GCAATCGTTT TTTTATTGAG CCTAGTAATA TCCATGCGGT GAAATTGGTT      120
GGGGAGGGTG AAGGGATCCC TAAATTTTAA ACCAACAATA TTTTCACCAA AGTGTTTTAT      180
GAGATTTTAA AAAAGCATGG GAATGACGGC TCGTTTAAAT TTTTATTGCA TAATAAAGTC      240
CCTATTACAA GGGGCATGGG GTCTAGCTCA GCGATGATTG TGGGGGCGGT CGCTTCAGCG      300
TTTGCGTTTT TAGGGTTTGC TTTTGATAGA GAAAACATTC TCAATACTGC TCTAATTTAT      360
GAAAACCACC CGGATAATAT CACCCCGGCG GTGTTTGGGG GGTATAATGC AGCGTTTGTG      420
GAAAAAAGA AAGTGATAAG TTAAAAACC AAAATCCCTT CTTTTTTAAA AGCGGTGATG      480
GTGATCCCTA ATAGGGTCAT TTCTACCAAG CAATCGCGCC ATCTCTGCCC AAGCGTTACA      540
CGGTGCAAGA AAGCGTGTTC AACCTTTCGC ATGCGAGTT

```

(2) INFORMATION FOR SEQ ID NO:372:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 312 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...312
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:372

```

GTGGCTAAAA ATTTGGTAGC GAGCGGGGTT TGCGATAAAG CGACCGTGCA GCTTGCTTAT      60
GCGATTGGGG TGATAGAGCC TGTGTCTATT TATGTGAACA CGCATAACAC GAGCAAGCAT      120
TCAAGCGCGG AGTTGGA AAAA ATGCGTGAAA TCGGTTTTCA AACTCAGGCC AAAAGGCATC      180
ATTGAAAGCT TGGATTTGTT AAGACCCATT TATTGCTTCA CTTCAGCTTA TGGGCATTTT      240
GGGCGCGAGT TAGAAGAATT CACTTGGGAA AAGACTAACA AGGTTGAAGA GATTAAAGCG      300
TTCTTTAAGC GT

```

(2) INFORMATION FOR SEQ ID NO:373:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1065 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

315

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373

```

GTGCGTTTGT TTAGATTTGT GGGGTGGTAT TATTTCAAAT ACTTTTAAAT CGTGCTTTTA      60
GCTTTGGAAT TGTTTTTGT AGGCATTGAC AGCCTGAAAT ACGCCGATAA AATGCCTGAT      120
TCTGCGAACA TGATCATTTT ATTTTTCACC TATGATATTT TATTCGCTCT CAATTACACC      180
TTGCCCATTT CCTTGCTTTT AGCGATGGTT TTATTTTATA TCACCTTCAT TAAATCCAAC      240
CAATACACCG CCCTGCTCTC TATTGGATTT TCCAAATGCC AGATTTTAAG CCCTATTTT      300
TTGATTAGCC TGTTTTTCAC GGCTGTTTAT GTGGGGTTGA ACGCGACTCC TTTTGTGTAT      360
ATGGAAGAAA AAACGCAAAA TTTAATTAT AAAGACAATT CTTTGAGCGT TTCAGAGCAT      420
TTGTTAGTGA AATACAACGA TGATTACGTG TATTTTGATA AGATTAATCC CTTATTGCAA      480
AAAGCCCAAA ATATCAAGGT TTTTCGCTTA AAAGATAAAA CTTTAGAATC TTATGCTGAA      540
GCTAAGAAG CTTTTTTTGA AGACAAATAT TGGATTTTAC ATGACACTAC TATCTATGAG      600
ATGCCCTTGA GTTTTGAAC TGGCGCGAAC GCTTTAAACA CCACGCATT AGAAACCTTT      660
AAAACGCTCA AAAATTTCCG CCCTAAAGTT TTAGACACCA TTTATCAAAA CAAGCCTGCG      720
GTTTCTATCA CAGACGCTCT TTTATCCTTG CATGCTTTAG TGCGCCAAAA CGCGGACACG      780
AAAAAAGTGC GCTCGTTTTT GTATGTGTTT GCGATTTTGC CCTTTTTTGT GCCGTTTTTA      840
AGCGTTTTTA TCGCTTATTT TTCGCCCAGT CTCGCCCGCT ATGAAAACCT GGCTCTTTTA      900
GGGCTAAAGT TTATCATTAT CACGCTCGTT GTTTGGGGGC TATTCCTTGC TTTAGGGAAG      960
TTCAGCATTT CAGGGATACT CATTCTGAA ATAGGCGTTC TATCGCCCTT TTTCTGATTT      1020
CTAGCTCTCA GTCTTTGTA TTTTAAAAA CTTAATAAGA GATTG                          1065

```

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 717 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374

```

ATGATTTATG GCGTTTTAGA CGGCTTGT TTGGCTATTT TACAGGCTCA AAATTACCGC      60
TTCCATTTCG TTTATTTGTT TGAAGAAAAT TTAGACTTGT TAAAATCAG TTGCTATTTT      120
GGCGGTTATG AAGATTTGAT TAAAAAGGG GCTAACTTT TTATTCAAGG GTTTTTTAAC      180
CCTAATGAAT TGAAATGGA TTTTGTGAAA CGCCTATCA CGCATTCTTT TTTAAAGCTA      240
GAAATCATGC CCTATAAAG CGCTTTAAT TTGCGCATGC GAGAAAACAT TCAAAGCTAT      300
TACAAACAAG CCTAAGGGG TTGGGGGAGT TTTGAAGACG AATTGCTAGG GTTAAAGAAC      360
ACGCTTAAAA ACTTACCCCT ATACCAAACC CTAAAAACCA AACCCAAAAA AATTAACGCC      420
CCCATTTCG TGGTGGGTAA TGGGCAAGC CTGGATTAT TGTTAGATTT TTTAAAGAA      480
AATGAAGAAA AATTCATCAT TTTTTCATGC GGAACCGCTT TAAAGCCTTT AAAAGCGCAT      540
GGCGTTAAAG TGGATTTTCA AATAGAAGTG GAGCGCATAG ACTATCTTAA GGAGGTTTTA      600
GAAAGAGCCC CCTAGAAGA CACCCCTTA ATGGGCGCTA ACATGCTCAA TCCTAACGCT      660
TTTGATTTAG CCAAAGAAGC GTTGATGTTT ATGCGTGGG GGAGCGCTTG CGCAGTA      717

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SUBSTITUTE SHEET (RULE 26)

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 867 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375

ATGCTGGCGT	TTTTAAAAAC	CCCTAGAAAC	AGCGCTTTTG	CTTTGGGTYT	TTTCGTGGGG	60
GCGTTATTGT	TTTACTGGTG	CGCTTTAAGG	CTTTCGCATT	CGGATTTCAC	YTATTTATTG	120
CCCTTAATCA	TTGTTTTAGT	AGCGTTAGTT	TATGGGGTTT	TATTTTATTT	GTGCTCTAT	180
TTTGAAAACC	CCTACTTCAG	GCTTTTGAGT	TTTTTAGGCT	CTAGTTTAT	CCACCCTTTT	240
GGATTGATT	GGTTAGTCCC	GGATAGCTTT	TTTTCTTATA	GCGTGTTAG	GGTGGATAAA	300
TTATCTTTAG	GGCTTATTTT	TTTAGCTTGC	ATTTTTTTGA	GCGCTCAAAA	TCTTAAAAAA	360
TACAGAATGA	TAGGGGTTTT	ATTGCTGCTT	GGCGCGTTGG	ATTTTCATTI	TTTTAAAATA	420
AGCGATTTAA	AAGAGGTTGG	AAATATTGAA	TTAGTCTCTA	CAAGAACGCC	CCAAGATTTG	480
AAATTGACT	CAAAATACCT	TAATAATATT	GAAAACAACA	TTCTTAAAGA	AATCAAACCTC	540
GCTCAAAGCA	AGCAAAAAAC	CTTGATTGTT	TTTCCAGAGA	CCGCTTACCC	TATCGCTTTA	600
GAAAACTCCC	CTTTTAAAAAC	CCAAC TAGAA	GATTTAAGCG	ACAAGATCGC	CATTTTAATA	660
GGGACATTGC	GCGCTCARGG	CTATAGCCTT	TATAACAGCT	CGTTTTTATT	TTCTAAAAAA	720
AGCGTTCAAA	TCGCTGATAA	AGTGATCTTA	GCCCCCTTTG	GCGAGATAAT	GCCTTTACCG	780
GAGTTTCTTC	AAAAACCCCT	TGAAAAGCTC	TTTTTTGCGA	GAGCGCTTAT	TTATACCGCA	840
ACGCTCCCCA	TTTCAGCGAT	TTTACAT				867

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376

317

ATGAACGATC	CTAAGCATGT	GGTGTATGTT	TGGCTGGACG	CTTTATTGAA	TTATGCGAGC	60
GCGTTAGGGT	ATTTGAACGG	TTTAGACAAT	AAAATGGCGC	ATTTTGAACG	CGCTAGGCAT	120
ATTGTGGGTA	AGGATATTTT	ACGCTTCCAT	GCCATTTATT	GGCCAGCCTT	TTTGATGAGT	180
TTGAATTTGC	CCTTATTCAA	ACAGCTCTGT	GTGCATGGGT	GGTGGACGAT	AGAGGGCGTG	240
AAAATGAGTA	AGAGCTTGGG	TAATGTTTAA	GACGCTCAAA	AGCTCGCCAT	GGAGTATGGG	300
ATTGAAGAAT	TACGCTATTT	TTTATTGCGT	GAGGTGCCTT	TTGGGCAAGA	TGGGGATTTT	360
TCTAAAAAAG	CGTTAGTAGA	ACGGATTAAT	GCGAATTTGA	ATAACGATTT	GGGGAATTTG	420
TTGAATCGTT	TGCTAGGCAT	GGCTAAAAAG	TATTTCAATT	ATTCTCTAAA	AAGCACCAAA	480
ATCACTGCGT	ATTATCCTAA	AGAGCTAGAA	AAAGCACATC	AAATTTTAGA	TAACGCTAAT	540
TCTTTTGTGC	CTAAATGCA	ATTGCATAAG	GCTTTAGAGG	AATTGTTTAA	TATTTATGAT	600
TTTTTGAATA	AACATCATCG	TAAAGAAGAG	CCGTGGGTCT	TGCACAAAAA	CAACGAATCA	660
GAAAAATTAG	AAGCCTTATT	GAGTTTGATC	GCAAACACGC	TACTACAATC	AAGCTTCTTG	720
CTCTATGCGT	TCATGCCAAA	GAGCGCTATG	AAATTAGCGA	GCGCTTTTCG	TGTAGAAATC	780
ACGCCCAATA	ATTACGAACG	CTTTTTTAAG	GCTAAAAAAT	TACAAGATAT	GGTTTTACAA	840
GACACCGAGC	CTTTATTTTC	CAAAATTGAG	AAAATTGAAA	AGATTGAAAA	GATTGAAAAG	900
ATTGAAAAGA	TTGAAAAGG	GGAGGAAGCC	CTAGCAGAAA	AAGCAGAAAA	AAAAGAAAAA	960
GAAAAAGCCC	CACCAACACA	AGAAAATTAT	ATTAGTATTG	AGGATTTCAA	GAAAGTAGAG	1020
ATTAAAGTGG	GGCTTATCAA	AGAAGCTCAA	AGGATTGAAA	AATCCAATAA	ATTACTGCGC	1080
TTAAAGTGG	ATTTAGGCGA	AAATCGTTTG	AGGCAGATCA	TCTCAGGGAT	CGCTTTGGAT	1140
TATGAGCCTG	AAAGCTTGGT	GGGTCAAATG	GTGTGCGTGG	TGGCTAATTT	AAAACCCGCA	1200
AAGCTTATGG	GTGAAATGAG	TGAGGGCATG	ATTTTAGCGG	TGCGAGATAA	TGATAATCTG	1260
GCTTTAATCA	GCCCTACCAG	AGAAAAAATT	GCAGGAAGTT	TGATCAGC		1308

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377

ATGAAACGAC	CGATCAGCAA	ATTGAAACAA	AACTTTTTAC	AATTCAAACA	TTCTTTCAAC	60
AAACATTAG	ATAAGTACAG	CCTTTATTAT	AGGCTGTTCA	ATATCAGCTC	TATCGTTATA	120
GGTTTTTTAA	TAGCGCTTTT	TTCTTATGGG	GCAGGGGTGA	TTTTAGTTTA	TCCAATATTA	180
TTCTTGTTTG	CTCTTATAAT	AAAACCTAGC	TTTTTTTATT	ACACTACTTA	TCTTTTGCTA	240
CTCGTTTCTC	TCAGCATAAT	AAGCAAATAC	TATCTCCTAA	GCCACGCAAA	TTTCACAATG	300
AAGCTAATCA	TGCTTATGAC	TCAATGGCAA	AATTGGTTCT	TA		342

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

318

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...5
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:378

ATGGG

5

(2) INFORMATION FOR SEQ ID NO:379:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...381
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:379

```

GTGTTCACTT ATTCCCTGGG GCAGGTTTTC TTTTCTCTAA GTATCGGTTT AGGGATCAAT      60
ATCACTTATG CTGCCGTTAC GGATAAAACG CAGAATTTCG TTAAAAGCAC GATTTGGGTG      120
GTTTTATCAG GRATTTTAAT TTCTCTGTG RCAGGGCTTA TGATTTTCAC TTTTGTGTTT      180
GAATATGGGG CTAATGTCTC ACAAGGCACA GGGTTAATCT TCACITCTTT ACCGGTGGTT      240
TTTGGCCAAA TGGGAGCGAT AGGCGTTCCT TGTTCATT CTTTCTTGC TCGCGCTCGC      300
TTTGTCTGGC ATCACTTCTA CGGTGGCTTT ATTAGAGCCA AGCGTGATGT ATCTTACCGA      360
AAAGTATCAA TACTCTCGTT T

```

(2) INFORMATION FOR SEQ ID NO:380:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 537 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

319

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...537

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380

ATGAAACCAT	TGCATTTTTC	ACACCTGGAC	AGAGAGCAAT	CAGGCGATGT	GGGTTTTATC	60
ATTAAAAACC	TTATTTTTTT	AGGGGTTTTT	TCCTTATGG	GTTGGTTGAA	TACCGAGTAT	120
TTTCTATGGC	CTAGCATGCT	GGAATTAAAA	AAATCCTTT	TAGAAGAAAA	TCGTAAAAAA	180
AGCGTTTTAG	AATACGCGCA	AAGGCATTTT	GAAACAGCCC	TAGCAAACTA	CCGCAATCAA	240
AAAGAAACCA	GCGAATCTTT	GTTAAAGATT	TTTAATGATG	AAGAGTCCAG	GCGGATTTTA	300
GAAAAGATCT	TAAAAAATG	TTTTGACGCC	TATAAATCA	AACCCTTGCT	CTCTCAAAAC	360
CCCTCCCAAA	AAACCCAATT	TTTTATCATG	GCTAGAGCGA	GCGAATTGGA	AAAACTTAT	420
CTTTTTTTCA	CCTTAATCAA	CAAGTATTTA	CCGAGCGCTC	AAAGCCAATT	GCCCTTAAAG	480
ATTTCTAAAG	ATAGCGACGG	GTTGTTGGTG	CAATTTGGCG	TGAGTATTGA	TCGCCAA	537

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381

ATGAATGCAT	TGAAGCGTGC	GTGTTTAAGA	TTGATGGGCG	AAACCAATAC	CGATGATTTA	60
ASCCCAARYGA	GCGACGCTTT	CACACGGAGC	GATATTCCTT	TACACGCCAA	AGCCATGCTA	120
AAAAACCGGA	TTGAAAATTA	CGAACAACGC	ATTGAAGCCA	TTAAAACTAA	AGGCGTTCCT	180
GTAGCGTATG	TGGGCGATGT	GGTTGGCACA	GGAAGCTCTA	GAAAAAGCGC	GACTAACTCT	240
ATCATGTGGC	ATTTTGGTAA	GGACATTCCT	TTTGTGCCTA	ATAAAAGGAG	TGGAGGCATT	300
GTGATTGGGG	GGGTGATCGC	TCCGATTTTC	TTTGCGACTT	GTGAAGATAG	CGGGGCGTTA	360
CCCATGTGGG	CTGATGTAA	GGATTTGAAA	GAGGGCGATA	TCATTAAAAT	CTACCCCTTAT	420
AAAGGCGAAA	TCACGCTGAA	CGATAAGGTG	GTTAGCACCT	TTAAGCTAGA	GCCTGAAACT	480
TTATTAGATG	AAGTCAGGGC	TTCTGGGCGT	ATCCCTTAA	TCATTGGTAG	GGGTTTGACC	540
AATAAAGCGC	GTAAATTTTT	GGGCCGGCGA	ATCGGAAGCG	TTCAAAAAAC	CTTCCGCCCC	600
TCAAGCGCGC	TAAGGCTACA	CTTTGCC				627

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

SUBSTITUTE SHEET (RULE 26)

320

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382

ATGCTTTCAG	CCCACCAACC	TTTAAAAAAT	TACCCTGATC	TGATTAAAAA	AGAGTTGCAA	60
GAGCATAACG	CCTATGCCGAG	CGTCGCTAGT	GGGGTGCCAG	CGATGTGTGA	TGGTATCACG	120
CAAGGTTATG	AGGGAATGGA	ATTGAGCTTG	TTTAGTAGAG	ATGTGATCGC	ATTAAGCACC	180
SCCGTAGGGT	TAAGCCATAA	TGTTTTTGAC	GGGGCGTTTT	TTTTGGGCGT	GTGCGATAAA	240
ATTGTGCCAG	GCTTGCTCAT	AGGAGCGTTA	AGCTTTGGGA	ATTTAGCGAG	CGTGTTTGTG	300
CCAAGCGGGC	CTATGGTGAG	CGGGATAGAA	AATTATAAAA	AAGCCAAAGC	GCGCCAAGAT	360
TTTGCAATGG	GAAAGATCAA	CAGAGAAGAG	CTTTTAAAAG	TGGAAATGCA	AAGCTATCAT	420
GATGTGGGCA	CTTGCACTTT	TTATGGCAGC	GCTAATTCTA	ATCAAATGAT	GATGGAGTTT	480
ATGGGGTTGC	ATGTGGCCAA	TTCTAGCTTT	ATCAACCCTA	ACAACCCCTT	ACGAAAGGTT	540
TTAGTAGAAG	AGAGCGCTAA	AAGATTAGCG	AGCGGGAAAG	TCCTGCCTTT	AGCCAAACTC	600
ATTGATGAAA	AAAGCATTCT	TAACGCTCTT	ATAGGCTTAA	TGGCAACAGG	GGGTTCTACT	660
AACCACACTT	TGCATTTGAT	CGCTATCGCA	GATCTGTGG	GG		702

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 795 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383

ATGAAATTTT	TAAAATTCTT	TGCCAGTAGC	GTAACCTCTAG	ATGAAAAAAT	TTTAATGTTT	60
CTTCTTTTGA	ACGCTCTTTC	TAACGCTTAC	AAAAATAGCG	ATTTGTTTTT	TTTCTCTAAA	120
GGCTTTTTAG	GCGCTTTTTT	AATCGGGTTT	GTGGTGTAAT	ATGGTTGCGC	GCTAATCCCT	180
AAAAAACGCT	TGAAATATTC	ATTAGAATGG	CTGTTTATAG	GAAGCGGTAT	TATTTTITAGC	240
GTGGCAGAAA	TTTTTACGCT	GTTTATGTTT	AAAAATGCCTT	TTTCCAAAGG	CTTGATTGAC	300
ACGCTTTTITAG	CCACAAACAG	CTCTGAAACG	ATGGCGTTTA	TAAAAAGCTA	TAAAAATTAT	360
TTGCTTTTACT	ACGCTTTGAT	TTTGATCGCT	TTGTTGATCG	CCATTAAAAAT	CATTGCTTTT	420
AGAGCGCTTG	TGCTGGTGT	GATAGCGAGC	GTTTTAGGGC	TTTCTATCCT	TACAATAGGG	480
AGCGTTTCGTA	ACATTAAACA	CCTTACAAAG	AACGATGCGA	TTTTAAAAAG	ATCACTCTTT	540
TCTCTTTCTT	TAGCTAGGGG	GTTTTATTCC	GCTTATTTGA	GTTTGTTTGA	TCGCCAACAA	600
GCCATAAAAT	TTTATAGCTT	TTTAAATAAT	CTTTATTTAC	CAAGCGATTA	TCTTTCTAGC	660
ACGGGCGGATA	TTTCAAATGT	CGTCTTAGTC	ATCGCGAAAG	CGCGAGCAGA	AATTTTCATGC	720
AACTCTATGG	CTATAGCGTT	CCTAATAATC	CCTTATSCGA	GCGAACTCGC	CAACGAGAGA	780
GAGAGAGAGA	GAGAG					795

(2) INFORMATION FOR SEQ ID NO:384:

SUBSTITUTE SHEET (RULE 26)

321

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384

```

Met Cys Ser Gln Glu Ile Leu Ser Ser Leu Gln Thr Ile Ile Ala Glu
1      5      10      15
Gln Phe Ser Ile Asn Ile Ile Thr Gln Leu Ala Asn Lys Leu Thr Gln
20      25      30
Val Lys Asn Leu Asn Phe Phe Glu Asn Lys Asp His Thr Ile Lys Leu
35      40      45
Asn Thr Ile His Asn Gly Leu His Ile Arg Pro Leu Asn Tyr Val Ser
50      55      60
Asn Leu Phe Phe Asn Leu Gln Arg Ile Ile Gly Leu Ile Ser Leu Phe
65      70      75      80
Gly Ile Leu Phe Ser Ile Ser Ile Tyr Leu Pro Phe Ile Met Ile Phe
85      90      95
Ala Thr Val Pro Cys Ile Leu Ile Ser Asn His Ile Ala Lys Lys His
100      105      110
Ser Ala Ser Ile Asp Lys Leu Gln Asp Gln Lys Glu Ser Met Gln Asn
115      120      125
Tyr Leu Tyr Ser Gly Leu Asp Asn Gln Lys Asn Lys Asp Asn Leu Leu
130      135      140
Phe Asn Phe Met Leu Asn Phe His His Lys Phe Ile Glu Thr Lys Glu
145      150      155      160
Leu Tyr Leu Asn Asn Phe Val Lys Val Ala Gln Lys Asn Leu Ile Phe
165      170      175
Thr Ile Tyr Ala Asp Val Leu Ile Thr Thr Leu Ser Ile Ala Leu Phe
180      185      190
Phe Leu Met Val Phe Ile Ile Leu Ser Lys Leu Ile Gly Val Gly Ala
195      200      205
Ile Ala Gly Tyr Ile Gln Ala Phe Ser Ser Thr Gln Gln Gln Leu Gln
210      215      220
Asp Leu Ser Phe Tyr Gly Lys Trp Phe Phe Ala Ile Asn Lys Tyr Phe
225      230      235      240
Glu Asn Tyr Phe Cys Ile Leu Asp Tyr Lys Ile Pro Lys Pro Glu Thr
245      250      255
Gln Ile Lys Leu Glu Glu Lys Ile His Ser Ile Thr Phe Glu Asn Ile
260      265      270
Ser Phe Ser Tyr Pro Asn Ser Lys Leu Ile Phe Glu Asn Phe Asn Leu
275      280      285
Ser Leu His Ser Asn Lys Ile Tyr Ala Leu Val Gly Lys Asn Ala Ser
290      295      300
Gly Lys Ser Thr Leu Ile Asn Leu Leu Leu Gly Phe Tyr Thr Pro Asn
305      310      315      320
Ser Gly Gln Ile Ile Ile Asn Asn Lys Tyr Pro Leu Gln Asp Leu Glu
325      330      335
Leu Asn Ser Tyr His Gln Gln Met Ser Ala Ile Phe Gln Asp Phe Ser
340      345      350
Leu Tyr Ala Gly Tyr Ser Ile Asp Asp Asn Leu Phe Met Gln Asn Asn
355      360      365

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SUBSTITUTE SHEET (RULE 26)

322

```

Ile Thr Lys Glu Gln Leu Lys Gln Lys Arg Glu Ile Leu Lys Ser Phe
  370                      375                      380
Asp Glu Asn Phe Gln Asn Cys Leu Asn Asp Cys Asn Asn Thr Leu Phe
  385                      390                      395                      400
Gly Ala Gln Tyr Asn Gly Val Asp Phe Ser Leu Gly Gln Lys Gln Arg
                      405                      410                      415
Ile Ala Thr Met Arg Ala Phe Leu Lys Pro Ser Asn Cys Ile Val Leu
                      420                      425                      430
Asp Glu Pro Ser Ser Ala Ile Asp Pro Ile Met Glu Lys Glu Phe Leu
                      435                      440                      445
Asp Phe Ile Phe Lys Lys Ser Gln Ser Lys Met Ala Leu Ile Ile Thr
                      450                      455                      460
His Arg Met Asn Ser Val Lys Gln Ala Asn Glu Ile Ile Val Leu Asp
  465                      470                      475                      480
Gln Gly Lys Leu Ile Glu Gln Gly Asn Phe Glu Thr Leu Met Lys Lys
                      485                      490                      495
Gln Gly Leu Phe Cys Glu Leu Phe Leu Lys Gln Gln Tyr
                      500                      505

```

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385

```

Met Lys Gly Pro Ile Leu Trp Pro Ala Phe Ser Gln Phe Ser Asp Gln
  1                      5                      10                      15
Asp Leu Ser Asp Ile Val Ala Tyr Leu Thr Ser Ile Leu Pro Lys Asn
  20                      25                      30
Leu Ser Asp Lys Glu Val Phe Ala Gln Ser Cys Gln Arg Cys His Ser
  35                      40                      45
Leu Asp Tyr Ala Lys Asp Lys Ala Phe Ser Asp Pro Lys Asp Leu Ala
  50                      55                      60
Asn Tyr Leu Gly Ser His Ala Pro Asp Leu Ser Met Met Ile Arg Ala
  65                      70                      75                      80
Lys Gly Glu His Gly Leu Asn Val Phe Ile Asn Asp Pro Gln Lys Leu
  85                      90                      95
Leu Pro Gly Thr Ala Met Pro Arg Val Gly Leu Asn Glu Lys Ala Gln
  100                     105                     110
Lys Gln Val Ile Ser Tyr Leu Glu Lys Ala Gly Asp Arg Lys Lys His
  115                     120                     125
Glu Arg Asn Thr Leu Gly Ile Lys Ile Met Ile Phe Phe Ala Val Leu
  130                     135                     140
Ser Phe Leu Ala Tyr Ala Gly Lys Glu Lys Phe Gly Ala Lys Cys Ile
  145                     150                     155                     160
Lys Phe Lys Lys Gly Gly Thr Trp Phe Tyr Asp Phe
  165                     170

```

(2) INFORMATION FOR SEQ ID NO:385:

SUBSTITUTE SHEET (RULE 26)

323

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385

```

Met Lys Gly Pro Ile Leu Trp Pro Ala Phe Ser Gln Phe Ser Asp Gln
 1             5             10             15
Asp Leu Ser Asp Ile Val Ala Tyr Leu Thr Ser Ile Leu Pro Lys Asn
      20             25             30
Leu Ser Asp Lys Glu Val Phe Ala Gln Ser Cys Gln Arg Cys His Ser
      35             40             45
Leu Asp Tyr Ala Lys Asp Lys Ala Phe Ser Asp Pro Lys Asp Leu Ala
      50             55             60
Asn Tyr Leu Gly Ser His Ala Pro Asp Leu Ser Met Met Ile Arg Ala
      65             70             75             80
Lys Gly Glu His Gly Leu Asn Val Phe Ile Asn Asp Pro Gln Lys Leu
      85             90             95
Leu Pro Gly Thr Ala Met Pro Arg Val Gly Leu Asn Glu Lys Ala Gln
      100            105            110
Lys Gln Val Ile Ser Tyr Leu Glu Lys Ala Gly Asp Arg Lys Lys His
      115            120            125
Glu Arg Asn Thr Leu Gly Ile Lys Ile Met Ile Phe Phe Ala Val Leu
      130            135            140
Ser Phe Leu Ala Tyr Ala Gly Lys Glu Lys Phe Gly Ala Lys Cys Ile
      145            150            155            160
Lys Phe Lys Lys Gly Gly Thr Trp Phe Tyr Asp Phe
      165            170

```

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386

```

Met Glu Arg Lys Thr Leu Gln Ser Ile Leu Cys Leu Ile Lys Lys Glu
 1             5             10             15

```

SUBSTITUTE SHEET (RULE 26)

324

```

Met Met Arg Pro Lys Gly Ile Leu Met Asn Cys Cys Arg Thr Trp Lys
      20      25      30
His Gln Val Leu Lys Gln Ser Thr Thr Gly Leu Val Val Leu Ser Ile
      35      40      45
Ile Ser Ser Thr Ala Pro Phe Ile Gly Leu Phe Gly Thr Val Val Glu
      50      55      60
Ile Leu Glu Ala Phe Asn Asn Leu Gly Ala Leu Gly Gln Ala Ser Phe
      65      70      75      80
Gly Val Ile Ala Pro Ile Ile Ser Lys Ala Leu Ile Ala Thr Ala Ala
      85      90      95
Gly Ile Leu Ala Ala Ile Pro Ala Tyr Ser Phe Tyr Leu Ile Leu Lys
      100      105      110
Arg Lys Val Tyr Asp Leu Ser Val Tyr Val Gln Met Gln Val Asp Ile
      115      120      125
Leu Ser Ser Lys Lys
      130

```

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387

```

Met His Glu Arg Ile Glu Arg Gly Ile Unk Asn Asn Glu Cys Lys Glu
1      5      10      15
Ile Phe Gly Asn Glu Leu Lys Gln Arg Lys Thr Lys Leu Ile Glu Asp
      20      25      30
Ile Glu Arg Arg Phe Lys Glu Cys Glu Glu Gln Phe Arg Gly Ser Val
      35      40      45
Gly Lys Asn Ile Glu Gln Leu Glu Glu Arg Val Lys Asp Ser Leu Ala
      50      55      60
Ile Ile Lys Arg Ile Asn Asn Leu Gly Leu Asn Pro Asn Ser Asn Phe
      65      70      75      80
Asn Met Asp Ser Gly Ile Asp Thr Ile Gly Leu Phe Ser Ser Ile Gly
      85      90      95
Gly Leu Val Leu Leu Leu Thr Pro Val Val Gly Glu Phe Ala Leu
      100      105      110
Ile Ala Gly Val Gly Leu Ala Leu Val Gly Val Gly Lys Ser Ile Trp
      115      120      125
Ser Phe Phe Asp Ser Asp Tyr Lys Lys Ser Gln Gln Arg Lys Glu Val
      130      135      140
Asp Lys Asn Leu His Gln Ile Cys Glu Lys Leu Cys Arg Met
      145      150      155

```

(2) INFORMATION FOR SEQ ID NO:388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid

SUBSTITUTE SHEET (RULE 26)

325

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388

```

Met Pro Gly Val Tyr Gln Met Ser Ile Glu Pro Leu Leu Lys Glu Cys
1          5          10          15
Glu Glu Leu Val Gly Leu Gly Ile Lys Ala Val Leu Leu Phe Gly Ile
20          25          30
Pro Lys His Lys Asp Ala Thr Gly Ser His Ala Leu Asn Lys Asp His
35          40          45
Ile Val Ala Lys Ala Thr Arg Glu Ile Lys Lys Arg Phe Lys Asp Leu
50          55          60
Ile Val Ile Ala Asp Leu Cys Phe Cys Glu Tyr Thr Asp His Gly His
65          70          75          80
Cys Gly Ile Leu Glu Asn Ala Ser Val Ser Asn Asp Lys Thr Leu Lys
85          90          95
Ile Leu Asn Leu Gln Gly Leu Ile Leu Leu Lys Ala Val Trp Ile Phe
100          105          110

```

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389

```

Val Glu Asn Asn Lys Ser Leu Lys His Ala Asn Glu Leu Arg Asp Lys
1          5          10          15
Arg Asp Glu Leu Glu Phe His Leu Arg Glu Leu Phe Gly Gly Asn Val
20          25          30
Phe Lys Ser Ser Ile Lys Thr His Ser Leu Thr Asp Lys Asp Ser Ala
35          40          45
Asp Phe Asp Glu Ser Tyr Asn Leu Asn Ile Gly His Gly Unk Asn Unk
50          55          60
Ile
65

```

(2) INFORMATION FOR SEQ ID NO:390:

SUBSTITUTE SHEET (RULE 26)

326

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390

```

Met Gln Glu Phe Ser Leu Trp Cys Asp Phe Ile Glu Arg Asp Phe Leu
1           5           10           15
Glu Asn Asp Phe Leu Lys Leu Ile Asn Lys Gly Ala Ile Cys Gly Unk
          20           25           30
Thr Ser Asn Pro Ser Leu Phe Cys Glu Ala Ile Thr Lys Ser Ala Phe
          35           40           45
Tyr Gln Asp Glu Ile Ala Lys Unk Gln Arg Gln Lys Ser
50           55           60

```

(2) INFORMATION FOR SEQ ID NO:390:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390

```

Met Gln Glu Phe Ser Leu Trp Cys Asp Phe Ile Glu Arg Asp Phe Leu
1           5           10           15
Glu Asn Asp Phe Leu Lys Leu Ile Asn Lys Gly Ala Ile Cys Gly Unk
          20           25           30
Thr Ser Asn Pro Ser Leu Phe Cys Glu Ala Ile Thr Lys Ser Ala Phe
          35           40           45
Tyr Gln Asp Glu Ile Ala Lys Unk Gln Arg Gln Lys Ser
50           55           60

```

(2) INFORMATION FOR SEQ ID NO:391:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 619 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

327

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391

```

Val Phe Val Ala Ser Lys Gln Ala Asp Glu Gln Lys Lys Leu Val Ile
1      5      10      15
Glu Gln Glu Val Gln Lys Arg Gln Phe Gln Lys Ile Glu Glu Leu Lys
20      25      30
Ala Asp Met Gln Lys Gly Val Asn Pro Phe Phe Lys Val Leu Phe Asp
35      40      45
Gly Gly Asn Arg Leu Phe Gly Phe Pro Glu Thr Phe Ile Tyr Ser Ser
50      55      60
Ile Phe Ile Leu Phe Val Thr Ile Val Leu Ser Val Ile Leu Phe Gln
65      70      75      80
Ala Tyr Glu Pro Val Leu Ile Val Ala Ile Val Ile Val Leu Val Ala
85      90      95
Leu Gly Phe Lys Lys Asp Tyr Arg Leu Tyr Gln Arg Met Glu Arg Ala
100     105     110
Met Lys Phe Lys Lys Pro Phe Leu Phe Lys Gly Val Lys Asn Lys Ala
115     120     125
Phe Met Ser Ile Phe Ser Met Lys Pro Ser Lys Glu Met Ala Asn Asp
130     135     140
Ile His Leu Asn Pro Asn Arg Glu Asp Arg Leu Val Ser Ala Ala Asn
145     150     155     160
Ser Tyr Leu Ala Asn Asn Tyr Glu Cys Phe Leu Asp Asp Gly Val Ile
165     170     175
Leu Thr Asn Asn Tyr Ser Leu Leu Gly Thr Ile Lys Leu Gly Gly Ile
180     185     190
Asp Phe Leu Thr Thr Ser Lys Lys Asp Leu Ile Glu Leu His Ala Ser
195     200     205
Ile Tyr Ser Val Phe Arg Asn Phe Val Thr Pro Glu Phe Lys Phe Tyr
210     215     220
Phe His Thr Val Lys Lys Lys Ile Val Ile Asp Glu Thr Asn Arg Asp
225     230     235     240
Tyr Gly Leu Ile Phe Ser Asn Asp Phe Met Arg Ala Tyr Asn Glu Lys
245     250     255
Gln Lys Arg Glu Ser Phe Tyr Asp Ile Ser Phe Tyr Leu Thr Ile Glu
260     265     270
Gln Asp Leu Leu Asp Thr Leu Asn Glu Pro Val Met Asn Lys Lys His
275     280     285
Phe Ala Asp Asn Asn Phe Glu Glu Phe Gln Arg Ile Ile Arg Ala Lys
290     295     300
Leu Glu Asn Phe Lys Asp Arg Ile Glu Leu Ile Glu Glu Leu Leu Ser
305     310     315     320
Lys Tyr His Pro Thr Arg Leu Lys Glu Tyr Thr Lys Asp Gly Ile Ile
325     330     335
Tyr Ser Lys Gln Cys Glu Phe Tyr Asn Phe Leu Val Gly Met Asn Glu
340     345     350
Ala Pro Phe Ile Cys Asn Arg Lys Asp Leu Tyr Leu Lys Glu Lys Met
355     360     365
His Gly Gly Val Lys Glu Val Tyr Phe Ala Asn Lys His Gly Lys Ile
370     375     380
Leu Asn Asp Asp Leu Ser Glu Lys Tyr Phe Ser Ala Ile Glu Ile Ser
385     390     395     400
Glu Tyr Ala Pro Lys Ser Gln Ser Asp Leu Phe Asp Lys Ile Asn Ala
405     410     415

```

SUBSTITUTE SHEET (RULE 26)

328

```

Leu Asp Ser Glu Phe Ile Phe Met His Ala Tyr Ser Pro Lys Asn Ser
    420                      425                      430
Gln Val Leu Lys Asp Lys Leu Ala Phe Thr Ser Arg Arg Ile Ile Ile
    435                      440                      445
Ser Gly Gly Ser Lys Glu Gln Gly Met Thr Leu Gly Cys Leu Ser Glu
    450                      455                      460
Leu Val Gly Asn Gly Asp Ile Thr Leu Gly Ser Tyr Gly Asn Ser Leu
    465                      470                      475                      480
Val Leu Phe Ala Asp Ser Phe Glu Lys Met Lys Gln Ser Val Lys Glu
    485                      490                      495
Cys Val Ser Ser Leu Asn Ala Lys Gly Phe Leu Ala Asn Ala Ala Thr
    500                      505                      510
Phe Ser Met Glu Asn Tyr Phe Phe Ala Lys His Cys Ser Phe Ile Thr
    515                      520                      525
Leu Pro Phe Ile Phe Asp Val Thr Ser Asn Asn Phe Ala Asp Phe Ile
    530                      535                      540
Ala Met Arg Ala Met Ser Phe Asp Gly Lys Glu Asp Asn Asn Ala Trp
    545                      550                      555                      560
Gly Asn Ser Val Met Thr Leu Lys Ser Glu Ile Asn Ser Pro Phe Tyr
    565                      570                      575
Leu Asn Phe His Met Pro Thr Asp Phe Gly Ser Ala Ser Ala Gly His
    580                      585                      590
Thr Leu Ile Leu Gly Ser Thr Gly Ser Gly Lys Asn Ser Val Tyr Val
    595                      600                      605
His Asp Ser Lys Arg Tyr Gly Ala Ile Cys Leu
    610                      615

```

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392

```

Val Lys Thr Ser Cys Leu Val Thr Ile Gly Arg Ile Arg Gly Val Phe
1      5      10      15
Ile Ile Lys Ala Gln Leu Leu Leu Arg Glu Gly Gly Phe Met Asn Phe
20      25      30
Thr Ala Tyr Asn Thr Lys Thr Pro Gly His Leu His Leu Tyr Val His
35      40      45
Lys Gly His Thr Glu Leu Gly Glu Gly Glu Arg Leu Ile Lys Thr Leu
50      55      60
Ser Met Lys Leu Ala Gln Gly Leu Pro Lys Glu Trp Arg Val Phe Pro
65      70      75      80
Ser Asn Glu Trp Pro Lys Glu Phe Asn Ile Leu Ala Leu Pro Tyr Glu
85      90      95
Val Phe Ala Lys Glu Arg Gly Ser Ser Trp Ala Lys His Leu
100      105      110

```

(2) INFORMATION FOR SEQ ID NO:393:

SUBSTITUTE SHEET (RULE 26)

329

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...68

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393

```

Val Ala Lys Asp Ile Ile Ser Glu Ser Gln Asn Leu Cys Ala Arg Lys
1          5          10          15
Phe Arg Arg Leu Tyr Ala Leu Leu Lys Glu Asn Glu Met Leu Ile Arg
          20          25          30
Ile Gly Ser Tyr Gln Met Gly Asn Asp Lys Glu Leu Asp Glu Ala Ile
          35          40          45
Lys Lys Lys Ala Leu Met Glu Gln Phe Leu Val Gln Asp Glu Asn Ala
50          55          60
Leu Unk Ala Phe
65

```

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394

```

Met Lys Ser Arg Pro Ile Leu Ala Gln Ala Tyr Ala Leu Gln Met Met
1          5          10          15
Val Lys Gln Ile Ala Phe Leu Glu Thr Ile Leu Val Glu Asn Glu Gln
          20          25          30
Asp Ala Leu Ile Leu Glu Asn Ser Leu Ile Lys Gln Leu Lys Pro Lys
          35          40          45
Tyr Asn Ile Leu Leu Arg Asp Asp Lys Thr Tyr Pro Tyr Ile Tyr Met
50          55          60
Asp Phe Ser Ile Asp Phe Pro Ile Pro Leu Ile Thr Arg Lys Ile Leu
65          70          75          80
Lys Gln Pro Gly Val Lys Tyr Phe Gly Pro Phe Thr Ser Gly Ala Lys
          85          90          95
Asp Ile Leu Asp Ser Leu Tyr Glu Leu Leu Pro Leu Val Gln Lys Lys
100          105          110

```

SUBSTITUTE SHEET (RULE 26)

330

```

Asn Cys Ile Lys Asp Lys Lys Ala Cys Met Phe Tyr Gln Ile Glu Arg
  115      120      125
Cys Lys Ala Pro Cys Glu Asp Lys Ile Thr Lys Glu Glu Tyr Leu Lys
  130      135      140
Ile Ala Lys Glu Cys Leu Glu Met Ile Glu Asn Lys Asp Arg Leu Ile
  145      150      155      160
Lys Glu Leu Glu Leu Lys Met Glu Arg Leu Ser Ser Asn Leu Arg Phe
      165      170      175
Glu Glu Ala Leu Ile Tyr Arg Asp Arg Ile Ala Lys Ile Gln Lys Ile
      180      185      190
Ala Pro Phe Thr Cys Met Asp Leu Ala Lys Leu Tyr Asp Leu Asp Ile
      195      200      205
Phe Ala Phe Tyr Gly Gly Asn Asn Lys Ala Val Leu Val Lys Met Phe
      210      215      220
Met Arg Gly Gly Lys Ile Ile Ser Ser Ala Phe Glu Lys Ile His Ser
  225      230      235      240
Leu Asn Gly Phe Asp Thr Asp Glu Ala Met Lys Gln Ala Ile Ile Asn
      245      250      255
His Tyr Gln Ser His Leu Pro Leu Met Pro Glu Gln Ile Leu Leu Ser
      260      265      270
Ala Cys Ser Asn Glu Thr Leu Lys Glu Leu Gln Glu Phe Ile Ser His
      275      280      285
Gln Tyr Ser Lys Lys Ile Ala Leu Ser Ile Pro Lys Lys Gly Asp Lys
  290      295      300
Leu Ala Leu Ile Glu Ile Ala Met Lys Asn Ala Gln Glu Ile Phe Ser
  305      310      315      320
Gln Glu Lys Thr Ser Asn Glu Asp Arg Ile Leu Glu Glu Ala Arg Ser
      325      330      335
Leu Phe Asn Leu Glu Cys Val Pro Tyr Arg Val Glu Ile Phe Asp Thr
      340      345      350
Ser His His Ser Asn Ser Gln Cys Val Gly Gly Met Val Val Tyr Glu
      355      360      365
Asn Asn Ala Phe Gln Lys Asp Ser Tyr Arg Arg Tyr His Leu Lys Gly
  370      375      380
Ser Asn Glu Tyr Asp Gln Met Ser Glu Leu Leu Thr Arg Arg Ala Leu
  385      390      395      400
Asp Phe Ala Lys Glu Pro Pro Pro Asn Leu Trp Val Ile Asp Gly Gly
      405      410      415
Arg Ala Gln Leu Asn Ile Ala Leu Glu Ile Leu Lys Ser Ser Gly Ser
      420      425      430
Phe Val Glu Val Ile Ala Ile Ser Lys Glu Lys Arg Gly Phe
      435      440      445

```

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395

Val Ser Leu Gly Ala Phe Gln Gly Tyr Tyr Gly Gly Leu Val Asp Leu

AMINO ACID SEQUENCE SHEET (RULE 26)

331

```

1           5           10           15
Val Gly Gln Arg Leu Ser Glu Ile Trp Ser Ala Ile Pro Met Leu Phe
                20           25           30
Leu Leu Ile Val Ile Ser Ser Ala Phe Asn Ser Asn Phe Trp Ile Ile
                35           40           45
Leu Phe Leu Val Leu Leu Phe Ser Trp Met Gly Leu Ser Gln Val Val
                50           55           60
Arg Thr Glu Phe Leu Lys Ala Arg Asn Met Asp Tyr Thr Lys Ala Ala
65           70           75           80
Arg Ala Leu Gly

```

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396

```

Met Ser Glu Ala Tyr Phe Leu His His Lys Asn Ala Ser Gln Val Ser
1           5           10           15
Leu Asn Glu Gln Val Leu Asn Val Met Lys Gln Val Gln Leu Asp Glu
                20           25           30
Asn Phe Trp Asn Val Ser Leu Met
                35           40

```

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397

```

Val Ile Leu Ile Phe Ile Ile Val Val Glu Asp Gln Lys Gly Ile Phe
1           5           10           15
Pro Ile Ala Ala Ser Lys Arg Lys Ser Gln Ser Ser Val Ile Ile Glu
                20           25           30

```

SUBSTITUTE SHEET (RULE 26)

332

```

Asp Val Cys Phe Ser Lys Glu Asp Phe Val Glu Gly Ala Lys Ala Ile
   35           40           45
Glu Gly Leu Leu Lys Lys His Gly Phe Lys Asp Asn Gly Ile Ile Phe
   50           55           60
Gly His Ala Leu Ser Gly Asn Leu His Phe Val Val Thr Pro Ile Leu
   65           70           75           80
Glu Asn Glu Ala Glu Arg Lys Ala Phe Glu Asn Leu Val Ser Glu Met
   85           90           95
Phe Leu Met Val Ser Lys Ser Ser Gly Ser Ile Lys Ala Glu His Gly
  100           105           110
Thr Gly Arg Met Val Ala Pro Phe Val Glu Met Glu Trp Gly Glu Lys
  115           120           125
Ala Tyr Lys Ile His Lys Gln Ile Lys Glu Leu Phe Asp Pro Asn Gly
  130           135           140
Leu Leu Asn Pro Asp Val Ile Ile Thr Asn Asp Lys Glu Ile His Thr
  145           150           155           160
Lys Asn Leu Lys Ser Ile Tyr Pro Ile Glu Glu His Leu Asp Met Cys
  165           170           175
Met Glu Cys Gly Phe Cys Glu Arg Ile Cys Pro Ser Lys Asp Leu Ser
  180           185           190
Leu Thr Pro Arg Gln Arg Ile Val Ile His Arg Glu Val Glu Arg Leu
  195           200           205
Lys Glu Arg Val Ser His Gly His Asp Glu Asp Gln Val Leu Leu Asp
  210           215           220
Glu Leu Leu Lys Glu Ser Glu Tyr Leu Ala His Ala Thr Cys Ala Val
  225           230           235           240
Cys His Met Cys Ser Thr Leu Cys Pro Leu Gly Ile Asp Thr Gly Unk
  245           250           255
Ile Ala Leu Asn His Tyr Gln Lys Asn Pro Lys Gly Glu Lys Ile Ala
  260           265           270
Ser Lys Ile Leu Lys Ser His Ala Asn Asp His Lys Arg Gly Ser Phe
  275           280           285
Phe Phe Lys Unk Arg Phe Arg Gly Phe Lys Asn Ser
  290           295           300

```

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398

```

Met Lys Glu Lys Asn Phe Trp Pro Leu Gly Ile Met Ser Val Leu Ile
1           5           10           15
Phe Gly Leu Gly Ile Val Val Phe Leu Val Val Phe Ala Leu Lys Asn
  20           25           30
Ser Pro Lys Asn Asp Leu Val Tyr Phe Lys Gly His Asn Glu Val Asp
  35           40           45
Leu Asn Phe Asn Ala Met Leu Lys Thr Tyr Glu Asn Phe Lys Ser Asn
  50           55           60
Tyr Arg Phe Ser Val Gly Leu Lys Pro Leu Thr Glu Ser Pro Lys Thr

```

SUBSTITUTE SHEET (RULE 26)

333

```

65          70          75          80
Pro Ile Leu Pro Tyr Phe Ser Lys Gly Thr His Gly Asp Lys Lys Ile
      85          90          95
Gln Glu Asn Leu Leu Asn Asn Ala Leu Ile Leu Glu Lys Ser Asn Thr
      100         105         110
Leu Tyr Ala Gln Leu Gln Pro Leu Lys Pro Ala Leu Asp Ser Pro Asn
      115         120         125
Ile Gln Val Tyr Leu Ala Phe Tyr Pro Ser Gln Ser Gln Pro Arg Leu
      130         135         140
Leu Gly Thr Leu Asp Cys Lys Asn Ala Cys Glu Pro Leu Lys Phe Asp
      145         150         155         160
Leu Leu Glu Gly Asp Lys Val Gly Arg Tyr Lys Ile Leu Phe Lys Phe
      165         170         175
Val Phe Lys Asn Lys Glu Glu Leu Ile Leu Glu Gln Leu Leu Phe Leu
      180         185         190
Ser Ser Met Ala Cys Met Gly Ile Ser Ile Leu Lys Asn Ala Lys Ala
      195         200         205
Phe Phe Lys Tyr Lys Ile
      210

```

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399

```

Met Pro Ile Lys Gly Ser Phe Leu Ala Arg Asn Arg Leu Val Ile Ala
1          5          10          15
Leu Thr Asp Ala Val Ile Ile Pro Gln Ala Asp Leu Lys Ser Gly Ser
      20         25         30
Met Ser Ser Ala Arg Leu Ala Gln Lys Tyr Gln Lys Pro Leu Phe Val
      35         40         45
Leu Pro Gln Arg Leu Asn Glu Ser Asp Gly Thr Asn Glu Leu Leu Glu
      50         55         60
Lys Gly Gln Ala Gln Gly Ile Phe Asn Ile Gln Asn Phe Ile Asn Thr
      65         70         75         80
Leu Leu Lys Asp Tyr His Leu Lys Glu Met Pro Glu Met Lys Asp Glu
      85         90         95
Phe Leu Glu Tyr Cys Ala Lys Asn Pro Ser Tyr Glu Glu Ala Tyr Leu
      100        105        110
Lys Phe Gly Asp Lys Leu Leu Glu Tyr Glu Leu Leu Gly Lys Ile Lys
      115        120        125
Arg Ile Asn His Leu Val Val Leu Ala
      130        135

```

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 amino acids

334

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400

```

Met Val Val Glu Leu Lys Asn Ile Glu Lys Ile Tyr Glu Asn Gly Phe
 1           5           10           15
His Ala Leu Lys Gly Val Asn Leu Glu Lys Lys Gly Asp Ile Leu
 20           25           30
Gly Val Ile Gly Tyr Ser Gly Ala Gly Lys Ser Thr Leu Ile Arg Leu
 35           40           45
Ile Asn Cys Leu Glu Arg Pro Ser Ser Gly Glu Val Leu Val Asn Gly
 50           55           60
Val Asn Leu Leu Asn Leu Lys Pro Lys Glu Leu Gln Lys Ala Arg Gln
 65           70           75           80
Lys Ile Gly Met Ile Phe Gln His Phe Asn Leu Leu Ser Ala Lys Asn
 85           90           95
Val Phe Glu Asn Val Ala Phe Ala Leu Glu Ile Ala Arg Trp Glu Lys
100           105           110
Thr Lys Ile Lys Ser Arg Val His Glu Leu Leu Glu Leu Val Gly Leu
115           120           125
Glu Asp Lys Val His Phe Tyr Pro Lys Gln Leu Ser Gly Gly Gln Lys
130           135           140
Gln Arg Val Ala Ile Ala Arg Ser Leu Ala Asn Cys Pro Asn Leu Leu
145           150           155           160
Leu Cys Asp Glu Ala Thr Ser Ala Leu Asp Ser Lys Thr Thr His Ser
165           170           175
Ile Leu Thr Leu Leu Ser Gly Ile Gln Lys Lys Phe Asp Leu Ser Ile
180           185           190
Val Phe Ile Thr His Gln Ile Glu Val Val Lys Glu Leu Cys Asn Gln
195           200           205
Met Cys Val Ile Ser Ser Gly Glu Ile Val Glu Arg Gly Ser Val Glu
210           215           220
Glu Ile Phe Ala Asn Pro Lys His Ala Val Thr Lys Glu Leu Leu Gly
225           230           235           240
Ile Lys Asn Glu His Ala Asp Gln Lys Ser Gln Asp Ile Tyr Arg Ile
245           250           255
Val Phe Leu Gly Glu His Leu Asp Glu Pro Ile Ile Ser Unk Phe Unk
260           265           270

```

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 286 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

SUBSTITUTE SHEET (RULE 26)

335

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401

```

Leu Unk Pro Met Lys Val Ile Gln Val Phe Leu Phe Ser Asn Pro Phe
1          5          10          15
Cys Ala Ile Val Pro Asn Thr Glu Pro Glu His Leu Glu His Tyr Asp
          20          25          30
His Asp Leu Glu Arg Phe Phe Phe Ala Tyr Lys Tyr Phe Leu Asp His
          35          40          45
Ala Gln Lys Arg Val Ile Tyr Lys Glu Asp Pro Phe Leu Lys Asn Tyr
          50          55          60
Ser Lys Asp Ala Ile Val Leu Glu Lys Lys Asp Ile Tyr Asn Ile Gln
65          70          75          80
Tyr Ile Leu Lys Asp Gly Glu Pro Tyr Thr Ser Phe Glu Leu Lys Asn
          85          90          95
Leu Gly Ala Phe Leu Val Trp Gly Leu Gly Glu His Asn Ala Thr Asn
          100          105          110
Ala Ser Leu Ala Ile Leu Ser Ala Leu Asp Glu Leu Asn Leu Glu Glu
          115          120          125
Ile Arg Asn Asn Unk Leu Asn Phe Lys Gly Ile Lys Lys Arg Phe Asp
130          135          140
Ile Leu Gln Lys Asn Asn Leu Ile Leu Ile Asp Asp Tyr Ala His His
145          150          155          160
Pro Thr Glu Ile Gly Unk Thr Leu Lys Ser Ala Arg Ile Tyr Ala Asn
          165          170          175
Leu Leu Asn Thr Gln Glu Lys Ile Ile Val Ile Trp Gln Ala His Lys
          180          185          190
Tyr Ser Arg Leu Met Asp Asn Leu Glu Glu Phe Lys Lys Cys Phe Leu
          195          200          205
Glu His Cys Asp Arg Leu Ile Ile Leu Pro Val Tyr Ser Ala Ser Glu
210          215          220
Val Lys Arg Asp Ile Asp Leu Lys Ala His Phe Lys His Tyr Asn Pro
225          230          235          240
Thr Phe Ile Asp Arg Val Arg Lys Lys Gly Asp Phe Leu Glu Leu Leu
          245          250          255
Val Asn Asp Asn Val Val Glu Thr Ile Glu Lys Gly Phe Val Ile Gly
          260          265          270
Phe Gly Ala Gly Asp Ile Thr Tyr Gln Leu Arg Gly Glu Met
          275          280          285

```

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401

336

```

Leu Unk Pro Met Lys Val Ile Gln Val Phe Leu Phe Ser Asn Pro Phe
1      5      10      15
Cys Ala Ile Val Pro Asn Thr Glu Pro Glu His Leu Glu His Tyr Asp
      20      25      30
His Asp Leu Glu Arg Phe Phe Phe Ala Tyr Lys Tyr Phe Leu Asp His
      35      40      45
Ala Gln Lys Arg Val Ile Tyr Lys Glu Asp Pro Phe Leu Lys Asn Tyr
      50      55      60
Ser Lys Asp Ala Ile Val Leu Glu Lys Lys Asp Ile Tyr Asn Ile Gln
65      70      75      80
Tyr Ile Leu Lys Asp Gly Glu Pro Tyr Thr Ser Phe Glu Leu Lys Asn
      85      90      95
Leu Gly Ala Phe Leu Val Trp Gly Leu Gly Glu His Asn Ala Thr Asn
      100      105      110
Ala Ser Leu Ala Ile Leu Ser Ala Leu Asp Glu Leu Asn Leu Glu Glu
      115      120      125
Ile Arg Asn Asn Unk Leu Asn Phe Lys Gly Ile Lys Lys Arg Phe Asp
130      135      140
Ile Leu Gln Lys Asn Asn Leu Ile Leu Ile Asp Asp Tyr Ala His His
145      150      155      160
Pro Thr Glu Ile Gly Unk Thr Leu Lys Ser Ala Arg Ile Tyr Ala Asn
      165      170      175
Leu Leu Asn Thr Gln Glu Lys Ile Ile Val Ile Trp Gln Ala His Lys
      180      185      190
Tyr Ser Arg Leu Met Asp Asn Leu Glu Glu Phe Lys Lys Cys Phe Leu
195      200      205
Glu His Cys Asp Arg Leu Ile Ile Leu Pro Val Tyr Ser Ala Ser Glu
210      215      220
Val Lys Arg Asp Ile Asp Leu Lys Ala His Phe Lys His Tyr Asn Pro
225      230      235      240
Thr Phe Ile Asp Arg Val Arg Lys Lys Gly Asp Phe Leu Glu Leu Leu
      245      250      255
Val Asn Asp Asn Val Val Glu Thr Ile Glu Lys Gly Phe Val Ile Gly
      260      265      270
Phe Gly Ala Gly Asp Ile Thr Tyr Gln Leu Arg Gly Glu Met
275      280      285

```

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402

```

Met Gly Ala Leu Ile Ala Met Phe Phe Leu Met Leu Ile Lys Lys Thr
1      5      10      15
Ile Ala Tyr Lys Glu Asp Lys Lys Ser Ala Ala Leu Lys Val Val Pro
      20      25      30
Tyr Leu Val Ala Leu Met Ser Leu Ala Phe Ser Trp Tyr Leu Ile Val
      35      40      45
Lys Val Leu Lys Arg Leu Tyr Ala Val Ser Phe Glu Ile Gln Leu Ala

```

SUBSTITUTE SHEET (RULE 26)

337

```

      50              55              60
Cys Gly Cys Val Leu Ala Leu Leu Ile Phe Ile Leu Phe Lys Arg Phe
65              70              75              80
Val Leu Lys Lys Ala Pro Gln Leu Glu Asn Ser His Glu Ser Val Asn
      85              90              95
Glu Leu Phe Asn Val Pro Leu Ile Phe Ala
      100              105

```

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403

```

Met Ile Lys Arg Ile Ala Cys Ile Leu Ser Leu Ser Ala Ser Leu Ala
1              5              10              15
Leu Ala Gly Glu Val Asn Gly Phe Phe Met Gly Ala Gly Tyr Gln Gln
      20              25              30
Gly Arg Tyr Gly Pro Tyr Asn Ser Asn Tyr Ser Asp Trp Arg His Gly
      35              40              45
Asn Asp Leu Tyr Gly Leu Asn Phe Lys Leu Gly Phe Val Gly Phe Ala
      50              55              60
Asn Lys Trp Phe Gly Ala Arg Val Tyr Gly Phe Leu Asp Trp Phe Asn
      65              70              75              80
Thr Ser Gly Thr Glu His Thr Lys Thr Asn Leu Leu Thr Tyr Gly Gly
      85              90              95
Gly Gly Asp Leu Ile Val Asn Leu Ile Pro Leu Asp Lys Phe Ala Leu
      100              105              110
Gly Leu Ile Gly Gly Val Gln Leu Ala Gly Asn Thr Trp Met Phe Pro
      115              120              125
Tyr Asp Val Asn Gln Thr Arg Phe Gln Phe Leu Trp Asn Leu Gly Gly
      130              135              140
Arg Met Arg Val Gly Asp Thr Val Arg Leu Lys Arg Ala
      145              150              155

```

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 278 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

338

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404

```

Met Tyr Arg His Val Leu Lys Asp Phe Ser Leu Asp Phe Ser Lys Glu
1          5          10          15
Ser Val Gln Glu Leu Phe Asn Gln Leu Ala Lys Asp Thr Phe Leu Leu
20          25          30
Leu Leu Pro Val Leu Ile Ile Leu Met Val Val Ala Phe Leu Ser Asn
35          40          45
Val Leu Gln Phe Gly Trp Leu Phe Ala Pro Lys Val Ile Glu Pro Lys
50          55          60
Phe Ser Lys Ile Asn Pro Ile Asn Gly Val Lys Asn Leu Phe Ser Leu
65          70          75          80
Lys Lys Ile Leu Asp Gly Ser Leu Ile Thr Leu Lys Val Phe Leu Ala
85          90          95
Phe Phe Leu Gly Phe Phe Ile Phe Ser Leu Phe Leu Gly Glu Leu Asn
100         105         110
His Ala Ala Leu Leu Asn Leu Gln Gly Gln Leu Leu Trp Phe Lys Ser
115         120         125
Lys Ala Leu Trp Leu Ile Ser Ser Leu Leu Phe Leu Phe Phe Val Leu
130         135         140
Ala Phe Val Asp Leu Ile Ile Lys Arg Arg Gln Tyr Thr Asn Ser Leu
145         150         155         160
Lys Met Thr Lys Gln Glu Val Lys Asp Glu Tyr Lys Gln Gln Glu Gly
165         170         175
Asn Pro Glu Ile Lys Ala Lys Ile Arg Gln Met Met Val Lys Asn Ala
180         185         190
Thr Asn Lys Met Met Gln Glu Ile Pro Lys Ser Asn Val Val Val Thr
195         200         205
Asn Pro Thr His Tyr Ala Val Ala Leu Lys Phe Asp Glu Glu His Pro
210         215         220
Val Pro Val Val Val Ala Lys Gly Thr Asp Tyr Leu Ala Ile Arg Ile
225         230         235         240
Lys Gly Ile Ala Arg Glu His Asp Ile Glu Ile Ile Glu Asn Lys Thr
245         250         255
Leu Ala Arg Glu Leu Tyr Arg Asp Val Lys Leu Asn Ala Thr Ile Pro
260         265         270
Glu Glu Leu Phe Glu Arg
275

```

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405

Met Asn Thr Unk Pro Leu Ile Ala Thr Leu Leu Gln Ala Pro Leu His

SUBSTITUTE SHEET (RULE 26)

339

```

1           5           10           15
Val Leu Gly Ile Arg Glu Pro Val Ser Phe Gln Pro Phe Tyr Pro Lys
                20           25           30
Thr Glu Lys Pro Asn Arg Pro Gln Lys Phe Ala His Val Ser Ser Met
                35           40           45
Pro Ser Leu Glu Phe Leu Glu Lys Leu Val Ile Arg Tyr Leu Leu Glu
                50           55           60
Asp Arg Ser Leu Leu Asp Leu Ala Val Gly Tyr Ile His Ser Gly Val
65           70           75           80
Phe Leu His Lys Lys Gln Glu Phe Asp Ala Leu Cys Gln Glu Lys Leu
                85           90           95
Asp Asp Pro Lys Leu Val Ala Leu Leu Leu Asp Ala Asn Leu Pro Leu
                100           105           110
Lys Lys Gly Gly Phe Glu Lys Glu
                115           120

```

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406

```

Met Gly Gln Ala Phe Phe Lys Lys Ile Val Gly Cys Phe Cys Leu Gly
1           5           10           15
Tyr Leu Phe Leu Ser Ser Ala Ile Glu Ala Val Ala Leu Asp Ile Lys
                20           25           30
Asn Phe Asn Arg Gly Arg Val Lys Val Val Asn Lys Lys Ile Ala Tyr
                35           40           45
Leu Gly Asp Glu Lys Pro Ile Thr Ile Trp Thr Ser Leu Asp Asn Val
                50           55           60
Thr Val Ile Gln Leu Glu Lys Asp Glu Thr Ile Ser Tyr Ile Thr Thr
65           70           75           80
Gly Phe Asn Lys Gly Trp Ser Ile Val Pro Asn Ser Asn His Ile Phe
                85           90           95
Ile Gln Pro Lys Ser Val Lys Ser Asn Leu Met Phe Glu Lys Glu Ala
                100           105           110
Val Asn Phe Ala Leu Met Thr Arg Asp Tyr Gln Glu Phe Leu Lys Thr
                115           120           125
Lys Lys Leu Ile Val Asp Ala Pro Asp Pro Lys Glu Leu Glu Glu Gln
130           135           140
Lys Lys Ala Leu Glu Lys Glu Lys Glu Ala Lys Glu Gln Ala Gln Lys
145           150           155           160
Ala Gln Lys Asp Lys Arg Glu Lys Arg Lys Glu Glu Arg Ala Lys Asn
                165           170           175
Arg Ala Asn Leu Glu Asn Leu Thr Asn Ala Met Ser Asn Pro Gln Asn
                180           185           190
Leu Ser Asn Asn Lys Asn Leu Ser Glu Leu Ile Lys Gln Gln Arg Glu
                195           200           205
Asn Glu Leu Asp Gln Met Glu Arg Thr Arg Gly His Ala Arg Ala Gly
210           215           220

```

SUBSTITUTE SHEET (RULE 26)

340

Ser Ser
225

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407

Leu	Leu	Leu	Phe	Phe	Leu	Leu	Lys	Gly	Val	Val	Phe	Ser	Leu	Gly	Phe
1				5					10					15	
Phe	Ser	Phe	Phe	Glu	Glu	Val	Ser	Gly	Ser	Phe	Unk	Ala	Val	Ser	Leu
			20					25				30			
Unk	Val	Leu	Ala	Leu	Val	Met	Gly	Ser	Ser	Unk	Gly	Leu	Glu	Glu	Phe
		35					40				45				
Cys	Val	Leu	Glu	Glu	Leu	Ile	Asn	Ser	Gly	Leu	Ser	Val			
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407

Leu	Leu	Leu	Phe	Phe	Leu	Leu	Lys	Gly	Val	Val	Phe	Ser	Leu	Gly	Phe
1				5					10					15	
Phe	Ser	Phe	Phe	Glu	Glu	Val	Ser	Gly	Ser	Phe	Unk	Ala	Val	Ser	Leu
			20					25				30			
Unk	Val	Leu	Ala	Leu	Val	Met	Gly	Ser	Ser	Unk	Gly	Leu	Glu	Glu	Phe
		35					40				45				
Cys	Val	Leu	Glu	Glu	Leu	Ile	Asn	Ser	Gly	Leu	Ser	Val			
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:408:

SUBSTITUTE SHEET (RULE 26)

341

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408

```

Met Asn Thr Glu Ile Leu Thr Ile Met Leu Val Val Ser Val Leu Met
1           5           10           15
Gly Leu Val Gly Leu Ile Ala Phe Leu Trp Gly Val Lys Ser Gly Gln
20           25           30
Phe Asp Asp Glu Lys Arg Met Leu Glu Ser Val Leu Tyr Asp Ala Arg
35           40           45
Ala Thr
50

```

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409

```

Met Gly Phe Leu Lys Val Leu Lys His Asp Ala Leu Gly Gln Val Gly
1           5           10           15
Asn Ile Val Ile Gly Asn Phe Leu Ile Thr Leu Thr Val Leu Ala Val
20           25           30
Cys Phe Ser Ser Gln Ser Ala Glu Glu Thr Thr Met Leu Thr Leu Ser
35           40           45
Tyr Thr Leu Phe Phe Ile Leu Gly Ala Phe Leu Leu Val Ala Ile Ser
50           55           60
Val Gly Ala Ile Lys Asn Leu Asn Ala Leu Phe Ser Lys Arg Gly Val
65           70           75           80
Leu Ser Phe Ser Leu Pro Ile Ser Leu Glu Ser Leu Leu Leu Pro Lys
85           90           95
Ile Leu Leu Pro Unk Val Phe Phe Tyr Leu Gln Phe Val Leu Val Cys
100          105          110
Gly Glu Arg Ala Phe Gly Leu Leu Pro Phe
115          120

```

SUBSTITUTE SHEET (RULE 26)

342

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409

```

Met Gly Phe Leu Lys Val Leu Lys His Asp Ala Leu Gly Gln Val Gly
1      5      10      15
Asn Ile Val Ile Gly Asn Phe Leu Ile Thr Leu Thr Val Leu Ala Val
20     25     30
Cys Phe Ser Ser Gln Ser Ala Glu Glu Thr Thr Met Leu Thr Leu Ser
35     40     45
Tyr Thr Leu Phe Phe Ile Leu Gly Ala Phe Leu Leu Val Ala Ile Ser
50     55     60
Val Gly Ala Ile Lys Asn Leu Asn Ala Leu Phe Ser Lys Arg Gly Val
65     70     75     80
Leu Ser Phe Ser Leu Pro Ile Ser Leu Glu Ser Leu Leu Leu Pro Lys
85     90     95
Ile Leu Leu Pro Unk Val Phe Phe Tyr Leu Gln Phe Val Leu Val Cys
100    105    110
Gly Glu Arg Ala Phe Gly Leu Leu Pro Phe
115    120

```

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410

```

Met Leu Lys Thr His Leu Ser Ser Ala Arg Gly Val Val Val Leu Ser
1      5      10      15
Lys Ile Leu Pro Val Asn Val Val Leu Met Val Ser Val Arg Leu Phe
20     25     30
Glu Lys Glu Leu Lys Arg Lys Pro Tyr Tyr Ile Ile Ala Ser Ala His

```

SUBSTITUTE SHEET (RULE 26)

343

```

      35              40              45
Ser Asp Glu Gly Leu Glu Lys Leu Lys Lys Unk Gly Unk Asp Met Val
  50              55              60
Unk Unk Pro Thr Lys Leu Met Ala Gln Arg Val Ser Ala Asn Unk Trp
  65              70              75
Cys Unk Leu Asp Met Glu Asn Ile Leu Glu Arg Phe Ile Asn Lys Lys
      85              90              95
Asp Thr Leu Leu Asp Leu Glu Glu Val Ile Val Pro Lys Thr Ser Trp
      100              105              110
Leu Val Leu Arg Lys Leu Lys Glu Ala His Phe Arg Glu Ile Ala Lys
      115              120              125
Ala Phe Val Ile Gly Ile Thr Gln Lys Asp Gly Lys Tyr Ile Pro Met
      130              135              140
Pro Asp Gly Glu Thr Ile Ile Ala Ser Glu Ser Lys Leu Leu Met Val
      145              150              155
Gly Thr Ser Glu Gly Val Ala Thr Cys Lys Gln Leu Ile Thr Ser His
      165              170              175
Gln Lys Pro Lys Glu Val Asp Tyr Ile Ser Leu
      180              185

```

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410

```

Met Leu Lys Thr His Leu Ser Ser Ala Arg Gly Val Val Val Leu Ser
  1              5              10              15
Lys Ile Leu Pro Val Asn Val Val Leu Met Val Ser Val Arg Leu Phe
      20              25              30
Glu Lys Glu Leu Lys Arg Lys Pro Tyr Tyr Ile Ile Ala Ser Ala His
      35              40              45
Ser Asp Glu Gly Leu Glu Lys Leu Lys Lys Unk Gly Unk Asp Met Val
      50              55              60
Unk Unk Pro Thr Lys Leu Met Ala Gln Arg Val Ser Ala Asn Unk Trp
      65              70              75
Cys Unk Leu Asp Met Glu Asn Ile Leu Glu Arg Phe Ile Asn Lys Lys
      85              90              95
Asp Thr Leu Leu Asp Leu Glu Glu Val Ile Val Pro Lys Thr Ser Trp
      100              105              110
Leu Val Leu Arg Lys Leu Lys Glu Ala His Phe Arg Glu Ile Ala Lys
      115              120              125
Ala Phe Val Ile Gly Ile Thr Gln Lys Asp Gly Lys Tyr Ile Pro Met
      130              135              140
Pro Asp Gly Glu Thr Ile Ile Ala Ser Glu Ser Lys Leu Leu Met Val
      145              150              155
Gly Thr Ser Glu Gly Val Ala Thr Cys Lys Gln Leu Ile Thr Ser His
      165              170              175
Gln Lys Pro Lys Glu Val Asp Tyr Ile Ser Leu
      180              185

```

SUBSTITUTE SHEET (RULE 26)

344

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411

```

Met Phe Val Ala Ala Gly Leu Gly Ala Tyr Ala Ile Ala Leu Phe His
1          5          10          15
Leu Phe Thr His Ala Phe Phe Lys Ser Leu Leu Phe Leu Gly Ser Gly
          20          25          30
Asn Val Met His Ala Met Glu Asp Asn Leu Asp Ile Thr Lys Met Gly
          35          40          45
Ala Leu Tyr Lys Pro Met Arg Ile Thr Ala Val Phe Met Ile Ile Gly
          50          55          60
Ser Val Ala Leu Cys Gly Ile Tyr Pro Phe Ala Gly Tyr Phe Ser Lys
          65          70          75          80
Asp Lys Ile Leu Glu Val Ala Phe Gly Met His His His Ile Leu Trp
          85          90          95
Phe Val Leu Leu Ile Gly Ala Ile Phe Thr Ala Phe Tyr Ser Phe Arg
          100          105          110
Leu Ile Met Leu Val Phe Phe Ala Pro Lys Gln His Glu Ile Asn His
          115          120          125
Pro Pro
          130

```

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412

```

Met Phe Ile Ser Ser Ser Tyr Thr Leu Ser Phe Val Trp Leu Phe Leu
1          5          10          15
Ile Phe Phe Phe Phe Lys Asn Lys Pro Leu Gly Leu Arg Phe Ser Leu

```

SUBSTITUTE SHEET (RULE 26)

345

```

      20      25      30
Ser Leu Ile Ser Val Ile Leu Ser Asn Ile Ala Leu Lys Asp Ser Leu
  35      40      45
Ser Leu Asn Glu Phe Leu Ser Ser Phe Thr Ala Pro Leu Ser Pro Phe
  50      55      60
Ser Cys Leu Leu Ile Leu Ala Tyr Ala Ser Phe Ser Cys His Ile Leu
  65      70      75      80
Lys Lys Pro Pro Leu Glu Thr Leu Gln Ser Tyr Ser Val Met Leu Phe
      85      90      95
Phe Asn Leu Leu Leu Leu Thr Asp Ile Leu Gly Phe Leu Pro Phe Ser
      100      105      110
Ile Tyr His His Phe Met Ala Ser Leu Ile Phe Ser Ala Leu Phe Cys
      115      120      125
Ser Ser Leu Phe Leu Ser Ser Pro Leu Leu Gly Val Ile Ala Leu Val
      130      135      140
Ala Leu Ser Ser Ser Leu Leu Met Arg Ser Asn Phe Gln Ile Leu Asp
      145      150      155      160
Ser Leu Leu Asp Phe Pro Leu Phe Leu Phe Val Phe Phe Lys Thr Leu
      165      170      175
Tyr Leu Ala Lys Lys Arg Leu
      180

```

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413

```

Val Gly Ser Phe Leu Phe Val Gly Pro Ser Gly Val Gly Lys Thr Glu
1      5      10      15
Leu Ala Lys Glu Leu Ala Leu Asn Leu Unk Leu His Phe Glu Arg Phe
  20      25      30
Asp Met Ser Glu Tyr Lys Glu Ala His Ser Val Ala Lys Leu Ile Gly
  35      40      45
Ser Pro Ser Gly Tyr Val Gly Phe Glu Gln Gly Gly Leu Leu Val Asn
  50      55      60
Ala Ile Lys Lys His Pro His Cys Leu Leu Leu Leu Asp Glu Ile Glu
  65      70      75      80
Lys Ala His Pro Asn Val Tyr Asp Leu Leu Leu Gln Val Met Unk Asn
      85      90      95
Ala Thr Leu Ser Asp Asn Leu Gly Asn Lys Ala Ser Phe Lys His Val
      100      105      110
Ile Leu Ile Met Thr Unk Unk Val Gly Ser Lys Asp Lys Asp Thr Leu
      115      120      125
Gly Phe Phe Ser Thr Lys Asn Ala Lys Tyr Asp Arg Ala Val Lys Glu
      130      135      140
Leu Leu Thr Pro Glu Leu Arg Ser Arg Ile Asp Ala Ile Val Pro Phe
      145      150      155      160
Asn Ala Leu Ser Leu Glu Asp Phe Glu Thr His Cys Phe Cys Gly Ile
      165      170      175

```

SUBSTITUTE SHEET (RULE 26)

346

Gly Arg Val Lys Ser Pro Ser Thr Arg Ala Arg Arg Asp Leu Lys Ile
 180 185 190
 Pro

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413

Val Gly Ser Phe Leu Phe Val Gly Pro Ser Gly Val Gly Lys Thr Glu
 1 5 10 15
 Leu Ala Lys Glu Leu Ala Leu Asn Leu Unk Leu His Phe Glu Arg Phe
 20 25 30
 Asp Met Ser Glu Tyr Lys Glu Ala His Ser Val Ala Lys Leu Ile Gly
 35 40 45
 Ser Pro Ser Gly Tyr Val Gly Phe Glu Gln Gly Gly Leu Leu Val Asn
 50 55 60
 Ala Ile Lys Lys His Pro His Cys Leu Leu Leu Asp Glu Ile Glu
 65 70 75 80
 Lys Ala His Pro Asn Val Tyr Asp Leu Leu Leu Gln Val Met Unk Asn
 85 90 95
 Ala Thr Leu Ser Asp Asn Leu Gly Asn Lys Ala Ser Phe Lys His Val
 100 105 110
 Ile Leu Ile Met Thr Unk Unk Val Gly Ser Lys Asp Lys Asp Thr Leu
 115 120 125
 Gly Phe Phe Ser Thr Lys Asn Ala Lys Tyr Asp Arg Ala Val Lys Glu
 130 135 140
 Leu Leu Thr Pro Glu Leu Arg Ser Arg Ile Asp Ala Ile Val Pro Phe
 145 150 155 160
 Asn Ala Leu Ser Leu Glu Asp Phe Glu Thr His Cys Phe Cys Gly Ile
 165 170 175
 Gly Arg Val Lys Ser Pro Ser Thr Arg Ala Arg Arg Asp Leu Lys Ile
 180 185 190
 Pro

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

SUBSTITUTE SHEET (RULE 26)

347

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414

```

Met Arg Leu Asp Tyr Ala Leu Phe Asn Gln His Leu Ala Asn Ser Arg
1      5      10      15
Glu Lys Ala Lys Ala Leu Val Leu Lys Lys Gln Val Leu Val Asn Lys
20     25     30
Met Val Val Ser Lys Pro Ser Phe Ile Val Lys Glu Gly Asp Gln Ile
35     40     45
Glu Leu Ile Ala Pro Asn Leu Phe Val Ser Arg Ala Gly Glu Lys Leu
50     55     60
Gly Ala Phe Leu Glu Asp His Phe Ile Asp Phe Lys Glu Lys Val Val
65     70     75     80
Leu Asp Val Gly Ala Ser Lys Gly Gly Phe Ser Gln Val Ala Leu Leu
85     90     95
Lys Gly Ala Lys Lys Val Leu Cys Val Asp Val Gly Lys Met Gln Leu
100    105    110
Asp Glu Ser Leu Lys Asn Asp Gln Arg Ile Glu Cys Tyr Glu Glu Cys
115    120    125
Asp Ile Arg Gly Phe Lys Thr Pro Glu Lys Ile Asp Leu Ala Leu Cys
130    135    140
Asp Val Ser Phe Ile Ser Leu Tyr Cys Ile Leu Glu Ala Ile Leu Pro
145    150    155    160
Leu Ser Gly Glu Phe Leu Thr Leu Phe Lys Pro Gln Phe Glu Val Gly
165    170    175
Arg Thr Ile Lys Arg Asn Lys Lys Gly Val Val Met Asp Lys Glu Ala
180    185    190
Ile Leu Asn Ala Leu Glu Asn Phe Lys Asn His Leu Lys Thr Lys Asp
195    200    205
Phe Gln Ile Leu Thr Ile Gln Glu Ser Leu Val Lys Gly Lys Asn Gly
210    215    220
Asn Val Glu Phe Phe Ile His Phe Lys Arg Ala
225    230    235

```

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...88

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415

```

Met Ser Leu Pro Pro Val Cys Ile Leu Lys Asp Val Asn His Leu Leu
1      5      10      15
Gln Val Leu His Ser Leu Val Ala Leu Gly Asn Ser Met Leu Val Ile
20     25     30

```

SUBSTITUTE SHEET (RULE 26)

348

Glu His Asn Leu Asp Ile Ile Lys Asn Ala Asp Tyr Ile Ile Asp Met
 35 40 45
 Gly Pro Asp Gly Gly Asp Lys Gly Gly Lys Val Ile Ala Ser Gly Thr
 50 55 60
 Pro Leu Glu Val Ala Gln Asn Cys Glu Lys Thr Gln Ser Tyr Thr Gly
 65 70 75 80
 Lys Phe Leu Ala Leu Glu Leu Lys
 85

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416

Met Gln Asn Arg Ser His Glu Ile Gln Gly Val Ser His Ile Lys Asn
 1 5 10 15
 Asn Tyr Lys Phe Phe Thr Lys Glu Leu Asp Asn Tyr Ile Ser Lys Gly
 20 25 30
 Tyr Arg Ile Glu Glu Ile Tyr Gly Ala Phe Leu Trp Leu Lys Ile Val
 35 40 45
 Ala Ile Gly Leu Glu Leu Gly Glu Asp Asp Pro Gln Val Val Phe Glu
 50 55 60
 Ser Ile Asn Ala Thr Gly Val Gln Leu Lys Gly Leu Asp Leu Ile Arg
 65 70 75 80
 Asn Tyr Leu Met Met Gly Glu Asn Unk Asp Asn Gln Asn Arg Leu Tyr
 85 90 95
 Asn Thr Tyr Trp Val Pro Leu Glu Asn Trp Leu Gly Glu
 100 105

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417

SUBSTITUTE SHEET (RULE 26)

349

```

Met Asp Thr Ile Lys Ser Ile Pro Ile Arg Thr Phe Ile Leu Leu Tyr
1      5      10      15
Lys Ser Ser Pro Lys Cys Val Val Leu Ala Ser Ile Thr Val Leu Phe
      20      25      30
Val Gly Ile Leu Unk Ser Leu Asn Ile Leu Val Met Ile Lys Leu Ile
      35      40      45
Asp Ile Val Val Asn Leu Leu Gln Lys His Thr His Phe Glu Tyr Ser
      50      55      60
Leu Leu Leu Pro Thr Leu Leu Trp Gly Ala Leu Leu Phe Leu Thr
65      70      75      80
His Val Phe Ser Gly Asn Phe Ile Lys Leu Ala Asn His Tyr Cys Arg
      85      90      95
Thr Ile Phe Tyr Lys Tyr His His Ser Ala Cys
      100      105

```

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418

```

Met Ile Phe Tyr Thr Thr Ile Lys Glu Pro Leu Lys Asn Leu Gln Tyr
1      5      10      15
Arg Tyr Ala Gln Phe Phe Gly Lys Ile Lys Pro Cys Ser Phe Leu Glu
      20      25      30
Ser Leu Lys Ser Cys Phe Phe Gln Thr Tyr Ser Phe Ser Leu Thr Arg
      35      40      45
Lys Gln Asp Phe Lys Ser His Leu Arg His Phe Ile Asp Ser Ala His
      50      55      60
Ser Asn Ala Leu Val Gly Asn Leu Tyr Arg Ala Leu Phe Ile Gly Asp
65      70      75      80
Ser Leu Asn Lys Asp Leu Arg Asp Arg Ala Asn Ala Leu Gly Ile Asn
      85      90      95
His Leu Leu Ala Ile Ser Gly Phe His Leu Gly Ile Leu Ser Ala Ser
      100      105      110
Val Tyr Phe Leu Phe Ser Leu Phe Tyr Thr Pro Leu Gln Lys Arg Tyr
      115      120      125
Phe Pro Tyr Arg Asn Ala Phe Unk
      130      135

```

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

350

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...54

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419

```

Met Asn Lys Pro Phe Leu Ile Leu Leu Ile Ala Leu Ile Ala Phe Ser
1          5          10          15
Gly Cys Asn Met Arg Lys Tyr Phe Lys Pro Ala Lys His Gln Ile Lys
          20          25          30
Ala Lys Arg Ile Ser Leu Thr Ile Cys Lys Lys Ala Ser Phe Arg Leu
          35          40          45
Ile Val Met Glu Pro Phe
          50

```

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420

```

Met Ala Ala Trp Asn Thr Leu Val Glu Lys Ile Ile Ala Pro Lys His
1          5          10          15
Lys Val Lys Ile Gly Phe Val Gly Lys Tyr Leu Ser Leu Lys Glu Ser
          20          25          30
Tyr Lys Ser Leu Ile Glu Ala Leu Ile His Ala Gly Ala His Leu Asp
          35          40          45
Thr Gln Val Asn Ile Glu Trp Leu Asp Ser Glu Asn Phe Asn Glu Lys
          50          55          60
Thr Asp Leu Glu Gly Val Asp Ala Ile Leu Val Pro Gly Gly Phe Gly
          65          70          75          80
Glu Arg Gly Ile Glu Gly Lys Ile Cys Ala Ile Gln Arg Ala Arg Leu
          85          90          95
Glu Lys Leu Pro Phe Leu Gly Ile Cys Leu Gly Met Gln Leu Ala Ile
          100          105          110
Val Glu Phe Cys Arg Lys Cys Phe Arg Leu Glu Arg Gly
          115          120          125

```

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 amino acids

(B) TYPE: amino acid

SUBSTITUTE SHEET (RULE 26)

351

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421

```

Met Thr Lys Ala Phe Val Pro Leu Ser Leu Leu Val Ser Ala Ile Leu
1      5      10      15
Leu Ala Phe Ser Leu Ile Leu Ile Pro Thr Ser Lys Ser Ala Tyr Tyr
20      25      30
Gly Phe Leu Arg Gln Lys Lys Asp Lys Ile Asp Ile Asn Ile Arg Ala
35      40      45
Gly Glu Phe Gly Gln Lys Leu Gly Asp Trp Leu Val Tyr Val Asp Lys
50      55      60
Thr Glu Asn Asn Ser Tyr Asp Asn Leu Val Leu Phe Ser Asn Lys Ser
65      70      75      80
Leu Ser Gln Glu Ser Phe Ile Leu Ala Gln Lys Gly Asn Ile Asn Asn
85      90      95
Gln Asn Gly Val Phe Glu Leu Asn Leu Tyr Asn Gly His Ala Tyr Phe
100     105     110
Thr Gln Gly Asp Lys Met Arg Lys Val Asp Phe Glu Glu Leu His Leu
115     120     125
Arg Asn Lys Leu Lys Ser Phe Asn Ser Asn Asp Ala Ala Tyr Leu Gln
130     135     140
Gly Thr Asp Tyr Leu Gly Tyr Trp Lys Lys Ala Phe Gly Lys Asn Ala
145     150     155     160
Asn Lys Asn Gln Lys Arg Arg Phe Ser Gln Ala Ile Leu Val Ser Leu
165     170     175
Phe Pro Leu Ala Ser Val Phe Leu Ile Pro Leu Phe Gly Ile Ala Asn
180     185     190
Pro Arg Phe Lys Thr Asn Trp Ser Tyr Phe Unk Val Leu Gly Ala Val
195     200     205
Gly Val Tyr Phe Leu Met Val His Val Ile Ser Thr Asp Leu Phe Leu
210     215     220
Met Thr Phe Phe Phe Pro Phe Ile Trp Ala Phe Ile Ser Tyr Leu Leu
225     230     235     240
Phe Arg Lys Phe Ile Leu Lys Arg Tyr
245

```

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

352

(B) LOCATION 1...86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422

```

Met Ser Lys Ser Ala Ile Phe Val Leu Ser Gly Phe Leu Ala Phe Leu
1          5          10          15
Leu Tyr Ala Leu Leu Leu Tyr Gly Leu Leu Leu Glu Arg His Asn Lys
          20          25          30
Glu Ala Glu Lys Ile Leu Leu Asp Leu Asn Lys Lys Asp Glu Gln Ala
          35          40          45
Ile Asp Leu Asn Leu Glu Asp Leu Pro Ser Glu Lys Lys Asn Glu Lys
          50          55          60
Ile Lys Lys Val Thr Glu Lys Gln Asp Asp Phe Leu Glu Pro Lys Arg
65          70          75          80
Arg Thr Gln Arg Gly Ala
          85

```

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423

```

Val Met Ala Gln Ser Leu Leu Val His Ala Phe Phe Ala Ala Leu Leu
1          5          10          15
Ala Leu Ala Phe Met Ile Asn Leu Tyr Thr Leu Phe Lys Glu Lys Asn
          20          25          30
Phe Ile Gln Leu Asn Arg Lys Ile Tyr Leu Val Met Pro Ala Ile Tyr
          35          40          45
Ile Leu Leu Ser Ile Ala Leu Leu Ser Gly Val Phe Ile Trp Ala Met
          50          55          60
Gln Gln Phe Glu Phe Ser Phe Ser Ala Val Val Met Leu Leu Gly Leu
65          70          75          80
Leu Leu Met Leu Ile Ala Glu Ile Lys Arg His Lys Ser Val Lys Phe
          85          90          95
Ala Ile Thr Lys Lys Glu Arg Met Lys Ala Tyr Ile Lys Lys Ala Lys
          100          105          110
Ile Leu Tyr Phe Leu Glu Thr Ile Leu Ile Ile Val Leu Met Gly Ile
          115          120          125

```

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

353

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424

```

Val Arg Asn Val Val Leu Phe Ile Leu Thr Ala Ile Phe Leu Ala Phe
1          5          10          15
Met Leu Leu Val Ser Tyr Cys Met Pro His Tyr Ser Val Ala Val Ile
          20          25          30
Ser Gly Val Glu Val Lys Arg Met Asn Glu Asn Glu Asn Thr Pro Asn
          35          40          45
Asn Lys Glu Val Lys Thr Leu Ala Arg Asp Val Tyr Phe Val Gln Thr
          50          55          60
Tyr Asp Pro Lys Asp Gln Lys Ser Val Thr Val Tyr Arg Asn Glu Asp
65          70          75          80
Thr Arg Phe Gly Phe Pro Phe Tyr Phe Lys Phe Asn Ser
          85          90

```

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...88

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425

```

Met Phe Lys Lys Ile Ile Phe Leu Cys Val Phe Leu Ile Gly Gly Phe
1          5          10          15
Val Ile Pro Pro Leu Glu Ala Met Pro Ile Leu Arg Asn Lys Thr Pro
          20          25          30
Lys Lys Asn Tyr Gln Glu Ala His Glu Lys Leu Tyr Arg Ser Ile Ile
          35          40          45
Asn Arg Gln Unk Unk Thr Arg Lys Lys Ser Gly Trp Tyr Phe Leu Gly
          50          55          60
Gly Val Gly Ala Val Glu Ala Ile Lys Asp Tyr Gln Gly Lys Glu Met
65          70          75          80
Lys Asp Trp Met Pro Arg Ser Ile
          85

```

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

354

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426

```

Val His Phe Thr Cys Ile Phe Leu Thr Leu Leu Lys Trp Ile Leu Pro
1          5          10          15
Ala Lys Asn Lys Gln Ala Cys Lys Lys Ala Thr Asn Gln Ile His Ser
          20          25          30
Arg Unk Ala Lys His Pro Ala Lys Tyr Pro Pro Ser Ser Ile Asn Pro
          35          40          45
Ser Ile Gln Ala Gly Ile Gln Gly Val Met Gln Gly Phe Gly Ala Leu
          50          55          60
Ser Ser Unk Leu Glu Unk Pro Unk Phe Val Unk Ala Lys Cys Gly
65          70          75          80
Trp Ile Gly Gly Phe Glu His Tyr Leu Ser Pro Leu Tyr Gly Trp Gly
          85          90          95
Lys Ile His Asp Gly Ala His Cys Asp Leu Met Gln Lys Asp Ala Asn
          100          105          110
Gly Arg Gly Ile Gly Leu Glu Lys Gly Leu Pro Pro Phe Lys Gly Leu
          115          120          125

```

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427

```

Met Gln Lys Phe Phe Ser Arg Phe Arg Arg Trp Ala Leu Pro Phe Tyr
1          5          10          15
Phe Val Ser Ala Leu Ala Ala Ile Asp Ile Asp Glu Val Thr Glu Ala
          20          25          30
Gln Ala Asn Ser Ile Lys Leu Ser Asp Gln Leu Val Ser Leu Ser Asp
          35          40          45
Lys Leu Leu Glu Lys Ala Val Asp Arg Gly Arg Asn Thr Asp His Leu
          50          55          60
Lys Asp Leu Asn Asp Leu His Glu Lys Ile Lys His Leu Arg Leu Ile
65          70          75          80
Leu Glu Pro Lys Pro Lys Gly Lys Glu Asp Ser Pro Asn Leu Gly Gly
          85          90          95
Asn Lys Asp Met Lys Thr Val Glu Ile Gly Ser Gly

```

SUBSTITUTE SHEET (RULE 26)

355

100

105

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428

```

Val Ile Leu Ala Phe Ala Phe Gly Met Ser Leu Leu Gly Leu Ala Gly
1           5           10           15
Met Phe Ile Asp Ile Pro Phe Leu Ser Thr Gly Val His Ile Pro Arg
20           25           30
Lys Glu Asp Ile Leu Trp Ile Ser Leu Ile Gly Ile Ser Gly Thr Leu
35           40           45
Gly Gln Tyr Phe Leu Thr Tyr Ala Tyr Met Asn Ala Pro Ala Gly Ile
50           55           60
Ile Ala Pro Ile Glu Tyr Thr Arg Ile Val Trp Gly Leu Leu Phe Gly
65           70           75           80
Leu Tyr Leu Gly Asp Thr Phe Leu Asp Leu Lys Ser Ser Leu Gly Val
85           90           95
Ala Leu Ile Leu Cys Ser Gly Leu Leu Ile Ala Leu Pro Ala Leu Leu
100          105          110
Lys Glu Leu Lys Lys Ile
115

```

(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...54

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429

```

Met Ile Tyr Leu Gly Lys Lys Asn Phe Asn Ala Leu Leu Lys Gly Ala
1           5           10           15
Tyr Leu Met Asp Glu His Phe Arg Asn Ala Pro Phe Glu Ser Asn Leu
20           25           30

```

SUBSTITUTE SHEET (RULE 26)

356

Pro Val Leu Met Gly Leu Ile Trp Arg Val Val Tyr Leu Thr Phe Phe
 35 40 45
 Pro Ile Gln Lys Ala Thr
 50

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430

Met Ala Ala Lys Ser Lys Ala Unk Thr Leu Lys Val Phe Ser Lys Phe
 1 5 10 15
 Phe Ser Asn Phe Lys Ile Thr Lys Leu Lys Asp Asn His Glu Glu Ala
 20 25 30
 His Lys Leu Phe Gly Glu Asn Ser Arg Lys Ala His Asp Thr Glu Ile
 35 40 45
 Ile Tyr Ser Thr Leu Gln Val Val Pro Arg Tyr Ser Ile Glu Thr Val
 50 55 60
 Gly Phe Ser Leu Leu Ile Leu Ala Val Ala Tyr Ile Leu Phe Lys Tyr
 65 70 75 80
 Gly Glu Ala Arg Met Val Leu Pro Thr Ile Ser Met Tyr Ala Leu Ala
 85 90 95
 Leu Tyr Arg Ile Leu Pro Ser Val Thr Gly Val Ile Ser Tyr Tyr Asn
 100 105 110
 Glu Ile Ala Tyr Asn Gln Leu Ala Thr Asn Val Val Phe Lys Ser Leu
 115 120 125
 Ser Lys Thr Ile Val Glu Glu Asp Leu Val Pro Leu Asp Phe Asn Glu
 130 135 140
 Lys Ile Thr Leu Gln Asn Ile Ser Phe Ala Tyr Lys Ser Lys His Pro
 145 150 155 160
 Val Leu Lys Asn Phe Asn Leu Thr Ile Gln Lys Gly Gln Lys Ile Ala
 165 170 175
 Leu Ile Gly His Ser Gly Cys Gly Lys Ser Thr Leu Ala Asp Ile Ile
 180 185 190
 Met Gly Leu Thr Tyr Pro Lys Ser Gly Glu Ile Phe Ile Asp Asn Thr
 195 200 205
 Leu Leu Thr Ser Glu Asn Arg Arg Ser Trp Arg Lys Lys Ile Gly Tyr
 210 215 220
 Ile Pro Gln Asn Ile Tyr Leu Phe Asp Gly Thr Val Gly Asp Asn Ile
 225 230 235 240
 Ala Phe Gly Ser Ala Ile Asp Glu Lys Arg Leu Ile Lys Val Cys Lys
 245 250 255
 Met Ala His Ile Tyr Asp Phe Leu Cys Glu His Glu Gly Leu Lys Thr
 260 265 270
 Gln Val Gly Glu Gly Ala Leu Ser Leu Ala Ala Val Lys Asn Ser Ala
 275 280 285

(2) INFORMATION FOR SEQ ID NO:431:

SUBSTITUTE SHEET (RULE 26)

357

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431

```

Met Ala Phe Gln Val Asn Thr Asn Ile Asn Ala Met Asn Ala His Val
1          5          10          15
Gln Ser Ala Leu Thr Gln Asn Ala Leu Lys Thr Ser Leu Glu Arg Leu
20          25          30
Ser Ser Gly Leu Arg Ile Asn Lys Ala Ala Asp Asp Ala Ser Gly Met
35          40          45
Thr Val Ala Asp Ser Leu Arg Ser Gln Ala Ser Ser Leu Gly Gln Ala
50          55          60
Ile Ala Asn Thr Asn Asp Gly Met Gly Ile Ile Gln Val Ala Asp Lys
65          70          75          80
Ala Met Asp Glu Gln Leu Lys Ile Leu Asp Thr Val Lys Val Lys Ala
85          90          95
Thr Gln Ala Ala Gln Asp Gly Gln Thr Thr Glu Ser Arg Lys Ala Ile
100         105         110
Gln Ser Asp Ile Val Arg Leu Ile Gln Gly Leu Asp Asn Ile Gly Asn
115         120         125
Thr Thr Thr Tyr Asn Gly Gln Ala Leu Leu Ser Gly Gln Phe Thr Asn
130         135         140
Lys Glu Phe Gln Val Gly Ala Tyr Ser Asn Gln Ser Ile Lys Ala Ser
145         150         155         160
Ile Gly Ser Thr Thr Ser Asp Lys Ile Gly Gln Val Arg Ile Ala Thr
165         170         175
Gly Ala Leu Ile Thr Ala Ser Gly Asp Ile Ser Leu Thr Phe Lys Gln
180         185         190
Val Asp Gly Val Asn Asp Val Thr Leu Glu Ser Val Lys Val Ser Ser
195         200         205
Ser Ala Gly Thr Gly Ile Gly Val Leu Ala Glu Val Ile Asn Lys Asn
210         215         220
Ser Asn Arg Thr Gly Val Lys Ala Tyr Ala Ser Val Ile Thr Thr Ser
225         230         235         240
Asp Val Ala Val Gln Ser Gly Ser Leu Ser Asn Leu Thr Leu Asn Gly
245         250         255
Ile His Leu Gly Asn Ile Ala Asp Ile Lys Unk Asn Asp Ser Asp Gly
260         265         270
Arg Leu Val Thr Ala Ile Asn Ala Val Thr Ser Glu Thr Gly Val Unk
275         280         285
Ala Tyr Thr Asp Gln Lys Gly Arg Leu Asn Leu Arg Ser Ile Gly
290         295         300

```

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

358

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431

```

Met Ala Phe Gln Val Asn Thr Asn Ile Asn Ala Met Asn Ala His Val
1      5      10      15
Gln Ser Ala Leu Thr Gln Asn Ala Leu Lys Thr Ser Leu Glu Arg Leu
20     25     30
Ser Ser Gly Leu Arg Ile Asn Lys Ala Ala Asp Asp Ala Ser Gly Met
35     40     45
Thr Val Ala Asp Ser Leu Arg Ser Gln Ala Ser Ser Leu Gly Gln Ala
50     55     60
Ile Ala Asn Thr Asn Asp Gly Met Gly Ile Ile Gln Val Ala Asp Lys
65     70     75     80
Ala Met Asp Glu Gln Leu Lys Ile Leu Asp Thr Val Lys Val Lys Ala
85     90     95
Thr Gln Ala Ala Gln Asp Gly Gln Thr Thr Glu Ser Arg Lys Ala Ile
100    105    110
Gln Ser Asp Ile Val Arg Leu Ile Gln Gly Leu Asp Asn Ile Gly Asn
115    120    125
Thr Thr Thr Tyr Asn Gly Gln Ala Leu Leu Ser Gly Gln Phe Thr Asn
130    135    140
Lys Glu Phe Gln Val Gly Ala Tyr Ser Asn Gln Ser Ile Lys Ala Ser
145    150    155    160
Ile Gly Ser Thr Thr Ser Asp Lys Ile Gly Gln Val Arg Ile Ala Thr
165    170    175
Gly Ala Leu Ile Thr Ala Ser Gly Asp Ile Ser Leu Thr Phe Lys Gln
180    185    190
Val Asp Gly Val Asn Asp Val Thr Leu Glu Ser Val Lys Val Ser Ser
195    200    205
Ser Ala Gly Thr Gly Ile Gly Val Leu Ala Glu Val Ile Asn Lys Asn
210    215    220
Ser Asn Arg Thr Gly Val Lys Ala Tyr Ala Ser Val Ile Thr Thr Ser
225    230    235    240
Asp Val Ala Val Gln Ser Gly Ser Leu Ser Asn Leu Thr Leu Asn Gly
245    250    255
Ile His Leu Gly Asn Ile Ala Asp Ile Lys Unk Asn Asp Ser Asp Gly
260    265    270
Arg Leu Val Thr Ala Ile Asn Ala Val Thr Ser Glu Thr Gly Val Unk
275    280    285
Ala Tyr Thr Asp Gln Lys Gly Arg Leu Asn Leu Arg Ser Ile Gly
290    295    300

```

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

SUBSTITUTE SHEET (RULE 26)

359

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432

```

Met Leu Asp Ile Trp Ile Asp Met Ile Ile Cys Ile Phe Tyr Leu Leu
1           5           10           15
Phe Phe Thr Thr Pro Tyr Ile Val Gly Asp Ile Leu Gln Leu Lys Phe
20           25           30
Ile Arg Gln Lys Leu Cys Glu Lys Pro Val Leu Leu Pro Gln Lys Asp
35           40           45
Tyr Glu Glu Ala Gly Asn Tyr Ala Ile Arg Lys Met Gln Leu Ser Ile
50           55           60
Ile Ser Gln Ile Leu Asp Gly Val Ile Phe Ala Gly Trp Val Phe Phe
65           70           75           80
Gly Leu Thr His Leu Glu Asp Leu Thr His Tyr Leu Asn Leu Pro Glu
85           90           95
Thr Leu Gly Tyr Leu Val Phe Ala Leu Phe Leu Ala Ile Gln Ser
100          105          110
Val Leu Ala Leu Pro Ile Ser Tyr Tyr Thr Thr Met His Leu Asp Lys
115          120          125
Glu Phe Gly Phe Ser Lys Val Ser Leu Ser Leu Phe Lys Asp Phe
130          135          140
Phe Lys Gly Leu Leu Leu Thr Leu Gly Val Gly Leu Leu Leu Ile Tyr
145          150          155          160
Thr Leu Ile Met Ile Ile Glu His Val Glu His Trp Glu Ile Ser Ser
165          170          175
Phe Phe Val Val Phe Val Phe Met Ile Leu Ala Asn Leu Phe Leu Pro
180          185          190

```

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433

```

Met Leu Lys Lys Ile Phe Leu Thr Asn Ser Leu Gly Ile Leu Cys Ser
1           5           10           15
Arg Ile Phe Gly Phe Leu Arg Asp Leu Met Met Ala Asn Ile Leu Gly
20           25           30
Ala Gly Val Tyr Ser Asp Ile Phe Phe Val Ala Phe Lys Leu Pro Asn
35           40           45
Leu Phe Arg Arg Ile Phe Ala Glu Gly Ser Phe Ser Gln Ser Phe Leu
50           55           60
Pro Ser Phe Ile Arg Ser Ser Ile Lys Gly Gly Phe Ala Ser Leu Val
65           70           75           80

```

SUBSTITUTE SHEET (RULE 26)

360

```

Gly Leu Ile Phe Cys Gly Val Leu Phe Met Trp Cys Leu Leu Val Ala
      85                      90                      95
Leu Asn Pro Leu Trp Leu Thr Lys Leu Leu Ala Tyr Gly Phe Asp Glu
      100                    105                    110
Glu Thr Leu Lys Leu Cys Thr Pro Ile Val Ala Ile Asn Phe Trp Tyr
      115                    120                    125
Leu Leu Leu Val Phe Ile Thr Thr Phe Leu Gly Ala Leu Leu Gln Tyr
      130                    135                    140
Lys His Ser Phe Phe Ala Ala Leu Met Arg Lys Leu Thr Gln Phe Met
145      150                    155                    160
His Asp Phe Ser Pro Phe Asp Phe
      165

```

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434

```

Met Asn Leu Glu Val Ala Leu Lys Ala Phe Glu Thr Leu Leu Pro Cys
1      5                      10                      15
Asn Lys Gln Glu Val Leu Lys Asn Leu Lys Pro Leu Asp Leu Ile Gly
      20                    25                    30
Arg Cys Glu Leu Leu Ser Pro Asn Ile Leu Ile Asp Val Gly His Asn
      35                    40                    45
Pro His Ser Ala Lys Ala Leu Lys Glu Glu Ile Lys Arg Ile Phe Asn
      50                    55                    60
Ala Pro Ile Val Leu Ile Tyr Asn Cys Tyr Gln Asp Lys Asp Ala Phe
65      70                    75                    80
Leu Val Leu Glu Ile Leu Lys Ser Val Val Lys Lys Val Leu Ile Leu
      85                    90                    95
Glu Leu His Asn Glu Arg Ile Ile Gln Leu Glu Lys Leu Lys Gly Ile
      100                   105                   110
Leu Glu Thr Leu Gly Leu Glu His Ala Leu Phe Glu Glu Leu Lys Glu
      115                   120                   125
Asn Glu Asn Tyr Leu Val Tyr Gly Ser Phe Leu Val Ala Asn Ala Phe
130      135                   140
Tyr Glu Arg Tyr Pro Lys Lys Arg Asp
145      150

```

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

361

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435

```

Met Phe Phe Lys Thr Tyr Gln Lys Leu Leu Gly Ala Ser Cys Leu Ala
1      5      10      15
Leu Tyr Leu Val Gly Cys Gly Asn Gly Gly Gly Glu Ser Pro Val
20      25      30
Glu Met Ile Unk Asn Ser Glu Gly Thr Phe Gln Ile Asp Ser Lys Ala
35      40      45
Asp Ser Ile Thr Ile Gln Gly Val Lys Leu Asn Arg Gly Asn Cys Ala
50      55      60
Val Asn Phe Val Pro Val Ser Glu Thr Phe Gln Met Gly Val Leu Ser
65      70      75      80
Gln Val Thr Pro Ile Ser Ile Gln Asp Phe Lys Asp Met Ala Ser Thr
85      90      95
Tyr Lys Ile Phe Asp Gln Lys Lys Gly Leu Ala Asn Ile Ala Asn Lys
100     105     110
Ile Ser Gln Leu Glu Gln Lys Gly Val Met Met Lys Pro Unk Thr Leu
115     120     125
Asn Phe Gly Glu Ser Leu Lys Gly Ile Ser Gln Gly Cys Asn Ile Ile
130     135     140
Glu Ala Glu Ile Gln Thr Asp Lys Gly Ala Trp Thr Phe Asn Phe Asp
145     150     155     160
Lys

```

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435

```

Met Phe Phe Lys Thr Tyr Gln Lys Leu Leu Gly Ala Ser Cys Leu Ala
1      5      10      15
Leu Tyr Leu Val Gly Cys Gly Asn Gly Gly Gly Glu Ser Pro Val
20      25      30
Glu Met Ile Unk Asn Ser Glu Gly Thr Phe Gln Ile Asp Ser Lys Ala
35      40      45
Asp Ser Ile Thr Ile Gln Gly Val Lys Leu Asn Arg Gly Asn Cys Ala
50      55      60
Val Asn Phe Val Pro Val Ser Glu Thr Phe Gln Met Gly Val Leu Ser
65      70      75      80

```

SUBSTITUTE SHEET (RULE 26)

362

Gln Val Thr Pro Ile Ser Ile Gln Asp Phe Lys Asp Met Ala Ser Thr
 85 90 95
 Tyr Lys Ile Phe Asp Gln Lys Lys Gly Leu Ala Asn Ile Ala Asn Lys
 100 105 110
 Ile Ser Gln Leu Glu Gln Lys Gly Val Met Met Lys Pro Unk Thr Leu
 115 120 125
 Asn Phe Gly Glu Ser Leu Lys Gly Ile Ser Gln Gly Cys Asn Ile Ile
 130 135 140
 Glu Ala Glu Ile Gln Thr Asp Lys Gly Ala Trp Thr Phe Asn Phe Asp
 145 150 155 160
 Lys

(2) INFORMATION FOR SEQ ID NO:436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...59

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436

Met Ala Ile Gly Phe Pro Leu Val Phe Gly Ile Leu Leu Thr Leu Phe
 1 5 10 15
 Ser Arg Ser Tyr Trp Arg Glu Phe Gly Gly Val Ser Gly Val Leu Trp
 20 25 30
 Arg Ala Ser Gly Phe Ser Gly Ala Lys Val Glu Arg Asn Leu Glu Arg
 35 40 45
 Asp Pro His Ala Phe Phe Thr His Cys Asp Phe
 50 55

(2) INFORMATION FOR SEQ ID NO:437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437

Met Lys Lys Lys Ala Lys Val Phe Trp Cys Cys Phe Lys Met Ile Arg

SUBSTITUTE SHEET (RULE 26)

363

```

1           5           10           15
Trp Leu Tyr Leu Ala Val Phe Phe Leu Leu Ser Val Ser Asp Ala Lys
20           25           30
Glu Ile Ala Met Gln Arg Phe Asp Lys Gln Asn His Lys Ile Phe Glu
35           40           45
Ile Leu Ala Asp Lys Val Ser Ala Lys Asp Asn Val Ile Thr Ala Ser
50           55           60
Gly Asn Ala Ile Leu Leu Asn Tyr Asp Val Tyr Ile Leu Ala Asp Lys
65           70           75           80
Val Arg Tyr Asp Thr Lys Thr Lys Glu Ala Leu Leu Glu Gly Asn Ile
85           90           95
Lys Val Tyr Arg Gly Glu Gly Leu Leu Val Lys Thr Asp Tyr Val Lys
100          105          110
Leu Ser Leu Asn Glu Lys Tyr Glu Ile Ile Phe Pro Phe Tyr Val Gln
115          120          125
Asp Ser Val Ser Gly Ile Trp Val Ser Ala Asp Ile Ala Ser Gly Lys
130          135          140
Asp Gln Lys Tyr Lys Ile Lys Asn Met Ser Ala Ser Gly Cys Ser Ile
145          150          155          160
Asp Asn Pro Ile Trp His Val Asn Ala Thr Ser Gly Ser Phe Asn Met
165          170          175
Gln Lys Ser His Leu Ser Met Trp Asn Pro Lys Ile Tyr Val Gly Asp
180          185          190
Ile Pro Val Leu Tyr Leu Pro Tyr Ile Phe Met Ser Thr Ser Asn Lys
195          200          205
Arg Thr Thr Gly Phe Leu Tyr Pro Glu Phe Gly Thr Ser Thr
210          215          220

```

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...53

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438

```

Met Leu Asp Phe Asp Leu Val Leu Phe Gly Ala Thr Gly Asp Leu Ala
1           5           10           15
Met Arg Lys Leu Phe Val Ser Leu Tyr Glu Ile Tyr Ile Ser Phe Met
20           25           30
Val Leu Lys Thr Ile Leu Gly Leu Ser His Arg Gly Val Arg Ser Tyr
35           40           45
Pro Met Lys Ser Phe
50

```

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

364

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439

```

Met Gln Asp Leu Pro Pro Cys Pro Lys Arg Asn Asp Ala Tyr Thr Tyr
1          5          10          15
His Asp Gly Thr Gln Phe Val Cys Ser Ser Cys Leu Tyr Glu Trp Asn
          20          25          30
Gly Asn Glu Ile Ser Asn Glu Glu Leu Ile Val Lys Asp Cys His Asn
          35          40          45
Asn Leu Leu Gln Asn Gly Asp Ser Val Ile Leu Ile Lys Asp Leu Lys
          50          55          60
Val Lys Gly Ser Ser Leu Val Leu Lys Lys Gly Thr Lys Ile Lys Asn
65          70          75          80
Ile Lys Leu Val Asn Ser Asp His Asn Val Asp Cys Lys Val Glu Gly
          85          90          95
Gln Ser Leu Ser Leu Lys Ser Glu Phe Leu Lys Lys Ala
          100          105

```

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...73

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440

```

Val Asp Gly Ala Ile Ile Thr Gly Asn Tyr Ala Leu Gln Ala Lys Leu
1          5          10          15
Thr Gly Ala Leu Phe Ser Glu Asp Lys Asp Ser Pro Tyr Ala Asn Leu
          20          25          30
Val Ala Ser Arg Glu Asp Asn Ala Gln Asp Glu Ala Ile Lys Ala Leu
          35          40          45
Ile Glu Ala Leu Gln Ser Glu Lys Thr Arg Lys Phe Ile Leu Asp Thr
          50          55          60
Tyr Lys Gly Ala Ile Ile Pro Ala Phe
65          70

```

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

365

(A) LENGTH: 237 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441

```

Val Phe Thr Met Leu Val Leu Val Leu Ser Asp Asn Phe Leu Gly Leu
1      5      10      15
Phe Ile Gly Trp Glu Gly Val Gly Leu Cys Ser Tyr Leu Leu Ile Gly
20      25      30
Phe Trp Tyr His Lys Lys Ser Ala Asn Asn Ala Ser Ile Glu Ala Phe
35      40      45
Val Met Asn Arg Ile Thr Asp Leu Gly Met Leu Met Gly Ile Ile Leu
50      55      60
Ile Phe Trp Asn Phe Gly Thr Leu Gln Tyr Lys Glu Val Phe Ser Met
65      70      75      80
Leu Asn Asn Ala Asp Tyr Ser Met Leu Phe Tyr Ile Ser Val Phe Leu
85      90      95
Phe Ile Gly Ala Met Gly Lys Ser Ala Gln Phe Pro Met His Thr Trp
100     105     110
Leu Ala Asn Ala Met Glu Gly Pro Thr Pro Val Ser Ala Leu Ile His
115     120     125
Ala Thr Thr Met Val Thr Ala Gly Val Tyr Leu Ile Ile Arg Ala Asn
130     135     140
Pro Leu Tyr Ser Ala Val Phe Glu Val Gly Tyr Phe Ile Ala Cys Leu
145     150     155     160
Gly Ala Phe Val Ala Leu Phe Gly Ala Ser Met Ala Leu Val Asn Lys
165     170     175
Asp Leu Lys Arg Ile Val Glu Tyr Ser Thr Leu Ser Gln Leu Gly Leu
180     185     190
Tyr Val Cys Ser Gly Arg Ala Trp Gly Leu Cys Asp Arg Ala Phe Pro
195     200     205
Pro Leu Tyr Ala Cys Val Leu Gln Ile Pro Pro Phe Leu Arg Leu Arg
210     215     220
Gln Cys His Ala Cys Asp Gly Arg Gln Ser Gly Tyr Tyr
225     230     235

```

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

366

(B) LOCATION 1...91

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442

```

Val Cys Leu Gly Leu Ala Asp Val Met Val Val Leu Ser Leu His Leu
1      5      10      15
Asn Leu Asn Pro Thr Asn Pro Lys Trp Leu Asn Arg Asp Arg Leu Val
      20      25      30
Phe Ser Gly Gly His Ala Ser Ala Leu Val Tyr Ser Leu Leu His Leu
      35      40      45
Trp Gly Phe Asp Leu Ser Leu Asp Asp Leu Lys Arg Phe Arg Gln Leu
      50      55      60
His Ser Lys Thr Pro Gly His Pro Glu Leu His His Thr Glu Gly Ile
65      70      75      80
Glu Ile Thr Thr Unk Phe Arg Ala Arg Phe Cys
      85      90

```

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...91

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442

```

Val Cys Leu Gly Leu Ala Asp Val Met Val Val Leu Ser Leu His Leu
1      5      10      15
Asn Leu Asn Pro Thr Asn Pro Lys Trp Leu Asn Arg Asp Arg Leu Val
      20      25      30
Phe Ser Gly Gly His Ala Ser Ala Leu Val Tyr Ser Leu Leu His Leu
      35      40      45
Trp Gly Phe Asp Leu Ser Leu Asp Asp Leu Lys Arg Phe Arg Gln Leu
      50      55      60
His Ser Lys Thr Pro Gly His Pro Glu Leu His His Thr Glu Gly Ile
65      70      75      80
Glu Ile Thr Thr Unk Phe Arg Ala Arg Phe Cys
      85      90

```

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori***SUBSTITUTE SHEET (RULE 26)**

367

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...97

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443

```

Met Met Ile Thr Lys Gln Ser Tyr Gln Arg Phe Ala Leu Met Arg Val
1      5      10      15
Phe Val Phe Ser Leu Ser Ala Phe Ile Phe Asn Thr Thr Glu Phe Val
20      25      30
Pro Val Ala Leu Leu Ser Asp Ile Ala Lys Ser Phe Glu Met Glu Ser
35      40      45
Ala Thr Val Gly Leu Met Ile Thr Ala Tyr Ala Trp Val Val Ser Leu
50      55      60
Gly Ser Leu Pro Leu Met Leu Leu Ser Ala Lys Ile Glu Arg Lys Arg
65      70      75      80
Leu Leu Leu Phe Leu Phe Ala Leu Phe Ile Phe Ser His Ile Leu Ser
85      90      95
Arg

```

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444

```

Met Lys Leu Arg Ala Ser Val Leu Ile Gly Val Ala Ile Leu Cys Leu
1      5      10      15
Ile Leu Ser Ala Cys Ser Asn Tyr Ala Lys Lys Val Val Lys Gln Lys
20      25      30
Asn His Val Tyr Thr Pro Val Tyr Asn Glu Leu Ile Glu Lys Tyr Ser
35      40      45
Glu Ile Pro Leu Asn Asp Lys Leu Lys Asp Thr Pro Phe Met Val Gln
50      55      60
Val Lys Leu Pro Asn Tyr Lys Asp Tyr Leu Leu Asp Asn Lys Gln Val
65      70      75      80
Val Leu Thr Phe Lys Leu Val His His Ser Lys Lys Ile Thr Leu Ile
85      90      95
Gly Asp Ala Asn Lys Ile Leu Gln Tyr Lys Asn Tyr Phe Gln Ala Asn
100      105      110
Gly Ala Arg Ser Asp Ile Asp Phe Tyr Leu Gln Pro Thr Leu Asn Gln
115      120      125
Lys Gly Val Val Met Ile Ala Ser Asn Tyr Asn Asp Asn Pro Asn Asn
130      135      140
Lys Glu Lys Pro Gln Thr Phe Asp Val Leu Gln Gly Ser Gln Pro Met
145      150      155      160
Leu Gly Ala Asn Thr Lys Asn Leu His Gly Tyr Asp Val Ser Gly Ala
165      170      175

```

SUBSTITUTE SHEET (RULE 26)

368

```

Asn Asn Lys Gln Val Ile Asn Glu Val Ala Arg Glu Lys Ala Gln Leu
      180      185      190
Glu Lys Ile Asn Gln Tyr Tyr Lys Thr Leu Leu Gln Asp Lys Glu Gln
      195      200      205
Glu Tyr Thr Thr Arg Lys Asn Asn Gln Arg Glu Ile Leu Glu Thr Leu
      210      215      220
Ser Asn Arg Ala Gly Tyr Gln Met Arg Gln Asn Val Ile Ser Ser Glu
      225      230      235      240
Ile Phe Lys Asn Gly Asn Leu Asn Met Gln Ala Lys Glu Glu Glu Val
      245      250      255
Arg Glu Lys Leu Gln Glu Glu Arg Glu Asn Glu Tyr Leu Arg Asn Gln
      260      265      270
Ile Arg Ser Leu Leu Ser Gly Lys
      275      280

```

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445

```

Met Thr Thr Pro Met Ile Ile Ile Ser Leu Glu Met Gly Leu Ser Leu
1      5      10      15
Val Pro Met Arg Gln Cys Leu Val Cys Gln Ala Leu Ala Arg Ser Ile
      20      25      30
Ser Trp Asn Gly Leu Gly Gly Asn Val Arg Asn Thr Lys Val Tyr Gly
      35      40      45
Lys Phe Ala Ala Tyr His His Leu Gln Lys Tyr Leu Leu Ile Asp Leu
      50      55      60
Ile Ala Arg Phe Lys Thr Gln Gly Gly Tyr Ile Phe Arg Tyr Asn Thr
      65      70      75      80
Asp Asp Tyr Leu Pro Leu Asn Ser Thr Phe Tyr Met Gly Gly Val Thr
      85      90      95
Thr Val Arg Gly Phe Arg Asn Gly Ser Ile Thr Pro Lys Asp Glu Phe
      100      105      110
Gly Leu Trp Leu Gly Gly Asp Gly Ile Phe Thr Unk Ser Thr Glu Leu
      115      120      125
Ser Tyr Gly Val Leu Lys Ala Ala Lys Met Arg Leu Ala Trp Phe Phe
      130      135      140
Asp Phe Gly Phe Leu Thr Phe Unk Thr Pro Thr Arg Gly Ser Phe Phe
      145      150      155      160
Tyr Asn Ala Unk Thr Thr Thr Ala Asn Phe Lys Asp Tyr Unk Val Val
      165      170      175
Gly Unk Unk Phe Glu Unk Ala Thr Trp Arg Ala
      180      185

```

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

369

(A) LENGTH: 187 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445

```

Met Thr Thr Pro Met Ile Ile Ile Ser Leu Glu Met Gly Leu Ser Leu
1      5      10      15
Val Pro Met Arg Gln Cys Leu Val Cys Gln Ala Leu Ala Arg Ser Ile
      20      25      30
Ser Trp Asn Gly Leu Gly Gly Asn Val Arg Asn Thr Lys Val Tyr Gly
      35      40      45
Lys Phe Ala Ala Tyr His His Leu Gln Lys Tyr Leu Leu Ile Asp Leu
      50      55      60
Ile Ala Arg Phe Lys Thr Gln Gly Gly Tyr Ile Phe Arg Tyr Asn Thr
      65      70      75      80
Asp Asp Tyr Leu Pro Leu Asn Ser Thr Phe Tyr Met Gly Gly Val Thr
      85      90      95
Thr Val Arg Gly Phe Arg Asn Gly Ser Ile Thr Pro Lys Asp Glu Phe
      100     105     110
Gly Leu Trp Leu Gly Gly Asp Gly Ile Phe Thr Unk Ser Thr Glu Leu
      115     120     125
Ser Tyr Gly Val Leu Lys Ala Ala Lys Met Arg Leu Ala Trp Phe Phe
      130     135     140
Asp Phe Gly Phe Leu Thr Phe Unk Thr Pro Thr Arg Gly Ser Phe Phe
      145     150     155     160
Tyr Asn Ala Unk Thr Thr Ala Asn Phe Lys Asp Tyr Unk Val Val
      165     170     175
Gly Unk Unk Phe Glu Unk Ala Thr Trp Arg Ala
      180     185

```

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...58

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446

```

Met Trp Leu Asp His Ile Ala Lys Glu Ile Arg Ser Leu Val Glu Asn
1      5      10      15

```

SUBSTITUTE SHEET (RULE 26)

370

```

Asp Ile Glu Val Gly Ile Val Ile Gly Gly Gly Asn Ile Ile Arg Gly
      20                25                30
Val Ser Ala Ala Leu Gly Gly Ile Ile Arg Arg Thr Ser Gly Asp Tyr
      35                40                45
Met Gly Met Leu Ala Thr Val Ile Lys Arg
      50                55

```

(2) INFORMATION FOR SEQ ID NO:447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...85

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447

```

Val His Asn Phe His Trp Asn Val Lys Gly Thr Asp Phe Phe Asn Val
1      5      10      15
His Lys Ala Thr Glu Glu Ile Tyr Glu Gly Phe Ala Asp Met Phe Asp
      20      25      30
Asp Leu Ala Glu Arg Ile Val Gln Leu Gly His His Pro Leu Val Thr
      35      40      45
Leu Ser Glu Ala Ile Lys Leu Thr Arg Val Lys Glu Glu Thr Lys Thr
      50      55      60
Ser Phe His Ser Lys Asp Ile Phe Lys Glu Ile Leu Glu Asp Tyr Lys
65      70      75      80
His Leu Glu Lys Glu
      85

```

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448

```

Met Asn Lys Thr Ile Lys Ala Ala Ala Leu Ala Tyr Asn Met Gly Gln
1      5      10      15
Asp His Ala Pro Lys Val Ile Ala Ser Gly Val Gly Glu Val Ala Lys

```

SUBSTITUTE SHEET (RULE 26)

371

```

      20      25      30
Arg Ile Ile Gln Lys Ala Lys Glu Tyr Asp Ile Ala Leu Phe Ser Asn
      35      40      45
Pro Met Leu Val Asp Ser Leu Leu Lys Val Glu Leu Asp Cys Ala Ile
      50      55      60
Pro Glu Glu Leu Tyr Glu Ser Val Val Gln Val Phe Leu Trp Leu Asn
      65      70      75      80
Ser Val Glu Asn Asn Ala Gln Met Ser Lys
      85      90

```

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449

```

Met Gln Ala Leu Lys Ser Leu Leu Glu Val Ile Thr Lys Leu Gln Asn
1      5      10      15
Leu Gly Gly Tyr Leu Met His Ile Ala Ile Phe Ile Ile Phe Ile Trp
      20      25      30
Ile Gly Gly Leu Lys Phe Val Pro Tyr Glu Ala Glu Gly Ile Ala Pro
      35      40      45
Phe Val Unk Asn Ser Pro Phe Phe Ser Phe Met Tyr Lys Phe Glu Lys
      50      55      60
Pro Ala Tyr Lys Gln His Lys Met Ser Glu Ser Gln Ser Met Gln Glu
      65      70      75      80
Glu Met Gln Asp Asn Pro Lys Ile Val Glu Asn Lys Unk Trp His Lys
      85      90      95
Glu Asn Arg Thr Ser Phe Ser Gly
      100

```

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...104

372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449

```

Met Gln Ala Leu Lys Ser Leu Leu Glu Val Ile Thr Lys Leu Gln Asn
1          5          10          15
Leu Gly Gly Tyr Leu Met His Ile Ala Ile Phe Ile Ile Phe Ile Trp
          20          25          30
Ile Gly Gly Leu Lys Phe Val Pro Tyr Glu Ala Glu Gly Ile Ala Pro
          35          40          45
Phe Val Unk Asn Ser Pro Phe Phe Ser Phe Met Tyr Lys Phe Glu Lys
          50          55          60
Pro Ala Tyr Lys Gln His Lys Met Ser Glu Ser Gln Ser Met Gln Glu
65          70          75          80
Glu Met Gln Asp Asn Pro Lys Ile Val Glu Asn Lys Unk Trp His Lys
          85          90          95
Glu Asn Arg Thr Ser Phe Ser Gly
          100

```

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450

```

Met Gly Lys Ile Ser Ala His Leu Ala His Glu Ile Arg Asn Pro Val
1          5          10          15
Gly Ser Ile Ser Leu Leu Ala Ser Val Leu Leu Lys His Ala Asn Glu
          20          25          30
Lys Thr Lys Pro Ile Val Val Glu Leu Gln Lys Ala Leu Trp Arg Val
          35          40          45
Glu Arg Ile Ile Lys Ala Thr Leu Leu Phe Ser Lys Gly Ile Gln Ala
          50          55          60
Asn Arg Thr Lys Gln Ser Leu Lys Thr Leu Glu Ser Asp Leu Lys Glu
65          70          75          80
Ala Leu Asn Cys Tyr Thr Tyr Ser Lys Asp Ile Asp Phe Leu Phe Asn
          85          90          95
Phe Ser Asp Glu Gly Phe Phe Asp Phe Asp Leu Met Gly Ile Val
          100          105          110
Leu Gln Asn Phe Leu Tyr Asn Ala Ile Asp Ala Ile Glu Ala Leu Glu
          115          120          125
Glu Ser Glu Gln Gly Gln Val Lys Ile Glu Ala Phe Ile Gln Asn Glu
          130          135          140
Phe Ile Val Phe Thr Ile Ile Asp Asn Gly Lys Glu Val Glu Asn Lys
145          150          155          160
Ser Ala Leu Phe Glu Pro Phe Glu Thr Thr Lys Leu
          165          170

```

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

373

(A) LENGTH: 212 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451

```

Val Ser Glu Phe His Gln Val Tyr Asp Pro Leu Gly Asn Ile Trp Leu
1          5          10          15
Ser Ala Leu Val Ala Leu Leu Pro Ile Leu Leu Phe Phe Leu Ser Leu
          20          25          30
Met Val Phe Lys Leu Lys Gly Tyr Thr Ala Ala Phe Leu Ser Val Ala
          35          40          45
Leu Ser Ala Ile Ile Ala Val Leu Val Tyr Lys Met Pro Val Ser Met
          50          55          60
Val Gly Ser Ser Phe Leu Tyr Gly Phe Leu Tyr Gly Leu Trp Leu Phe
65          70          75          80
Ala Trp Ile Ile Ile Ala Ala Ile Phe Leu Tyr Lys Leu Ser Val Lys
          85          90          95
Ser Gly Tyr Phe Glu Ile Leu Lys Glu Ser Val Gln Ser Ile Thr Leu
          100         105         110
Asp His Arg Ile Leu Val Ile Leu Ile Gly Phe Cys Phe Gly Ser Phe
          115         120         125
Leu Glu Gly Ala Ile Gly Phe Gly Gly Pro Ile Ala Ile Thr Ala Ala
130         135         140
Ile Leu Val Gly Leu Gly Leu Ser Pro Leu Tyr Ser Ala Gly Leu Cys
145         150         155         160
Leu Ile Ala Asn Thr Ala Pro Val Ala Phe Gly Ala Val Gly Ile Pro
          165         170         175
Ile Ser Ala Met Ala Ser Ala Val Gly Val Pro Ala Ile Leu Ile Ser
          180         185         190
Ala Met Thr Gly Lys Ile Leu Phe Val Ser Leu Leu Val Pro Phe
          195         200         205
Phe Ile Val Phe
210
  
```

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...182

SUBSTITUTE SHEET (RULE 26)

374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452

```

Met Glu Ile Lys Met Ala Lys Asp Tyr Gly Phe Cys Phe Gly Val Lys
1      5      10      15
Arg Ala Ile Gln Ile Ala Glu Lys Asn Gln Asn Ser Leu Ile Phe Gly
20      25      30
Ser Leu Ile His Asn Ala Lys Glu Ile Asn Arg Leu Glu Lys Asn Phe
35      40      45
Asn Val Lys Ile Glu Glu Asp Pro Lys Lys Ile Pro Lys Asn Lys Ser
50      55      60
Val Ile Ile Arg Thr His Gly Ile Pro Lys Gln Asp Leu Glu Tyr Leu
65      70      75      80
Lys Asn Lys Gly Val Lys Ile Thr Asp Ala Thr Cys Pro Tyr Val Ile
85      90      95
Lys Pro Gln Gln Ile Val Glu Ser Met Ser Lys Glu Gly Tyr Gln Ile
100     105     110
Val Leu Phe Gly Asp Ile Asn His Pro Glu Val Lys Gly Val Ile Ser
115     120     125
Tyr Ala Thr Asn Gln Ala Leu Val Gly Asn Ser Leu Glu Glu Leu Gln
130     135     140
Glu Lys Lys Leu Gln Arg Lys Val Ala Leu Val Ser Gln Thr Thr Gln
145     150     155     160
Ala Asn Pro Lys Thr Leu Ala Asn Arg Phe Leu Phe Gly Gly Unk Cys
165     170     175
Thr Glu Val Arg Ile Phe
180

```

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear.

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453

```

Met Asp His Glu Phe Leu Ile Thr Met Arg Leu Ser Phe Ser Leu Ala
1      5      10      15
Leu Ile Thr Thr Leu Ile Leu Leu Pro Ile Gly Ile Phe Leu Gly Tyr
20      25      30
Phe Leu Ser Leu Lys Arg Asn Leu Leu Thr Ser Leu Thr Glu Thr Leu
35      40      45
Val Tyr Met Pro Leu Val Leu Pro Pro Ser Val Leu Gly Phe Tyr Leu
50      55      60
Leu Leu Ile Phe Ser Pro Ser Ser Phe Leu Gly Ala Phe Leu Gln Asp
65      70      75      80
Val Leu Asn Val Lys Leu Val Phe Ser Phe Gln Gly Leu Ile Leu Gly
85      90      95
Ser Val Ile Phe Ser Leu Pro Phe Met Val Ser Pro Ile Lys Ser Ala
100     105     110
Leu Ile Ser Leu Pro Thr Ser Leu Lys Glu Ala Ser Tyr Ser Leu Gly
115     120     125
Lys Gly Glu Tyr Tyr Thr Leu Phe Phe Val Leu Leu Pro Asn Ile Lys

```

SUBSTITUTE SHEET (RULE 26)

375

130		135		140											
Pro	Ser	Val	Leu	Met	Ala	Ile	Ile	Thr	Thr	Phe	Met	His	Thr	Ile	Gly
145					150					155					160
Glu	Phe	Gly	Val	Val	Met	Met	Leu	Gly	Gly	Asp	Ile	Leu	Gly	Glu	Thr
				165					170					175	
Arg	Val	Ala	Ser	Ile	Thr	Ile	Phe	Asn	Glu	Ala	Glu	Ala	Leu	Asn	Tyr
			180					185					190		
Ser	Lys	Ala	His	Gln	Tyr	Ala	Leu	Thr	Leu	Thr	Leu	Ile	Ser	Phe	Ser
		195					200					205			
Leu	Leu	Phe	Val	Thr	Leu	Phe	Leu	Asn	Lys	Lys	Gln	Ser	Ser	Phe	Leu
210						215					220				

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454

Met	His	Pro	Ile	Met	Phe	Ala	Tyr	Ile	Ala	Asn	Ala	Leu	Ala	Gln	Ala
1				5				10						15	
Arg	Lys	Ile	Asn	Gly	Thr	Leu	Cys	Met	Ala	Phe	Gln	Lys	Ile	Ser	Gln
			20				25					30			
Val	Lys	Glu	Leu	Gly	Ile	Asp	Lys	Ala	Lys	Ser	Leu	Ile	Gly	Asn	Leu
		35				40					45				
Ser	Gln	Val	Ile	Ile	Tyr	Pro	Thr	Lys	Asp	Thr	Asp	Glu	Leu	Ile	Glu
		50			55				60						
Cys	Gly	Val	Pro	Leu	Ser	Asp	Ser	Glu	Ile	Asn	Phe	Leu	His	Asn	Thr
65				70				75						80	
Asp	Met	Arg	Ala	Arg	Gln	Val	Leu	Val	Lys	Asn	Ile	Val	Thr	Asn	Ala
			85					90						95	
Ser	Ala	Phe	Ile	Glu	Ile	Asp	Leu	Lys	Lys	Ile	Cys	Lys	Asn	Tyr	Phe
		100					105					110			
Ile	Phe	Leu	Ile	Ala	Met	Leu	Val	Ile	Glu	Lys	Ser	Ser	Met	Ile	Leu
		115				120						125			
Lys	Lys	Gln													
130															

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

SUBSTITUTE SHEET (RULE 26)

376

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...73

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455

```

Met Cys Leu Thr Gly Gly Leu Met Arg Trp Leu Lys Ser Val Lys Pro
1      5      10      15
Glu Arg Ile Leu His Ser Val Val Glu Phe Val Asp Ile Ala Gly Leu
      20      25      30
Ile Lys Gly Ala Ser Lys Gly Glu Gly Leu Gly Asn Gln Phe Leu Ala
      35      40      45
Asn Ile Lys Glu Cys Glu Val Ile Leu Gln Val Val Arg Cys Phe Glu
      50      55      60
Asp Asp Asn Asn His Ala Cys Glu Arg
65      70

```

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...92

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456

```

Met His Val Ala Cys Leu Leu Ala Leu Gly Asp Asn Leu Ile Thr Leu
1      5      10      15
Ser Leu Leu Lys Glu Ile Ala Ser Lys Lys Gln Gln Gln Ser Leu Lys Ile
      20      25      30
Leu Gly Thr His Leu Thr Leu Lys Ile Ala Lys Leu Leu Glu Cys Glu
      35      40      45
Lys His Phe Glu Ile Ile Pro Val Phe Glu Asn Ile Pro Ala Phe Tyr
      50      55      60
Asp Leu Lys Lys Gln Gly Val Phe Trp Ala Met Lys Asp Phe Leu Trp
      65      70      75      80
Leu Leu Lys Gln Leu Lys Asn Ile Lys Ser Asn Val
      85      90

```

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

SUBSTITUTE SHEET (RULE 26)

377

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457

```

Met Lys Lys Lys Pro Leu Met Trp Arg Ile Cys Ala Leu Arg Arg Leu
1      5      10      15
Leu Leu Gly Phe Lys Arg Glu Arg Glu Leu Leu Ser Phe Ala Lys His
20      25      30
Trp Asn Ile Pro Thr Ile Val Val Phe Thr His Thr Gln Ala Glu Ala
35      40      45
Gly Asp Ala Phe Val Gln Glu Thr Lys Gly Ile Ile Asp Glu Glu Trp
50      55      60
Gly Phe Lys Gly Phe Val Arg Ala Tyr Val Arg Val Asn Ser Val Ala
65      70      75      80
Phe Ser Phe Arg Gly Leu Lys Val Pro Val Glu Gly Leu Glu Glu Leu
85      90      95
Val Asp Glu Thr Lys Lys Cys Leu Ser Asp Ala Glu Lys Asn Lys Lys
100     105     110
Arg His Phe Leu Ser Ile Gln Arg Val Lys Ile Gln Glu Arg Lys Gln
115     120     125
Ala Met Ile Glu Glu Cys Lys Thr Ile Ile His Val Ala Ser Gly Ala
130     135     140
Ala Gly Val Ala Gly Leu Ile Pro Ile Pro Phe Ser Asp Ala Leu Ala
145     150     155     160
Ile Ala Pro Ile Gln Ala Gly Met Ile Tyr Lys Met Asn Asp Ala Phe
165     170     175
Gly Met Asp Leu Asp Lys Ser Val Gly Ala Ser Leu Val Ala Gly Leu
180     185     190
Leu Gly Val Asn Cys Arg Ala Ser Gly Glu Asp Ser Arg
195     200     205

```

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...41

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458

```

Val Leu Gly Val Unk Asn Leu Arg Gly Asn Val Phe Pro Leu Ile Ser
1      5      10      15
Leu Arg Leu Lys Phe Gly Leu Lys Ala Glu Lys Gln Asn Lys Asp Thr
20      25      30
Arg Tyr Leu Val Val Arg His Asn Asp
35      40

```

SUBSTITUTE SHEET (RULE 26)

378

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459

```

Val Lys Ser Val Phe Ser Glu Glu Lys Glu Thr Pro Val Thr Lys Glu
1      5      10      15
Asn Gly Ser Tyr Leu Ile Ala Tyr Asp Pro Leu Asp Gly Ser Ser Val
      20      25      30
Met Glu Ala Asn Phe Leu Val Gly Thr Ile Ile Gly Val Tyr Glu Lys
      35      40      45
Asp Tyr Lys Ala Gln Asn Leu Val Ala Ser Leu Tyr Val Val Phe Gly
      50      55      60
His Lys Ile Glu Leu Val Val Ala Leu Glu Glu Val Tyr Arg Tyr Ala
      65      70      75      80
Phe Tyr Gln Asn Lys Phe His Phe Ile Glu Thr Ile Val Leu Glu Asn
      85      90      95
Lys Gly Lys Ile Ile Ala Ser Gly Gly Asn Gln Lys Asp Phe Ser Leu
      100      105      110
Gly Leu Lys Lys Ala Leu Glu Gly Phe Phe Ala Glu Asn Tyr Arg Leu
      115      120      125
Arg Tyr Ser Gly Ser Met Val Ala Asp Val His His Val Leu Val Lys
      130      135      140
Lys Gly Gly Met Phe Ser Tyr Pro Gln Lys Lys Leu Arg Lys Leu Phe
      145      150      155      160
Glu Val Phe Pro Leu Ala Leu Met Val Glu Lys Ala Lys Gly Glu Ala
      165      170      175
Phe Tyr Phe Asp Lys Gly Val Lys Lys Arg Leu Leu Asp Gln Ser Val
      180      185      190
Glu Ser Tyr His Glu Lys Ser Glu Cys Tyr Leu Ala Ser Pro His Glu
      195      200      205
Ala Gln Ile Leu Glu Lys His Leu Lys Gly Glu
      210      215

```

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

SUBSTITUTE SHEET (RULE 26)

379

(A) NAME/KEY: misc_feature
(B) LOCATION 1...188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460

```

Met Lys Ser Ile Gly Glu Val Met Ala Ile Gly Gly Asn Phe Leu Glu
1      5      10      15
Ala Leu Gln Lys Ala Leu Cys Ser Leu Glu Asn Asn Trp Leu Gly Phe
      20      25      30
Glu Ser Leu Ser Lys Asp Leu Glu Ala Ile Lys Lys Glu Ile Arg Arg
      35      40      45
Pro Asn Pro Lys Arg Leu Leu Tyr Ile Ala Asp Ala Phe Arg Leu Gly
      50      55      60
Val Ser Val Asp Glu Val Phe Glu Leu Cys Gln Ile Asp Arg Trp Phe
      65      70      75      80
Leu Ser Gln Ile Gln Lys Leu Val Lys Ala Glu Glu Gly Ile Asn Ser
      85      90      95
Ser Val Leu Thr Asp Ala Lys Lys Leu Arg Gly Leu Lys Asn Leu Gly
      100     105     110
Phe Ser Asp Ala Arg Ile Ala Thr Lys Ile Lys Glu Asn Glu Asn Leu
      115     120     125
Glu Val Ser Pro Phe Glu Val Glu Leu Ala Arg Ser Asn Leu Gln Ile
      130     135     140
Ala Pro His Phe Glu Glu Val Asp Thr Cys Ala Ala Glu Phe Leu Ser
      145     150     155     160
Leu Thr Leu Ile Cys Ile Pro Pro Met Pro Leu Thr Leu Cys Pro Leu
      165     170     175
Leu Glu Thr Asn Lys Lys Asn Lys Lys Arg Lys Ser
      180     185

```

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461

```

Met Phe Gly Asn Lys Gln Leu Gln Ile Ser Gln Lys Asp Ser
1      5      10      15
Glu Ile Ala Glu Leu Lys Lys Glu Val Asn Leu Tyr Gln Ser Leu Leu
      20      25      30
Asn Leu Cys Leu His Glu Gly Phe Val Gly Ile Lys Asn Asn Lys Val
      35      40      45
Val Phe Lys Ser Gly Asn Leu Ala Ser Leu Asn Asn Leu Glu Glu Gln
      50      55      60
Ser Val His Phe Lys Glu Asn Ala Glu Ser Val Asn Leu Gln Gly Val
      65      70      75      80
Ser Tyr Ser Leu Lys Ser Gln Asn Ile Asp Gly Val Gln Tyr Phe Ser
      85      90      95
Leu Ala Lys Lys Thr Gly Gly Val Gly Glu Tyr His Lys Asn Asp Leu
      100     105     110

```

SUBSTITUTE SHEET (RULE 26)

380

```

Phe Lys Thr Phe Cys Thr Ser Leu Lys Glu Gly Leu Glu Asn Ala Gln
      115                      120                      125
Glu Ser Met Gln Tyr Phe His Gln Glu Thr Gly Leu Leu Leu Asn Ala
      130                      135                      140
Ala Lys Asn Gly Glu Glu His Ser Asn Glu Gly Leu Ile Thr Val Asn
145                      150                      155                      160
Lys Thr Gly Gln Asp Ile Glu Ser Leu Tyr Glu Lys Met Gln Asn Ala
      165                      170                      175
Thr Ser Leu Ala Asp Ser Leu Asn Gln Arg Ser Asn Glu Ile Thr Gln
      180                      185                      190
Val Ile Ser Leu Ile Asp Asp Ile Ala Glu Gln Thr Asn Leu Leu Ala
      195                      200                      205
Leu Asn Ala Ala Ile Glu Ala Ala Arg Ala Val Asn Met Ala Glu Gly
210                      215                      220
Leu Arg Trp Trp Leu Met Arg
225                      230

```

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462

```

Met Trp Ile Met Ser Ser Leu Ser Ser Ser Phe Phe His Ser Leu Phe
1           5           10           15
Phe Ile Lys Ser Asn Pro Gly Gln Leu Leu Lys Gly Trp Gly Ser Lys
      20           25           30
Ile Phe Phe Ile Asn Arg Lys Phe Val Leu Ala Gln Tyr Asn Pro Ser
      35           40           45
Val Ser Ile Phe Ile Leu Leu Asn Arg Val Phe Gly Val Gly Val
50           55           60

```

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...182

SUBSTITUTE SHEET (RULE 26)

381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463

```

Met Gln Phe Glu Glu Met Lys Glu Leu Ala His Gln Ile Gly Val Phe
1      5      10      15
Tyr His Val Gly Val Asp Gly Ile Ala Leu Phe Leu Leu Leu Asn
      20      25      30
Ala Ile Val Val Leu Leu Ser Val Val Tyr Val Lys Glu Arg Arg Lys
      35      40      45
Asp Phe Val Ile Cys Leu Leu Leu Leu Unk Gly Ile Leu Met Gly Val
      50      55      60
Phe Ser Ser Leu Asn Val Ile Phe Phe Tyr Ala Phe Trp Glu Ile Ser
      65      70      75      80
Leu Leu Pro Val Leu Tyr Leu Ile Gly Arg Phe Gly Arg Asn Asn Lys
      85      90      95
Ile Tyr Ser Gly Met Lys Phe Phe Leu Tyr Thr Phe Leu Ala Ser Leu
      100      105      110
Cys Met Leu Leu Gly Ile Leu Tyr Ile Gly Tyr Asp Tyr Ala Asn Asn
      115      120      125
Tyr Gly Met Met Ser Phe Asp Ile Leu Asp Trp Tyr Gln Leu Asn Phe
      130      135      140
Ser Ser Gly Ile Lys Thr Trp Leu Phe Val Ala Phe Leu Ile Gly Ile
      145      150      155      160
Ala Val Lys Ile Pro Leu Phe Pro Phe Thr His Gly Cys Leu Met Arg
      165      170      175
Ile Leu Thr Pro Pro Leu
      180

```

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463

```

Met Gln Phe Glu Glu Met Lys Glu Leu Ala His Gln Ile Gly Val Phe
1      5      10      15
Tyr His Val Gly Val Asp Gly Ile Ala Leu Phe Leu Leu Leu Asn
      20      25      30
Ala Ile Val Val Leu Leu Ser Val Val Tyr Val Lys Glu Arg Arg Lys
      35      40      45
Asp Phe Val Ile Cys Leu Leu Leu Leu Unk Gly Ile Leu Met Gly Val
      50      55      60
Phe Ser Ser Leu Asn Val Ile Phe Phe Tyr Ala Phe Trp Glu Ile Ser
      65      70      75      80
Leu Leu Pro Val Leu Tyr Leu Ile Gly Arg Phe Gly Arg Asn Asn Lys
      85      90      95
Ile Tyr Ser Gly Met Lys Phe Phe Leu Tyr Thr Phe Leu Ala Ser Leu
      100      105      110
Cys Met Leu Leu Gly Ile Leu Tyr Ile Gly Tyr Asp Tyr Ala Asn Asn
      115      120      125

```

SUBSTITUTE SHEET (RULE 26)

382

Tyr Gly Met Met Ser Phe Asp Ile Leu Asp Trp Tyr Gln Leu Asn Phe
 130 135 140
 Ser Ser Gly Ile Lys Thr Trp Leu Phe Val Ala Phe Leu Ile Gly Ile
 145 150 155 160
 Ala Val Lys Ile Pro Leu Phe Pro Phe Thr His Gly Cys Leu Met Arg
 165 170 175
 Ile Leu Thr Pro Pro Leu
 180

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464

Val Lys Lys Tyr Ala Glu Asp Phe Ile Thr Lys Asp Glu Val Lys Ser
 1 5 10 15
 Leu Leu Glu Arg Leu Ala Lys Asp Tyr Pro Thr Ile Val Glu Glu Ser
 20 25 30
 Lys Lys Ile Pro Thr Gly Ala Ile Arg Ser Val Leu Gln Ala Leu Leu
 35 40 45
 His Glu Lys Ile Pro Ile Lys Asp Met Leu Thr Ile Leu Glu Thr Ile
 50 55 60
 Thr Asp Ile Ala Pro Leu Val Gln Asn Asp Val Asn Ile Leu Thr Glu
 65 70 75 80
 Gln Val Arg Ala Arg Leu Ser Arg Val Ile Thr Asn Ala Phe Lys Ser
 85 90 95
 Glu Asp Gly Arg Leu Lys Phe Leu Thr Phe Ser Thr Asp Unk Glu Gln
 100 105 110
 Phe Unk Ala Gln
 115

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...116

SUBSTITUTE SHEET (RULE 26)

383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464

```

Val Lys Lys Tyr Ala Glu Asp Phe Ile Thr Lys Asp Glu Val Lys Ser
1      5      10      15
Leu Leu Glu Arg Leu Ala Lys Asp Tyr Pro Thr Ile Val Glu Glu Ser
      20      25      30
Lys Lys Ile Pro Thr Gly Ala Ile Arg Ser Val Leu Gln Ala Leu Leu
      35      40      45
His Glu Lys Ile Pro Ile Lys Asp Met Leu Thr Ile Leu Glu Thr Ile
      50      55      60
Thr Asp Ile Ala Pro Leu Val Gln Asn Asp Val Asn Ile Leu Thr Glu
      65      70      75      80
Gln Val Arg Ala Arg Leu Ser Arg Val Ile Thr Asn Ala Phe Lys Ser
      85      90      95
Glu Asp Gly Arg Leu Lys Phe Leu Thr Phe Ser Thr Asp Unk Glu Gln
      100      105      110
Phe Unk Ala Gln
      115

```

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465

```

Val Gly Ala Asn Pro Val Pro His Ala Gln Ile Leu Gln Ser Val Val
1      5      10      15
Asp Asp Leu Lys Glu Lys Gly Ile Lys Leu Val Ile Val Ser Phe Thr
      20      25      30
Asp Tyr Val Leu Pro Asn Leu Ala Leu Asn Asp Gly Ser Leu Asp Ala
      35      40      45
Asn Tyr Phe Gln His Arg Pro Tyr Leu Asp Arg Phe Asn Leu Asp Arg
      50      55      60
Lys Met His Leu Val Gly Leu Ala Asn Ile His Val Glu Pro Leu Arg
      65      70      75      80
Phe Tyr Ser Gln Lys Ile Thr Asp Ile Lys Asn Leu Lys Lys Gly Ser
      85      90      95
Val Ile Ala Val Pro Asn Asp Pro Ala Asn Gln Gly Arg Ala Leu Ile
      100      105      110
Leu Leu His Lys Gln Gly Leu Ile Ala Leu Lys Asp Pro Ser Asn Leu
      115      120      125
Tyr Ala Thr Glu Phe Asp Ile Val Lys Asn Pro Tyr Asn Ile Lys Ile
      130      135      140
Lys Pro Leu Glu Ala Ala Val Ile Ala
      145      150

```

(2) INFORMATION FOR SEQ ID NO:466:

SUBSTITUTE SHEET (RULE 26)

384

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...43

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466

```

Met Gly Leu Val Ala Ser Gly Ile Asn Asp Glu Glu Leu Leu Lys Trp
1           5           10           15
Leu Gln Ala Phe Gly Leu Lys Met Gly Leu Cys Phe Gln Val Leu Asp
          20           25           30
Asp Ile Ile Asp Val Thr Gln Asp Glu Lys Glu
      35           40

```

(2) INFORMATION FOR SEQ ID NO:467:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 240 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467

```

Met Met Lys Asn Lys Arg Ser Gln Asn Ser Pro Tyr Val Thr Pro Asp
1           5           10           15
Asn Pro Tyr Leu Thr Leu Glu Lys Ala Leu Gly Tyr Ser Phe Lys Asp
          20           25           30
Lys Arg Leu Leu Glu Gln Ala Leu Thr His Lys Ser Cys Lys Leu Ala
      35           40           45
Leu Asn Asn Glu Arg Leu Glu Phe Leu Gly Asp Ala Val Leu Gly Leu
      50           55           60
Val Ile Gly Glu Leu Leu Tyr His Lys Phe Unk Unk Asp Gly Gly
      65           70           75           80
Lys Leu Ser Lys Leu Arg Ala Ser Ile Val Ser Ala His Gly Phe Thr
          85           90           95
Lys Leu Ala Lys Ala Ile Ala Leu Gln Asp Tyr Leu Arg Val Ser Ser
          100          105          110
Ser Glu Glu Ile Ser Lys Gly Arg Glu Lys Pro Ser Ile Leu Ser Ser
          115          120          125
Ala Phe Glu Ala Leu Met Ala Gly Val Tyr Leu Glu Ala Gly Leu Ala
          130          135          140
Lys Val Arg Lys Ile Ile Gln Asn Leu Leu Asn Arg Ala Tyr Lys Arg

```

SUBSTITUTE SHEET (RULE 26)

385

145		150		155		160
Leu Asp	Leu Glu	His Leu	Phe Met	Asp Tyr	Lys Thr	Ala Leu
		165		170		175
Leu Thr	Gln Unk	Gln Phe	Cys Val	Ile Pro	Thr Tyr	Gln Leu
		180		185		190
Glu Lys	Gly Pro	Asp His	His Lys	Glu Phe	Glu Met	Ala Leu
		195		200		205
Gln Asp	Lys Met	Tyr Ala	Thr Ala	Lys Gly	Lys Ser	Lys Lys
		210		215		220
Glu Gln	Gln Cys	Ala Tyr	Gln Ala	Leu Gln	Asn Leu	Arg Lys
225		230		235		240

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467

Met	Met	Lys	Asn	Lys	Arg	Ser	Gln	Asn	Ser	Pro	Tyr	Val	Thr	Pro	Asp
1				5					10					15	
Asn	Pro	Tyr	Leu	Thr	Leu	Glu	Lys	Ala	Leu	Gly	Tyr	Ser	Phe	Lys	Asp
			20					25					30		
Lys	Arg	Leu	Leu	Glu	Gln	Ala	Leu	Thr	His	Lys	Ser	Cys	Lys	Leu	Ala
			35					40					45		
Leu	Asn	Asn	Glu	Arg	Leu	Glu	Phe	Leu	Gly	Asp	Ala	Val	Leu	Gly	Leu
			50				55				60				
Val	Ile	Gly	Glu	Leu	Leu	Tyr	His	Lys	Phe	Unk	Unk	Unk	Asp	Gly	Gly
65					70					75				80	
Lys	Leu	Ser	Lys	Leu	Arg	Ala	Ser	Ile	Val	Ser	Ala	His	Gly	Phe	Thr
				85					90					95	
Lys	Leu	Ala	Lys	Ala	Ile	Ala	Leu	Gln	Asp	Tyr	Leu	Arg	Val	Ser	Ser
				100				105					110		
Ser	Glu	Glu	Ile	Ser	Lys	Gly	Arg	Glu	Lys	Pro	Ser	Ile	Leu	Ser	Ser
			115				120					125			
Ala	Phe	Glu	Ala	Leu	Met	Ala	Gly	Val	Tyr	Leu	Glu	Ala	Gly	Leu	Ala
			130				135					140			
Lys	Val	Arg	Lys	Ile	Ile	Gln	Asn	Leu	Leu	Asn	Arg	Ala	Tyr	Lys	Arg
145					150					155				160	
Leu	Asp	Leu	Glu	His	Leu	Phe	Met	Asp	Tyr	Lys	Thr	Ala	Leu	Gln	Glu
				165					170					175	
Leu	Thr	Gln	Unk	Gln	Phe	Cys	Val	Ile	Pro	Thr	Tyr	Gln	Leu	Leu	Gln
			180					185					190		
Glu	Lys	Gly	Pro	Asp	His	His	Lys	Glu	Phe	Glu	Met	Ala	Leu	Tyr	Ile
			195				200					205			
Gln	Asp	Lys	Met	Tyr	Ala	Thr	Ala	Lys	Gly	Lys	Ser	Lys	Lys	Glu	Ala
			210				215				220				
Glu	Gln	Gln	Cys	Ala	Tyr	Gln	Ala	Leu	Gln	Asn	Leu	Arg	Lys	Pro	Asn
225					230				235					240	

SUBSTITUTE SHEET (RULE 26)

386

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468

```

Met Gly Phe Asn Arg Leu Val Asp Arg Asp Ile Asp Lys Asp Asn Pro
1          5          10          15
Arg Thr Lys Asn Arg Pro Ser Val Asp Gly Arg Ile Ser Val Lys Gly
20          25          30
Met Val Ile Phe Ser Val Ser Asn Ala Leu Leu Phe Val Gly Val Ser
35          40          45
Tyr Phe Ile Asn Pro Leu Ala Phe Lys Leu Ser Leu Pro Phe Leu Ile
50          55          60
Ile Leu Gly Gly Tyr Ser Tyr Phe Lys Arg Phe Ser Ser Leu Ala His
65          70          75          80
Phe Val Val Gly Leu Ala Leu Gly Leu Ala Pro Ile Ala Gly Ser Val
85          90          95
Ala Val Leu Gly Asp Ile Pro Leu Trp Asn Val Phe Leu Ala Leu Gly
100         105         110
Val Met Leu Trp Val Ala Gly Phe Asp Leu Leu Tyr Ser Leu Gln Asp
115         120         125
Met Glu Phe Asp Lys Glu Arg Gly Leu Phe Ser Ile Pro Ser Gln Leu
130         135         140
Gly Glu Lys Trp Cys Leu Asn Leu Ser Arg Leu Ser His Leu Val Ala
145         150         155         160
Leu Ile Cys Trp Leu Cys Phe Val Lys Cys Tyr His Gly Gly Leu Phe
165         170         175
Ala Tyr Leu Gly Leu Gly Val Ser Ala Leu Ile Leu Leu Tyr Glu Gln
180         185         190
Ile Leu Val Ala Arg Asp Tyr Lys Asn Ile Pro Lys Ser Leu Phe Cys
195         200         205
Glu

```

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

SUBSTITUTE SHEET (RULE 26)

387

(A) NAME/KEY: misc_feature
(B) LOCATION 1...95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469

Val	Glu	Gln	Asn	Lys	Ile	Ile	Lys	Leu	Phe	Thr	Val	Ala	Thr	Met	Ala
1				5					10					15	
Met	Met	Pro	Pro	Thr	Leu	Ile	Gly	Thr	Ile	Asn	Gly	Met	Asn	Phe	Lys
			20					25					30		
Phe	Met	Pro	Glu	Leu	Glu	Trp	Gln	Tyr	Gly	Tyr	Leu	Phe	Ala	Leu	Ile
		35				40					45				
Val	Met	Ala	Ile	Ser	Thr	Ile	Leu	Pro	Val	Ile	Tyr	Phe	Lys	Lys	Lys
	50					55					60				
Gly	Leu	Val	Val	Ala	Phe	His	Gly	Ile	Phe	Ile	Leu	Thr	Leu	Arg	Arg
65				70					75					80	
Ser	Phe	Tyr	Thr	Ala	Trp	His	Ser	Leu	Leu	Gly	Tyr	Ala	Thr	Leu	
			85					90						95	

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470

Leu	Leu	Val	Leu	Leu	Asn	Leu	Lys	Unk	Thr	Pro	Asn	Leu	Met	Trp	Pro
1				5					10					15	
Leu	Asp	Ile	Ile	Val	Val	Val	Ala	Trp	Val	Leu	Trp	Gly	Val	Asn	Met
			20					25					30		
Phe	Gly	Ser	Met	Ser	Val	Arg	Arg	Glu	Asn	Thr	Ile	Tyr	Val	Ser	Leu
		35				40					45				
Trp	Tyr	Tyr	Ile	Ala	Thr	Tyr	Val	Gly	Ile	Ala	Val	Met	Tyr	Ile	Phe
	50					55				60					
Asn	Asn	Leu	Ser	Ile	Pro	Thr	Tyr	Phe	Val	Ala	Asp	Met	Gly	Ser	Val
65				70					75					80	
Trp	His	Unk	Ile	Ser	Met	Tyr	Ser	Gly	Ser	Asn	Asp	Ala	Leu	Ile	Gln
		85						90					95		
Trp	Trp	Trp	Gly	His	Asn	Ala	Val	Ala	Phe	Val	Phe	Thr	Ser	Gly	Val
		100				105						110			
Ile	Gly	Thr	Ile	Tyr	Tyr	Phe	Leu	Pro	Lys	Glu	Ser	Gly	Gln	Pro	Ile
	115					120						125			
Phe	Ser	Tyr	Lys	Leu	Thr	Leu	Phe	Ser	Phe	Trp	Ser	Leu	Met	Phe	Val
	130					135				140					
Tyr	Ile	Trp	Ala	Gly	Gly	His	His	Leu	Ile	Tyr	Ser	Thr	Val	Unk	Asp
145			150						155					160	
Unk	Val	Gln	Thr	Leu	Ser	Ser	Unk	Phe	Ser	Val	Val	Leu	Ile	Leu	Pro
		165						170					175		
Ser	Unk	Gly	Thr	Ala	Ile	Asn	Met	Leu	Leu	Unk	Met	Arg	Gly	Gln	Trp
	180					185						190			
His	Gln	Unk	Lys	Glu	Ser	Pro	Leu	Ile	Lys	Phe	Leu	Val	Leu	Ala	Ser
	195					200						205			

SUBSTITUTE SHEET (RULE 26)

388

Thr Phe Tyr Met Leu Ser Thr Leu Glu Gly Ser Ile Gln Ala Ile Lys
 210 215 220
 Ser Val Asn Ala
 225

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470

Leu Leu Val Leu Leu Asn Leu Lys Unk Thr Pro Asn Leu Met Trp Pro
 1 5 10 15
 Leu Asp Ile Ile Val Val Val Ala Trp Val Leu Trp Gly Val Asn Met
 20 25 30
 Phe Gly Ser Met Ser Val Arg Arg Glu Asn Thr Ile Tyr Val Ser Leu
 35 40 45
 Trp Tyr Tyr Ile Ala Thr Tyr Val Gly Ile Ala Val Met Tyr Ile Phe
 50 55 60
 Asn Asn Leu Ser Ile Pro Thr Tyr Phe Val Ala Asp Met Gly Ser Val
 65 70 75 80
 Trp His Unk Ile Ser Met Tyr Ser Gly Ser Asn Asp Ala Leu Ile Gln
 85 90 95
 Trp Trp Trp Gly His Asn Ala Val Ala Phe Val Phe Thr Ser Gly Val
 100 105 110
 Ile Gly Thr Ile Tyr Tyr Phe Leu Pro Lys Glu Ser Gly Gln Pro Ile
 115 120 125
 Phe Ser Tyr Lys Leu Thr Leu Phe Ser Phe Trp Ser Leu Met Phe Val
 130 135 140
 Tyr Ile Trp Ala Gly Gly His His Leu Ile Tyr Ser Thr Val Unk Asp
 145 150 155 160
 Unk Val Gln Thr Leu Ser Ser Unk Phe Ser Val Val Leu Ile Leu Pro
 165 170 175
 Ser Unk Gly Thr Ala Ile Asn Met Leu Leu Unk Met Arg Gly Gln Trp
 180 185 190
 His Gln Unk Lys Glu Ser Pro Leu Ile Lys Phe Leu Val Leu Ala Ser
 195 200 205
 Thr Phe Tyr Met Leu Ser Thr Leu Glu Gly Ser Ile Gln Ala Ile Lys
 210 215 220
 Ser Val Asn Ala
 225

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

389

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...92

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471

```

Met Phe Asp Ser Ile Val Tyr Phe Phe Asn Lys Ser Gly Phe Val Thr
1      5      10      15
Thr Leu Val Leu Val Trp Ile Ser Leu Tyr Leu Val Met Thr Leu Trp
      20      25      30
Val Phe Leu Tyr Lys Ser Ile Val Leu Lys Ile Glu Leu Arg Arg Glu
      35      40      45
Met Gln Ser Leu Ser Asn Ile Leu Asn Gly Ala Gln Asp Ala Pro Glu
50      55      60
His Phe Met Phe Asn Lys Lys Arg Asn Asp Glu Thr Lys Arg Tyr Ser
65      70      75      80
Asn Glu Leu Leu Gln Asp Leu Glu Thr Pro Gly Ser
      85      90

```

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...96

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472

```

Met Ala Met Leu Tyr Cys Met Arg Leu Leu Met Pro Ile Leu Gly Ala
1      5      10      15
Ile Lys Gly Gly Asp Ile Gly Glu Trp Phe Pro Asp Asn Asp Pro Lys
      20      25      30
Tyr Lys Asn Ala Ser Ser Lys Glu Leu Leu Lys Ile Val Leu Asp Phe
      35      40      45
Ser Gln Ser Ile Gly Phe Glu Leu Leu Glu Met Gly Ala Thr Ile Phe
50      55      60
Ser Glu Ile Pro Lys Ile Thr Pro Tyr Lys Pro Ala Ile Leu Glu Asn
65      70      75      80
Leu Ser Gln Leu Leu Gly Leu Glu Lys Ser Gln Ile Ser Leu Lys Ala
      85      90      95

```

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1178 amino acids

SUBSTITUTE SHEET (RULE 26)

390

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473

```

Met Ile Pro Asn Leu Asp Ile Glu Gly Glu Thr Met Thr Asn Glu Ala
1      5      10      15
Ile Asn Gln Gln Pro Gln Thr Glu Ala Ala Phe Asn Pro Gln Gln Phe
      20      25      30
Ile Asn Asn Leu Gln Val Ala Phe Ile Lys Val Asp Asn Val Val Ala
      35      40      45
Ser Phe Asp Pro Asn Gln Lys Pro Ile Val Asp Lys Asn Asp Arg Asp
50      55      60
Asn Arg Gln Ala Phe Glu Lys Ile Ser Gln Leu Arg Glu Glu Phe Ala
65      70      75      80
Asn Lys Ala Ile Lys Asn Pro Thr Lys Lys Asn Gln Tyr Phe Ser Ser
      85      90      95
Phe Ile Ser Lys Ser Asn Asp Leu Ile Asp Lys Asp Asn Leu Ile Asp
      100      105      110
Thr Gly Ser Ser Ile Lys Ser Phe Gln Lys Phe Gly Thr Gln Arg Tyr
      115      120      125
Gln Ile Phe Met Asn Trp Val Ser His Gln Asn Asp Pro Ser Lys Ile
130      135      140
Asn Thr Gln Lys Ile Arg Gly Phe Met Glu Asn Ile Ile Gln Pro Pro
145      150      155      160
Ile Ser Asp Asp Lys Glu Lys Ala Glu Phe Leu Arg Ser Ala Lys Gln
      165      170      175
Ala Phe Ala Gly Ile Ile Ile Gly Asn Gln Ile Arg Ser Asp Gln Lys
      180      185      190
Phe Met Gly Val Phe Asp Glu Ser Leu Lys Glu Arg Gln Glu Ala Glu
195      200      205
Lys Asn Gly Glu Pro Asn Gly Asp Pro Thr Gly Gly Asp Trp Leu Asp
210      215      220
Ile Phe Leu Ser Phe Val Phe Asn Lys Lys Gln Ser Ser Asp Leu Lys
225      230      235      240
Glu Thr Leu Asn Gln Glu Pro Val Pro His Val Gln Pro Asp Val Ala
      245      250      255
Thr Thr Thr Thr Asp Ile Gln Ser Leu Pro Pro Glu Ala Arg Asp Leu
260      265      270
Leu Asp Glu Arg Gly Asn Phe Ser Lys Phe Thr Leu Gly Asp Met Asn
275      280      285
Met Leu Asp Val Glu Gly Val Ala Asp Ile Asp Pro Asn Tyr Lys Phe
290      295      300
Asn Gln Leu Leu Ile His Asn Asn Ala Leu Ser Ser Val Leu Met Gly
305      310      315      320
Ser His Asn Gly Ile Glu Pro Glu Lys Val Ser Leu Leu Tyr Gly Asn
      325      330      335
Asn Gly Gly Pro Glu Ala Arg His Asp Trp Asn Ala Thr Val Gly Tyr
      340      345      350
Lys Asn Gln Arg Gly Asp Asn Val Ala Thr Leu Ile Asn Val His Met
355      360      365
Lys Asn Gly Ser Gly Leu Val Ile Ala Gly Gly Glu Lys Gly Ile Asn
370      375      380
Asn Pro Ser Phe Tyr Leu Tyr Lys Glu Asp Gln Leu Thr Gly Ser Gln

```

SUBSTITUTE SHEET (RULE 26)

391

385		390		395		400									
Arg	Ala	Leu	Ser	Gln	Glu	Glu	Ile	Gln	Asn	Lys	Val	Asp	Phe	Met	Glu
				405					410					415	
Phe	Leu	Ala	Gln	Asn	Asn	Ala	Lys	Leu	Asp	Asn	Leu	Ser	Lys	Lys	Glu
			420					425						430	
Lys	Glu	Lys	Phe	Gln	Asn	Glu	Ile	Glu	Asp	Phe	Gln	Lys	Asp	Ser	Lys
			435					440					445		
Ala	Tyr	Leu	Asp	Ala	Leu	Gly	Asn	Asp	His	Ile	Ala	Phe	Val	Ser	Lys
			450				455				460				
Lys	Asp	Lys	Lys	His	Leu	Ala	Leu	Val	Ala	Glu	Phe	Gly	Asn	Gly	Glu
				470						475					480
Leu	Ser	Tyr	Thr	Leu	Lys	Asp	Tyr	Gly	Lys	Lys	Ala	Asp	Lys	Ala	Leu
				485					490					495	
Asp	Arg	Glu	Ala	Lys	Thr	Thr	Leu	Gln	Gly	Ser	Leu	Lys	His	Asp	Gly
			500					505					510		
Val	Met	Phe	Val	Asp	Tyr	Ser	Asn	Phe	Lys	Tyr	Thr	Asn	Ala	Ser	Lys
			515				520					525			
Ser	Pro	Asp	Lys	Gly	Val	Gly	Ala	Thr	Asn	Gly	Val	Ser	His	Leu	Glu
			530				535				540				
Ala	Gly	Phe	Ser	Lys	Val	Ala	Val	Phe	Asn	Leu	Pro	Asn	Leu	Asn	Asn
			545			550				555				560	
Leu	Ala	Ile	Thr	Ser	Val	Val	Arg	Gln	Asp	Leu	Glu	Asp	Lys	Leu	Ile
			565					570						575	
Ala	Lys	Gly	Leu	Ser	Pro	Gln	Glu	Ala	Asn	Lys	Leu	Val	Lys	Asp	Phe
			580					585					590		
Leu	Ser	Ser	Asn	Lys	Glu	Leu	Val	Gly	Lys	Ala	Leu	Asn	Phe	Asn	Lys
			595				600				605				
Ala	Val	Ala	Glu	Ala	Lys	Asn	Thr	Gly	Asn	Tyr	Asp	Glu	Val	Lys	Gln
			610				615				620				
Ala	Gln	Lys	Asp	Leu	Glu	Lys	Ser	Leu	Lys	Lys	Arg	Glu	Arg	Leu	Glu
			625			630				635				640	
Lys	Asp	Val	Ala	Lys	Asn	Leu	Glu	Ser	Lys	Ser	Gly	Asn	Lys	Asn	Lys
			645						650					655	
Met	Glu	Ala	Lys	Ser	Gln	Ala	Asn	Ser	Gln	Lys	Asp	Glu	Ile	Phe	Ala
			660					665					670		
Leu	Ile	Asn	Lys	Glu	Ala	Asn	Arg	Asp	Ala	Arg	Ala	Ile	Ala	Tyr	Ala
			675				680					685			
Gln	Asn	Leu	Lys	Gly	Ile	Lys	Arg	Glu	Leu	Ser	Asp	Lys	Leu	Glu	Asn
			690			695					700				
Ile	Asn	Lys	Asp	Leu	Lys	Asp	Phe	Ser	Lys	Ser	Phe	Asp	Glu	Phe	Lys
			705			710				715				720	
Asn	Gly	Lys	Asn	Lys	Asp	Phe	Ser	Lys	Ala	Glu	Glu	Thr	Leu	Lys	Ala
			725						730					735	
Leu	Lys	Gly	Ser	Val	Lys	Asp	Leu	Gly	Ile	Asn	Pro	Glu	Trp	Ile	Ser
			740					745					750		
Lys	Val	Glu	Asn	Leu	Asn	Ala	Ala	Leu	Asn	Glu	Phe	Lys	Asn	Gly	Lys
			755				760				765				
Asn	Lys	Asp	Phe	Ser	Lys	Val	Thr	Gln	Ala	Lys	Ser	Asp	Leu	Glu	Asn
			770			775					780				
Ser	Ile	Lys	Asp	Val	Ile	Asn	Gln	Lys	Ile	Thr	Asp	Lys	Val	Asp	
			785			790				795				800	
Asn	Leu	Asn	Gln	Ala	Val	Ser	Val	Ala	Lys	Ala	Thr	Gly	Asp	Phe	Ser
			805					810						815	
Gly	Val	Glu	Gln	Ala	Leu	Ala	Asp	Leu	Lys	Asn	Phe	Ser	Lys	Glu	Gln
			820					825					830		
Leu	Ala	Gln	Gln	Ala	Gln	Lys	Asn	Glu	Asp	Phe	Asn	Thr	Gly	Lys	Asn
			835				840					845			
Ser	Ala	Leu	Tyr	Gln	Ser	Val	Lys	Asn	Gly	Val	Asn	Gly	Thr	Leu	Val
			850			855					860				
Gly	Asn	Gly	Leu	Ser	Lys	Ala	Glu	Ala	Thr	Thr	Leu	Ser	Lys	Asn	Phe
			865			870				875				880	
Ser	Asp	Ile	Lys	Lys	Glu	Leu	Asn	Ala	Lys	Leu	Gly	Asn	Phe	Asn	Asn
			885						890					895	
Asn	Asn	Asn	Asn	Gly	Leu	Glu	Asn	Ser	Thr	Glu	Pro	Ile	Tyr	Thr	Gln
			900					905						910	

SUBSTITUTE SHEET (RULE 26)

392

```

Val Ala Lys Lys Val Lys Ala Lys Ile Asp Arg Leu Asp Gln Ile Ala
    915                      920                      925
Ser Gly Leu Gly Asp Val Gly Gln Ala Ala Ser Phe Leu Leu Lys Arg
    930                      935                      940
His Asp Lys Val Asp Asp Leu Ser Lys Val Gly Leu Ser Ala Asn His
    945                      950                      955                      960
Glu Pro Ile Tyr Ala Thr Ile Asp Asp Leu Gly Gly Pro Phe Pro Leu
    965                      970                      975
Lys Arg His Asp Lys Val Asp Asp Leu Ser Lys Val Gly Leu Ser Arg
    980                      985                      990
Glu Gln Lys Leu Thr Gln Lys Ile Asp Asn Leu Asn Gln Ala Val Ser
    995                      1000                      1005
Glu Ala Lys Ala Ser His Phe Asp Asn Leu Asp Gln Met Ile Asp Lys
    1010                      1015                      1020
Leu Lys Asp Ser Thr Lys Lys Asn Val Val Asn Leu Tyr Val Glu Ser
    1025                      1030                      1035                      1040
Ala Lys Lys Val Pro Thr Ser Leu Ser Ala Lys Leu Asp Asn Tyr Ala
    1045                      1050                      1055
Thr Asn Ser His Thr Arg Ile Asn Ser Asn Val Lys Asn Gly Thr Ile
    1060                      1065                      1070
Asn Glu Lys Ala Thr Gly Met Leu Thr Gln Lys Asn Ser Glu Trp Leu
    1075                      1080                      1085
Lys Leu Val Asn Asp Lys Ile Val Ala His Asn Val Gly Ser Ala Pro
    1090                      1095                      1100
Leu Ser Ala Tyr Asp Lys Ile Gly Phe Asn Gln Lys Asn Met Lys Asp
    1105                      1110                      1115                      1120
Tyr Ser Asp Ser Phe Lys Phe Ser Thr Arg Leu Ser Asn Ala Val Lys
    1125                      1130                      1135
Asp Ile Lys Ser Gly Phe Val Gln Phe Leu Thr Asn Ile Phe Ser Met
    1140                      1145                      1150
Gly Ser Tyr Ser Leu Met Lys Ala Ser Val Glu His Gly Val Lys Asn
    1155                      1160                      1165
Thr Asn Thr Lys Gly Gly Phe Gln Lys Ser
    1170                      1175

```

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474

```

Met Lys Ala Pro Ser Gln Unk Asp Leu Lys Lys Ile Leu Gly Ile Glu
1          5          10          15
Glu Val Ile Unk Unk Ser Thr Ser Pro Met Glu Leu Arg Leu Ala Asn
20          25          30
Gln Lys Leu Gly Asn Arg Phe Ile Lys Thr Leu Gln Ala Met Asn Glu
35          40          45
Leu Asp Met Gly Ala Phe Phe Asn Ala Tyr Ala Gln Thr Thr Lys Asp
50          55          60
Pro Thr His Ala Thr Ser Tyr Gly Val Phe Ala Ala Ser Leu Asn Met

```

SUBSTITUTE SHEET (RULE 26)

393

```

65          70          75          80
Glu Leu Lys Lys Ala Leu Arg His Tyr Leu Tyr Ala Gln Thr Ser Asn
      85          90          95
Met Val Ile Asn Cys Val Lys Ser Val Pro Leu Ser Gln Asn Asp Gly
      100          105          110
Gln Lys Ile Leu Leu Ser Leu Gln Ser Pro Phe Asn Gln Leu Ile Glu
      115          120          125
Lys Thr Leu Glu Leu Asp Glu Ser His Leu Cys Ala Ala Ser Val Gln
      130          135          140
Asn Asp Ile Lys Ala Met Gln His Glu Ser Leu Tyr Ser Arg Leu Tyr
145          150          155          160
Met Ser

```

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474

```

Met Lys Ala Pro Ser Gln Unk Asp Leu Lys Lys Ile Leu Gly Ile Glu
1          5          10          15
Glu Val Ile Unk Unk Ser Thr Ser Pro Met Glu Leu Arg Leu Ala Asn
      20          25          30
Gln Lys Leu Gly Asn Arg Phe Ile Lys Thr Leu Gln Ala Met Asn Glu
      35          40          45
Leu Asp Met Gly Ala Phe Phe Asn Ala Tyr Ala Gln Thr Thr Lys Asp
50          55          60
Pro Thr His Ala Thr Ser Tyr Gly Val Phe Ala Ala Ser Leu Asn Met
65          70          75          80
Glu Leu Lys Lys Ala Leu Arg His Tyr Leu Tyr Ala Gln Thr Ser Asn
      85          90          95
Met Val Ile Asn Cys Val Lys Ser Val Pro Leu Ser Gln Asn Asp Gly
      100          105          110
Gln Lys Ile Leu Leu Ser Leu Gln Ser Pro Phe Asn Gln Leu Ile Glu
      115          120          125
Lys Thr Leu Glu Leu Asp Glu Ser His Leu Cys Ala Ala Ser Val Gln
      130          135          140
Asn Asp Ile Lys Ala Met Gln His Glu Ser Leu Tyr Ser Arg Leu Tyr
145          150          155          160
Met Ser

```

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

394

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...466

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475

```

Met Lys Ala Leu Lys Thr Phe Leu Lys Lys Ser Leu Ile Leu Leu Leu
1      5      10      15
Ala Ile Ala Leu Asn His Leu Asn Ala Val Ala Met Ile Val Asp Asn
20      25      30
Pro Thr Gln Asn Ala Trp Asn Gly Ala Lys Arg Ala Trp Asp Glu Ser
35      40      45
Lys Trp Ala Lys His Leu Ala Thr Ile Thr Glu Arg Ile Lys Leu Ala
50      55      60
Gln Asp Thr Leu Asp Arg Ala Asn Gln Thr Leu Asn Ser Ile Asn Lys
65      70      75      80
Val Asn Asp Val Leu Asn Lys Thr Asn Gln Phe Leu Thr Gly Ser Ile
85      90      95
Leu Ser Ile Pro Asn Pro Met Gln Tyr Val Glu Lys Ile Gln Ser Phe
100     105     110
Ala Lys Gln Val Gln Ala Asn Thr Glu Arg Ile Lys Glu Asn Ala Gln
115     120     125
Asn Tyr Asp Ile Arg Asn Gln Ile Ala Ala Lys Arg Ile Ser Glu Lys
130     135     140
Cys Pro Glu Leu Asn Trp Asp Val Ser Gln Asp Ala Ser Pro Thr Glu
145     150     155     160
Lys Asn Leu His Gln Phe Phe Thr Ser Lys Gly Lys Glu Ser Ala Asn
165     170     175
Thr Lys Ala Leu Lys Asp Phe Ala Asn Ala Ile Gly Asn Thr Gln Ile
180     185     190
Ser Thr Ala Asn Asp Leu Gly Ala Gly Leu Arg Gly Arg Ala Leu Leu
195     200     205
Glu Tyr Ile Cys Ile Gln Lys Gly Asn Leu Glu Ala Ala Lys Lys Ile
210     215     220
Gln Leu Leu Asp Ser Gln Met Thr Leu Ala Leu Leu Asn Asn Asp Tyr
225     230     235     240
Thr Ala Tyr Glu Lys Leu Arg Ala Glu Lys Glu Glu Leu Lys Arg Gln
245     250     255
Ile Ala Ser Asn Val Tyr Ala Lys Val Lys Gln Leu Val Val Ala Ser
260     265     270
Gln Asp Arg Ala Phe Ser Gln Met Asp Asn Glu Leu Gly Val Lys Thr
275     280     285
Phe Gly Phe Asn Asp Glu Asn Val Lys Lys Gly Tyr Cys Lys Lys Glu
290     295     300
Asn Arg Asn Gly Lys Ser Glu Cys Ile Pro Asn Met Leu Asn Val Asn
305     310     315     320
Arg Leu Lys Ala Gln Phe Asp Glu Leu Asn Leu Asp Tyr Ser Arg Asp
325     330     335
Ile Ala Gly Lys Lys Gly Glu Ala Ala Ala Lys Val Phe Asn Asp Tyr
340     345     350
Lys His Arg Phe Gln Gln Leu Ser Val Glu Thr Ala Leu Glu Ile Ala
355     360     365
Gln Asn Leu Ser Phe Met Asn Lys Thr Leu Gly Leu Met Val Gln Met
370     375     380
Gln Ser Tyr Ala Phe Lys Gln Gln Met Gly Tyr Phe Glu Asp Ile Ile
385     390     395     400
Pro Ala Asp Ala Leu Lys Asp Asp Lys Glu His Gln Glu Asn Leu Glu

```

SUBSTITUTE SHEET (RULE 26)

395

```

          405          410          415
Gln Lys Gln Gln Glu Ile Glu Lys Val Tyr Arg Ala Lys Leu Asp Ala
          420          425          430
Tyr Gly Phe Pro Asn Gly Ser Val Gly Lys Ala Ser Gly Val Asn Ser
          435          440          445
Asn Ser Asn Asn Glu Ala Pro Ser Ser Asp Asn Ile Gln Ser Phe Asn
          450          455          460
Pro Tyr
465

```

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...59

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476

```

Met Ala Phe Ile Leu Thr Thr Asn Leu Phe Ile Lys Ser Phe Thr Asn
1          5          10          15
Ser Ile Arg Ile Thr Gly Cys Ile Ile Ser Pro Asn Val Phe Phe Ala
          20          25          30
Tyr Glu Phe Cys Ala Leu Gly Phe Arg Lys Gly Gly Leu Ile Leu Asp
          35          40          45
Asn Phe Ser Lys Phe Val Ser His Arg Leu Gln
50          55

```

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...59

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476

```

Met Ala Phe Ile Leu Thr Thr Asn Leu Phe Ile Lys Ser Phe Thr Asn
1          5          10          15
Ser Ile Arg Ile Thr Gly Cys Ile Ile Ser Pro Asn Val Phe Phe Ala
          20          25          30

```

SUBSTITUTE SHEET (RULE 26)

396

Tyr Glu Phe Cys Ala Leu Gly Phe Arg Lys Gly Gly Leu Ile Leu Asp
 35 40 45
 Asn Phe Ser Lys Phe Val Ser His Arg Leu Gln
 50 55

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477

Val Arg Phe Phe Ile Phe Leu Ile Leu Ile Cys Pro Leu Ile Cys Pro
 1 5 10 15
 Leu Met Ser Ala Asp Ser Ala Leu Pro Ser Val Asn Leu Ser Leu Asn
 20 25 30
 Ala Pro Ser Asp Pro Lys Gln Leu Val Thr Thr Leu Asn Val Ile Ala
 35 40 45
 Leu Leu Thr Leu Leu Val Leu Ala Pro Ser Leu Ile Leu Val Met Thr
 50 55 60
 Ser Phe Thr Arg Leu Ile Val Val Phe Ser Phe Leu Arg Thr Ala Leu
 65 70 75 80
 Gly Thr Gln Gln Thr Pro Pro Thr Gln Ile Leu Val Ser Leu Ser Leu
 85 90 95
 Ile Leu Thr Phe Phe Ile Met Glu Pro Ser Leu Lys Lys Ala Tyr Asp
 100 105 110
 Thr Gly Ile Lys Pro Tyr Met Asp Lys Lys Ile Ser Tyr Thr Glu Ala
 115 120 125
 Phe Glu Lys Ser Thr Leu Pro Phe Lys Glu Phe Met Leu Lys Asn Thr
 130 135 140
 Arg Glu Lys Asp Leu Ala Leu Phe Phe Arg Ile Arg Asn Leu Pro Asn
 145 150 155 160
 Pro Lys Thr Pro Asp Asp Val Ser Leu Ser Val Leu Ile Pro Ala Phe
 165 170 175
 Met Ile Ser Glu Leu Lys Thr Ala Phe Gln Ile Gly Phe Leu Leu Tyr
 180 185 190
 Leu Pro Phe Leu Val Ile Asp Met Val Ile Ser Ser Ile Leu Met Ala
 195 200 205
 Met Gly Met Met Met Leu Pro Pro Val Met Ile Ser Leu Pro Phe Lys
 210 215 220
 Ile Leu Val Phe Ile Leu Val Asp Gly Phe Asn Leu Leu Thr Glu Asn
 225 230 235 240
 Leu Val Ala Ser Phe Lys Met Val
 245

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
 (B) TYPE: amino acid

SUBSTITUTE SHEET (RULE 26)

397

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477

```

Val Arg Phe Phe Ile Phe Leu Ile Leu Ile Cys Pro Leu Ile Cys Pro
1      5      10      15
Leu Met Ser Ala Asp Ser Ala Leu Pro Ser Val Asn Leu Ser Leu Asn
20      25      30
Ala Pro Ser Asp Pro Lys Gln Leu Val Thr Thr Leu Asn Val Ile Ala
35      40      45
Leu Leu Thr Leu Leu Val Leu Ala Pro Ser Leu Ile Leu Val Met Thr
50      55      60
Ser Phe Thr Arg Leu Ile Val Val Phe Ser Phe Leu Arg Thr Ala Leu
65      70      75      80
Gly Thr Gln Gln Thr Pro Pro Thr Gln Ile Leu Val Ser Leu Ser Leu
85      90      95
Ile Leu Thr Phe Phe Ile Met Glu Pro Ser Leu Lys Lys Ala Tyr Asp
100     105     110
Thr Gly Ile Lys Pro Tyr Met Asp Lys Lys Ile Ser Tyr Thr Glu Ala
115     120     125
Phe Glu Lys Ser Thr Leu Pro Phe Lys Glu Phe Met Leu Lys Asn Thr
130     135     140
Arg Glu Lys Asp Leu Ala Leu Phe Phe Arg Ile Arg Asn Leu Pro Asn
145     150     155     160
Pro Lys Thr Pro Asp Asp Val Ser Leu Ser Val Leu Ile Pro Ala Phe
165     170     175
Met Ile Ser Glu Leu Lys Thr Ala Phe Gln Ile Gly Phe Leu Leu Tyr
180     185     190
Leu Pro Phe Leu Val Ile Asp Met Val Ile Ser Ser Ile Leu Met Ala
195     200     205
Met Gly Met Met Met Leu Pro Pro Val Met Ile Ser Leu Pro Phe Lys
210     215     220
Ile Leu Val Phe Ile Leu Val Asp Gly Phe Asn Leu Leu Thr Glu Asn
225     230     235     240
Leu Val Ala Ser Phe Lys Met Val
245

```

(2) INFORMATION FOR SEQ ID NO:478:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

398

(B) LOCATION 1...44

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478

```

Val Met Asp Ala Glu Asn Gly Glu Leu Leu Val Ala Gly Ser Tyr Pro
1           5           10           15
Glu Tyr Asn Leu Asn Asp Phe Val Gly Gly Ile Ser Gln Asp Lys Trp
          20           25           30
Gln Lys Leu Gln Asp Asp Ile Tyr Asn Pro Leu Leu
          35           40

```

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 421 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...421

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479

```

Met Asn Phe Phe Asp Thr Leu Met Gly Met Phe Val Glu Pro Ser Gln
1           5           10           15
Lys Val Ala Lys Ser Leu Ala Glu His Val Gly Ser Phe Phe His Ala
          20           25           30
Gln Leu Ile Leu Asn Thr Ile Ile Thr Ile Leu Phe Met Ile Trp Ala
          35           40           45
Tyr Lys Arg Val Lys Glu Gly Asp Met Phe Glu Phe Lys Thr Ala Met
          50           55           60
Gly Val Val Val Phe Ile Ala Phe Val Gly Phe Ile Asn Trp Gly Ile
          65           70           75           80
Lys Asn Pro Asn Asp Phe Asn Thr Tyr Phe Ile Asn Thr Ile Phe Tyr
          85           90           95
Pro Ser Glu Lys Leu Ala Ile Leu Ile Ala Gln Ser Leu Asn Asp Gly
          100          105          110
Leu Glu Ile Pro Thr Asn Thr Asn Leu Ser Pro Ser Glu Ile Phe Ser
          115          120          125
Ile Gly Asn Leu Ala Ser Ser Ala Tyr Ala Met Ile Val Asn Leu Trp
          130          135          140
Asp Asn Ala Phe Asp Gly Ile Asn Met Phe Asn Trp Leu Thr Met Ile
          145          150          155          160
Pro Lys Ile Ile Met Phe Phe Leu Val Ile Leu Gly Glu Leu Leu Phe
          165          170          175
Leu Gly Leu Leu Leu Ile Ile Val Leu Leu Val Thr Ala Glu Ile Phe
          180          185          190
Met Trp Ser Ala Leu Gly Leu Ile Val Leu Pro Leu Gly Leu Ile Pro
          195          200          205
Gln Thr Lys Gly Met Leu Phe Ser Tyr Leu Lys Lys Leu Ile Ser Leu
          210          215          220
Thr Leu Tyr Lys Pro Cys Met Met Leu Val Ala Phe Phe Asn Tyr Gly
          225          230          235          240
Ile Ile Tyr Lys Val Asn Thr Leu Ile Pro Thr Lys His Glu Val Thr
          245          250          255
Gln Gly Phe Tyr Gly Asn Ala Asp Lys Met Ala Asn Glu Gly Lys Ile

```

SUBSTITUTE SHEET (RULE 26)

399

```

      260      265      270
Ile Asp Val Phe Gly Asn Val Leu Glu Gly Asp Trp Asn Ser Tyr Ile
      275      280      285
Ala His Ser Ser Ile Val Gly Phe Leu Thr Ile Ile Val Leu Gly Ser
      290      295      300
Val Ile Cys Phe Phe Leu Val Lys Arg Val Pro Asp Phe Ile Asn Asn
      305      310      315
Ile Phe Gly Thr Ser Gly Gly Val Gly Ala Val Thr Glu Met Met Gln
      325      330      335
Lys Ile Gly Met Thr Ile Gly Gly Ala Val Phe Gly Gly Ser Ala Val
      340      345      350
Met Val Ala Asn Gln Val Lys Gln Ala Tyr Gln Ser Ala Gly Gly Gly
      355      360      365
Leu Ala Gly Leu Gln Ala Gly Ala Lys Ala Phe Gly Leu Gly Ala Ile
      370      375      380
Ser Gly Gly Ala Ser Ala Met Ala Asn His Arg Ser Val Lys Ala Gly
      385      390      395
Val Lys His Phe Val Ala Ser Val Lys Ser Gly Phe Gly Phe Asp Asn
      405      410      415
Asp Lys Asn Asn Lys
      420

```

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480

```

Leu Leu Val Thr Phe Leu Asn Gly Phe Asp Pro Lys Ile Ala Asn Leu
1      5      10      15
Arg Lys Ala Cys Asn Val Tyr Ser Val Gly Val Ile Tyr Ile Val Thr
      20      25      30
Thr Asn Thr Leu Asn Ile Leu Ser Cys Glu Ser Phe Glu Ile Leu Glu
      35      40      45
Lys Arg Glu Leu Asp Thr Ser Gly Val Thr Lys Thr Ser Thr Pro Phe
      50      55      60
Phe Ser Arg Val Glu Gly Ile Asp Ala Gly Thr Leu Gly Lys Leu Phe
      65      70      75      80
Ser Gly Ser Gln Ser Lys Asn Tyr Phe Ala Tyr Tyr Asp Ala Leu Val
      85      90      95
Lys Lys Glu Lys Arg Lys Glu Val Arg Ile Glu Lys Lys Glu Glu Arg
      100      105      110
Ile Asp Ala Arg Glu Asn Lys Arg Glu Ile Lys Gln Glu Ala Ile Lys
      115      120      125
Glu Pro Lys Lys Ala Asn Gln Gly Thr Glu Asn Ala Pro Thr Leu Glu
      130      135      140
Glu Lys Unk Tyr Gln Lys Ala Glu Arg Lys Phe Asp Ala Lys Unk Unk
      145      150      155      160
Arg Arg Ser Phe Lys Unk
      165

```

SUBSTITUTE SHEET (RULE 26)

400

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480

```

Leu Leu Val Thr Phe Leu Asn Gly Phe Asp Pro Lys Ile Ala Asn Leu
1          5          10          15
Arg Lys Ala Cys Asn Val Tyr Ser Val Gly Val Ile Tyr Ile Val Thr
20          25          30
Thr Asn Thr Leu Asn Ile Leu Ser Cys Glu Ser Phe Glu Ile Leu Glu
35          40          45
Lys Arg Glu Leu Asp Thr Ser Gly Val Thr Lys Thr Ser Thr Pro Phe
50          55          60
Phe Ser Arg Val Glu Gly Ile Asp Ala Gly Thr Leu Gly Lys Leu Phe
65          70          75          80
Ser Gly Ser Gln Ser Lys Asn Tyr Phe Ala Tyr Tyr Asp Ala Leu Val
85          90          95
Lys Lys Glu Lys Arg Lys Glu Val Arg Ile Glu Lys Lys Glu Glu Arg
100         105         110
Ile Asp Ala Arg Glu Asn Lys Arg Glu Ile Lys Gln Glu Ala Ile Lys
115         120         125
Glu Pro Lys Lys Ala Asn Gln Gly Thr Glu Asn Ala Pro Thr Leu Glu
130         135         140
Glu Lys Unk Tyr Gln Lys Ala Glu Arg Lys Phe Asp Ala Lys Unk Unk
145         150         155         160
Arg Arg Ser Phe Lys Unk
165

```

(2) INFORMATION FOR SEQ ID NO:481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...89

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481

SUBSTITUTE SHEET (RULE 26)

401

```

Met Asp Glu Pro Glu Thr Ser Leu Glu Gln Asn Ala Leu Ile Arg Leu
1          5          10          15
Ser Asn Leu Ile Ser Leu Arg Asn Thr Gln Gln Leu Thr Ser Ile Ile
20          25          30
Ala Thr His Asp Pro Ile Val Leu Asp Ser Cys Glu Trp Val Leu Leu
35          40          45
Leu Lys Asn Gly Asn Ile Ala Gln Tyr Lys Pro Leu Asn Ser Ile Leu
50          55          60
Lys Ser Val Ala Lys Thr Phe Asn Phe Lys Glu Lys Pro Thr Thr Lys
65          70          75          80
Asp Leu Leu Ala Leu Leu Lys Asp Ile
85

```

(2) INFORMATION FOR SEQ ID NO:482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482

```

Val Lys Thr Leu Gly Leu Ser Ser Leu Gly Gly Thr Leu Glu Phe Tyr
1          5          10          15
Asp Phe Ile Ile Phe Val Phe Phe Thr Ser Ile Ile Ala Lys His Phe
20          25          30
Phe Pro Asn Thr Leu Ser Pro Ile Trp Ser Glu Ile Asn Thr Tyr Gly
35          40          45
Ile Phe Ala Ala Gly Tyr Leu Ala Arg Pro Leu Gly Gly Ile Val Met
50          55          60
Ala His Phe Gly Asp Lys Phe Gly Arg Lys Asn Met Phe Met Leu Ser
65          70          75          80
Ile Leu Leu Met Val Ile Pro Thr Phe Ala Leu Ala Leu Met Pro Thr
85          90          95
Phe Asn Asp Leu Val Gly Phe Gly Val Asp Ser Met Gly Leu Thr Pro
100          105          110
Lys Asn Ala His Tyr Leu Gly Tyr Ile Ala Pro Val Phe Leu Val Leu
115          120          125
Val Arg Ile Cys Gln Gly Val Ala Val Gly Gly Glu Leu Pro Gly Ala
130          135          140
Trp Val Phe Val His Glu His Ala Pro Gln Gly Gln Lys Asn Thr Tyr
145          150          155          160
Ile Gly Phe Leu Thr Ala Ser Val Val Ser Gly Ile Leu Leu Gly Ser
165          170          175
Leu Val Tyr Ile Gly Ile Tyr Met Val Phe Asp Lys Pro Val Val Glu
180          185          190
Asp Trp Ala Trp Arg Val Ala Phe Gly Leu Gly Gly Ile Phe Gly Ile
195          200          205
Ile Ser Val Tyr Leu Arg Arg Phe Leu Glu Glu Thr Pro Val Phe Gln
210          215          220
Gln Met Lys Gln Gly Arg Cys Leu Ser Gln Ile Pro Ala
225          230          235

```

SUBSTITUTE SHEET (RULE 26)

402

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483

```

Met Arg Lys Phe Leu Asp Gly Ala Lys Ser Glu Val Leu Lys Tyr Asp
1      5      10      15
Val Ile Ser Phe Asp Ile Phe Asp Thr Leu Leu Leu Arg Pro Phe Ile
20     25     30
Lys Pro Thr Asp Leu Phe Leu Tyr Ile Glu Thr Lys Tyr Asn Ile Lys
35     40     45
Gly Phe His Gln Ala Arg Ile Leu Ala Glu Met Gln Ser Arg Lys Leu
50     55     60
Ser Lys Arg Gln Asp Ile Thr Leu Asp Glu Ile Tyr His Gln Ile Pro
65     70     75     80
Lys Glu Phe His Ser Tyr Lys Gly Val Glu Ile Ala Thr Glu Lys Glu
85     90     95
Val Leu Val Pro Asn Leu Glu Met Leu Glu Leu Tyr Arg Phe Ala Lys
100    105    110
Glu Asn Asn Lys Arg Val Ile Ile Val Ser Asp Met Tyr Leu Pro Leu
115    120    125
Glu Val Leu Glu Asp Ile Leu Ile Ser Lys Gly Phe Asp Gly Tyr Thr
130    135    140
Asn Phe Tyr Leu Ser Asn His Ile Met Leu Thr Lys His Ser Lys Asp
145    150    155    160
Leu Phe Lys His Val Leu Lys Gln Glu Asn Ile Thr Asn Thr Gln Ile
165    170    175
Leu His Ile Gly Asp Asn Ser Trp Ala Asp Asp Ala Met Pro Lys Ser
180    185    190
Leu Gly Ile Ala Thr Leu Phe Arg Lys Ser Val Leu Lys Gln Leu Glu
195    200    205
Glu Val Phe Pro Lys Tyr Lys Thr Phe Asn Pro Thr Ser Val Ala Gln
210    215    220
Ser Phe Ile Leu Gly Ser Leu Cys Val Phe Tyr Lys Asn Tyr Ile Gln
225    230    235    240
Lys His Glu Lys Phe Asp Tyr Trp Phe Leu Leu Gly Ala Met Gln Ala
245    250    255
Gly Ile Ala Ala Val Ala Tyr Cys Gln Phe Ile Tyr Lys Glu Ile His
260    265    270
Lys Arg Asn Ile Asp Thr Leu Val Phe Val Ala Arg Asp Gly Tyr Leu
275    280    285
Leu Gln Lys Ile Phe Asn Ile Leu Tyr Pro Asn Ser Tyr Lys Thr Thr
290    295    300
Tyr Val Tyr Ala Pro Arg Ile Leu Lys Lys Ala Val Phe Leu Glu Val
305    310    315    320
Val Glu Gly Glu Ser Leu Glu Ile Leu Arg Ile Leu Glu Gly Glu Glu
325    330    335
Glu Val Lys Lys Lys Gln Ile Thr Thr Asn Gln Gln Ala Tyr Val Tyr

```

SUBSTITUTE SHEET (RULE 26)

403

```

          340          345          350
Leu Tyr Ser Asn Phe Glu His Cys Arg His Leu Ala Leu Lys Cys Leu
          355          360          365
Asp Asn Tyr Arg Lys Tyr Leu Phe Ser Ser Asn Leu Glu Gly Asn Ile
          370          375          380
Ala Ile Val Asp Thr Ile Thr Leu Gly Tyr Ser Ser Gln Gly Leu Ile
          385          390          395          400
Gln Lys Ala Leu Asn Lys Glu Val Phe Gly Cys Tyr Val Asp Leu Leu
          405          410          415
Arg Ile Leu Asn Tyr Asp Cys Val Ser Phe Leu Pro Phe Ser His Pro
          420          425          430
Lys Pro Val Tyr Phe His Asn Trp Asp Phe Met Glu Phe Leu Leu Thr
          435          440          445
Ser Pro Glu Tyr Pro Ile Leu Asn Val Glu Asn Gly Val Pro Ile Leu
          450          455          460
Ser Lys Arg Arg Phe Ile Leu
          465          470

```

(2) INFORMATION FOR SEQ ID NO:484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484

```

Val Leu Lys Phe Phe Glu Asp Ser Lys Gln Leu Ser Thr Pro Met Gly
1          5          10          15
Lys Ser Ala Val Gly Ile Leu Ile Phe Gln Asp Ile Ala Ala Ile Pro
          20          25          30
Met Leu Leu Ile Leu Thr Ile Leu Gly Ser Lys Asp Ser His Val Asn
          35          40          45
Leu Leu Ile Leu Lys Thr Leu Ile Ser Ala Gly Ile Ile Leu Ile Leu
          50          55          60
Leu Leu Leu Pro Gly Lys Lys Gly Ala Asn Leu Ile Leu Glu Gln Ala
          65          70          75          80
Lys Asp Thr Arg Leu Pro Glu Ile Phe Ile Gly Thr Asp Phe Ser Asp
          85          90          95
Cys Leu Gln Arg Gly Gly Val Glu Pro Phe Phe Trp Val Phe Tyr Val
          100          105          110
Phe Gly Gly Val His Cys Gly His Gly Asp Phe
          115          120

```

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

404

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485

```

Met Glu Asn Ser Thr Leu Tyr Ile Val Ile Ala Gly Leu Trp Leu Ala
1           5           10           15
Val Gly Phe Gly Ile Phe Leu Lys Lys Leu Asp Met Pro Val Ile Ile
          20           25           30
Gly Tyr Ile Cys Thr Gly Thr Val Leu Ala Ala Phe Phe Lys Ile Asn
          35           40           45
Asp Phe Asn Leu Leu Ser Asp Ile Gly Glu Phe Gly Ile Val Phe Leu
          50           55           60
Met Phe Met Ile Gly Ile Glu Phe Asn Phe Asp Lys Leu Lys Ser Ile
          65           70           75           80
Lys Gln Glu Val Leu Val Phe Gly Leu Leu Gln Val Val Leu Cys Ala
          85           90           95
Leu Ile Ala Phe Leu Leu Gly Tyr Phe Val Leu Gly Leu Ser Pro Ile
          100          105          110
Phe Ser Leu Val Leu Gly Met Gly Leu Ser Leu Ser Ser Thr Ala
          115          120          125

```

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485

```

Met Glu Asn Ser Thr Leu Tyr Ile Val Ile Ala Gly Leu Trp Leu Ala
1           5           10           15
Val Gly Phe Gly Ile Phe Leu Lys Lys Leu Asp Met Pro Val Ile Ile
          20           25           30
Gly Tyr Ile Cys Thr Gly Thr Val Leu Ala Ala Phe Phe Lys Ile Asn
          35           40           45
Asp Phe Asn Leu Leu Ser Asp Ile Gly Glu Phe Gly Ile Val Phe Leu
          50           55           60
Met Phe Met Ile Gly Ile Glu Phe Asn Phe Asp Lys Leu Lys Ser Ile
          65           70           75           80
Lys Gln Glu Val Leu Val Phe Gly Leu Leu Gln Val Val Leu Cys Ala
          85           90           95
Leu Ile Ala Phe Leu Leu Gly Tyr Phe Val Leu Gly Leu Ser Pro Ile
          100          105          110
Phe Ser Leu Val Leu Gly Met Gly Leu Ser Leu Ser Ser Thr Ala

```

SUBSTITUTE SHEET (RULE 26)

405

115

120

125

(2) INFORMATION FOR SEQ ID NO:486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486

```

Met Ile Leu Ala Leu Leu Ile Ser Lys Glu Lys Thr His Leu Glu Ala
1      5      10      15
Leu Tyr Tyr Leu Ser Tyr Gly Val Leu Leu Gly Gly Val Ala Gln Ile
      20      25      30
Leu Leu His Phe Tyr Pro Leu Val Lys Leu Gly Leu Trp Asp Leu Leu
      35      40      45
Phe Lys Gly Leu Leu Gly Phe Lys Thr Lys Asn Thr Asn Lys Lys Glu
      50      55      60
Tyr Arg Leu Asn Arg Ala Lys Lys Asp Leu Lys Ala Phe Phe Lys Gln
      65      70      75      80
Phe Phe Pro Ser Val Leu Gly Asn Ser Ser Ala Gln Ile Ala Ser Phe
      85      90      95
Leu Asp Thr Thr Ile Ala Ser Phe Leu Ala Ser Gly Ser Val Ser Tyr
      100     105     110
Leu Tyr Tyr Ala Asn Arg Val Phe Gln Leu Pro Leu Ala Leu Phe Ala
      115     120     125
Ile Ala Ile Ser Thr Ala Leu Phe Pro Ser Ile Ala Ile Ala Leu Lys
      130     135     140
Asn Asn Gln Gln Asp Leu Ile Leu Gln Arg Leu Gln Lys Ala Trp Phe
      145     150     155     160
Phe Leu Val Gly Val Leu Leu Leu Cys Ser Ile Gly Gly Ile Met Leu
      165     170     175
Ser Lys Glu Ile Thr Glu Leu Leu Phe Glu Arg Gly Gln Phe Ser Pro
      180     185     190
Lys Asp Thr Leu Ile Thr Ser Gln Val Phe Ser Leu Tyr Leu Leu Gly
      195     200     205
Leu Leu Pro Phe Gly Leu Thr Lys Leu Phe Ser Leu Trp Leu Tyr Ala
      210     215     220
Lys Leu Glu Gln Lys Lys Ala Ala Lys Ile Ser Leu Ile Ser Leu Phe
      225     230     235     240
Leu Gly Leu Ala Ala Ser Leu Ser Leu Met Pro Leu Leu Gly Val Leu
      245     250     255
Gly Leu Arg

```

(2) INFORMATION FOR SEQ ID NO:487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

406

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...16
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:487

Leu Leu Leu Met Leu Asn Lys Pro Lys Pro Leu Phe Leu Unk Leu Gly
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:487:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...16
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:487

Leu Leu Leu Met Leu Asn Lys Pro Lys Pro Leu Phe Leu Unk Leu Gly
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:488:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...77
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:488

Val Leu Lys Tyr Pro Thr Met Phe Met Cys Ala Asp Ala Val Ile Ile
 1 5 10 15
 Ser Lys Ala Asp Met Ile Glu Val Phe Asn Phe Arg Val Ser Gln Val

SUBSTITUTE SHEET (RULE 26)

407

```

      20      25      30
Lys Glu Asp Met Gln Lys Leu Lys Pro Glu Ala Pro Ile Phe Leu Met
      35      40      45
Ser Ser Lys Asp Pro Lys Ser Leu Glu Asp Phe Lys Asn Phe Leu Leu
      50      55      60
Glu Lys Lys Arg Glu Asn Tyr Gln Ser Thr His Ser Phe
      65      70      75

```

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489

```

Met Leu Leu Cys Ala Gly Arg Asn Glu Thr Leu Lys Lys Ala Val Pro
1      5      10      15
Ile Gly Val Gly Leu Ile Glu Ser Ala Ile Asn Leu Thr Arg Met Cys
      20      25      30
Leu Lys Asn Pro Asp Thr Glu Ser Leu Ile Phe Ile Gly Ser Ala Gly
      35      40      45
Ser Tyr Ser Pro Glu Thr Glu Ile Leu Ser Val Phe Glu Ser Ile Glu
      50      55      60
Gly Tyr Gln Ile Glu Glu Ser Phe Ser His Leu Asn Ser Tyr Thr Pro
      65      70      75      80
Leu Asp Asn Phe Ile His Ile Glu Thr Lys Glu Gln Ala Leu Phe Glu
      85      90      95
Arg Val Arg Val Asn Ser Ser Asn Tyr Ile His Thr Ser Glu Met Phe
      100      105      110
Ala Lys Lys Met Val Gln Lys Gly Val Leu Leu Glu Asn Met Glu Phe
      115      120      125
Phe Ser Val Leu Ser Val Ala Lys Ile Phe Ser Leu Lys Ala Lys Gly
      130      135      140
Ile Phe Cys Val Ser Asn His Val Gly Leu Asn Ala His Lys Glu Phe
      145      150      155      160
Lys Glu Asn His Ala Lys Val Lys Gln Ile Leu Glu Asn Ile Ile Asp
      165      170      175
Ser Leu Ile Val
      180

```

(2) INFORMATION FOR SEQ ID NO:490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

SUBSTITUTE SHEET (RULE 26)

408

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490

```

Val Tyr Glu Glu Arg Ile Thr Leu Ala Ser Gln Gly Ile Pro Lys Thr
1          5          10          15
Ser Lys Val Gly Phe Glu Ile Phe Asp Thr Lys Asp Phe Gly Ala Thr
          20          25          30
Asp Phe Asp Gln Asn Ile Lys Leu Ile Arg Ala Ile Glu Gly Glu Leu
          35          40          45
Ser Arg Thr Ile Glu Ser Leu Asn Pro Ile Leu Lys Ala Asn Val His
          50          55          60
Ile Ala Ile Pro Lys Asp Ser Val Phe Val Ala Lys Glu Val Pro Pro
65          70          75          80
Ser Ala Ser Val Met Leu Lys Leu Lys Pro Asp Met Lys Leu Ser Pro
          85          90          95
Thr Gln Ile Leu Gly Ile Lys Asn Leu Ile Ala Ala Ala Val Pro Lys
          100          105          110
Leu Thr Ile Glu Asn Val Lys Ile Val Asn Glu Asn Gly Glu Ser Ile
          115          120          125
Gly Glu Gly Asp Ile Leu Glu Asn Ser Lys Glu Leu Ala Leu Glu Gln
130          135          140
Leu Arg Tyr Lys Gln Asn Phe Glu Asn Ile Leu Glu Asn Lys Ile Val
145          150          155          160
Asn Ile Leu Ala Pro Ile Val Gly Unk Lys Asn Unk Val Val Unk Unk
          165          170          175
Val Asn Unk Glu Phe Unk Phe Unk Gln Lys Lys Ser Thr Lys Glu Thr
          180          185          190
Phe Asp Pro Asn Asn Val Gly Lys Glu Arg Ala Lys Phe Arg Arg Lys
195          200          205
Lys Arg Arg Arg Ser
210

```

(2) INFORMATION FOR SEQ ID NO:491:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491

```

Val Ile Lys Lys Gly Tyr Ile Arg Gly Asp Leu Met Arg Ile Val Arg
1          5          10          15
Asn Leu Phe Leu Val Ser Phe Val Ala Tyr Ser Ser Ala Phe Ala Ala
          20          25          30
Asp Leu Glu Thr Gly Thr Lys Asn Asp Lys Lys Ser Gly Lys Lys Phe

```

SUBSTITUTE SHEET (RULE 26)

409

```

      35              40              45
Tyr Lys Leu His Lys Asn His Gly Ser Glu Thr Glu Thr Lys Asn Asp
  50              55              60
Lys Lys Leu Tyr Asp Phe Thr Lys Asn Ser Gly Leu Glu Gly Val Asp
  65              70              75              80
Leu Glu Lys Ser Pro Asn Leu Lys Ser His Lys Lys Ser Asp Lys Lys
      85              90              95
Phe Tyr Lys Gln Leu Ala Lys Asn Asn Ile Ala Glu Gly Val Ser Met
      100              105              110
Pro Ile Val Asn Phe Asn Lys Ala Leu Ser Phe Gly Pro Tyr Phe Glu
      115              120              125
Arg Thr Lys Ser Lys Lys Thr Gln Tyr Met Asp Gly Gly Leu Met Met
      130              135              140
His Ile Arg Phe
145

```

(2) INFORMATION FOR SEQ ID NO:492:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 281 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...281
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:492

```

Val Met Ile Asp Pro Lys Met Val Glu Phe Ser Ile Tyr Ala Asp Ile
1              5              10              15
Pro His Leu Leu Thr Pro Ile Ile Thr Asp Pro Lys Lys Ala Ile Gly
      20              25              30
Ala Leu Gln Ser Val Ala Lys Glu Met Glu Arg Arg Tyr Ser Leu Met
      35              40              45
Ser Glu Tyr Lys Val Lys Thr Ile Asp Ser Tyr Asn Glu Gln Ala Gln
      50              55              60
Ser Asn Asp Val Glu Ala Phe Pro Tyr Leu Ile Val Val Ile Asp Glu
      65              70              75              80
Leu Ala Asp Leu Met Met Thr Gly Gly Lys Glu Ala Glu Phe Pro Ile
      85              90              95
Ala Arg Ile Ala Gln Met Gly Arg Ala Ser Gly Leu His Leu Ile Val
      100              105              110
Ala Thr Gln Arg Pro Ser Val Asp Val Val Thr Gly Leu Ile Lys Thr
      115              120              125
Asn Leu Pro Ser Arg Val Ser Phe Arg Val Gly Thr Lys Ile Asp Ser
      130              135              140
Lys Val Ile Leu Asp Thr Asp Gly Ala Gln Ser Leu Leu Gly Arg Gly
      145              150              155              160
Asp Met Leu Phe Thr Pro Pro Gly Thr Asn Gly Leu Val Arg Leu His
      165              170              175
Ala Pro Phe Ala Thr Glu Asp Glu Ile Lys Lys Ile Val Asp Phe Ile
      180              185              190
Lys Ala Gln Lys Glu Val Glu Tyr Asp Lys Asp Phe Leu Leu Glu Glu
      195              200              205
Ser Arg Met Pro Leu Asp Thr Pro Asn Tyr Gln Gly Asp Asp Ile Leu
      210              215              220

```

SUBSTITUTE SHEET (RULE 26)

410

Glu Arg Ala Lys Ala Val Ile Leu Glu Lys Lys Ile Thr Ser Thr Ser
 225 230 235 240
 Phe Leu Gln Arg Gln Leu Lys Ile Gly Tyr Asn Gln Ala Ala Thr Ile
 245 250 255
 Thr Asp Glu Leu Glu Ala Gln Gly Phe Leu Ser Pro Arg Asn Ala Lys
 260 265 270
 Gly Asn Arg Glu Ile Leu Gln Asn Phe
 275 280

(2) INFORMATION FOR SEQ ID NO:493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493

Met Asn Phe Phe Lys Ile Leu Leu Met Glu Leu Arg Ala Ile Val Ser
 1 5 10 15
 His Lys Gly Val Leu Leu Ile Leu Ile Gly Ala Pro Leu Ile Tyr Gly
 20 25 30
 Leu Leu Tyr Pro Leu Pro Tyr Leu Lys Asp Ile Val Thr Gln Gln Lys
 35 40 45
 Ile Ala Leu Val Asp Glu Asp Asn Ser Phe Leu Ser Arg Gln Leu Ala
 50 55 60
 Phe Met Val Gln Ser Ser Asn Glu Leu Glu Ile Ala Phe Phe Ser Pro
 65 70 75 80
 Ser Met Leu Glu Ala Lys Lys Leu Leu Lys Glu Glu Lys Ile Tyr Gly
 85 90 95
 Ile Leu His Ile Pro Ser His Phe Glu Ala Asn Ile Tyr Lys Gln Ser
 100 105 110
 Ala Cys Asn Asp Arg Phe Leu Cys Glu Arg Gln Leu Leu Phe Asp Leu
 115 120 125
 Trp Cys Val Ser Glu Cys Gly Gly Gly Glu His Gln Arg Leu Lys Arg
 130 135 140

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

SUBSTITUTE SHEET (RULE 26)

411

(A) NAME/KEY: misc_feature
(B) LOCATION 1...73

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494

```

Val Gly Gly Leu Ala Met Leu Gly Phe Phe Tyr Asn Ile Glu Lys Ile
1      5      10      15
Ser Leu Ala Thr Ala Thr Ala Phe Ser Gln Cys Ala Pro Unk Tyr Thr
      20      25      30
Val Leu Leu Ser Pro Leu Leu Leu Lys Glu Lys Leu Lys Arg Ser Ala
      35      40      45
Leu Ile Ser Ala Cys Ile Gly Leu Val Gly Val Val Leu Ile Ser Asp
      50      55      60
Pro Ser Val Glu Asn Val Gly Pro Ser
65      70

```

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 311 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495

```

Val Cys Trp Thr Asp Leu Ile Gln Gly Leu Leu Met Met Ser Ala Leu
1      5      10      15
Ile Val Val Pro Ile Val Met Ile Ile His Leu Gly Gly Ile Gly Glu
      20      25      30
Gly Ile Lys Ile Ile Arg Glu Ile Lys Pro Glu Asn Leu Ser Phe Unk
      35      40      45
Gln Gly Ser Ser Val Val Ala Ile Ile Ser Ser Leu Ala Trp Gly Leu
      50      55      60
Gly Tyr Phe Gly Gln Pro His Ile Leu Val Arg Phe Met Ser Ile Arg
      65      70      75      80
Ser Ile Arg Asp Val Pro Lys Ala Thr Thr Ile Gly Ile Ser Trp Met
      85      90      95
Val Ile Ser Leu Ile Gly Ala Cys Val Met Gly Leu Leu Gly Val Ala
      100      105      110
Tyr Val His Lys Unk Asp Leu Ser Leu Glu Asp Pro Glu Lys Ile Phe
      115      120      125
Ile Val Met Ser Gln Leu Leu Phe Asn Pro Trp Ile Thr Gly Ile Leu
      130      135      140
Leu Ser Ala Ile Leu Ala Ala Val Met Ser Thr Ala Ser Ser Gln Leu
      145      150      155      160
Leu Val Ser Ser Ser Thr Ile Ala Glu Asp Phe Tyr Ala Thr Ile Phe
      165      170      175
Asn Lys Asn Ala Pro Gln Lys Leu Val Met Thr Ile Ser Arg Leu Ser
      180      185      190
Val Leu Gly Val Ala Cys Ile Ala Phe Phe Ile Ser Thr Asp Lys Asn
      195      200      205
Ala Ser Ile Leu Ser Ile Val Ser Tyr Ala Trp Ala Gly Phe Gly Ala
      210      215      220

```

SUBSTITUTE SHEET (RULE 26)

412

```

Ser Phe Gly Ser Val Ile Leu Phe Ser Leu Phe Trp Ser Arg Met Thr
225                230                235                240
Arg Ile Gly Ala Ile Ala Gly Met Leu Ser Gly Ala Ser Thr Val Ile
                245                250                255
Leu Tyr Asp Lys Phe Gly Lys Ser Phe Leu Asp Ile Tyr Glu Ile Val
                260                265                270
Pro Gly Phe Ile Val Ala Ser Val Ala Ile Val Ala Phe Ser Leu Phe
                275                280                285
Ser Ser Val Arg Ser Gly Thr Lys Glu Ala Phe Glu Thr Met Leu Lys
                290                295                300
Glu Ile Glu Ser Leu Lys His
305                310

```

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496

```

Val Gly Leu Phe Ile Val Leu Phe Leu Ile Ile Met Lys His Gln Thr
1          5          10          15
Ser Pro Tyr Ala Phe Thr His Asn Gln Ala Leu Val Thr Gln Thr Pro
          20          25          30
Pro Tyr Phe Thr Gln Leu Thr Ile Pro Lys Pro Asn Asp Ala Leu Ser
          35          40          45
Ala His Ala Ser Ser Leu Ile Ser Leu Pro Asn Asp Asn Leu Leu Ser
          50          55          60
Ala Tyr Phe Ser Gly Thr Lys Glu Gly Ala Arg Asp Val Lys Ile Ser
          65          70          75          80
Ala Asn Leu Phe Asp Ser Lys Thr Asn Arg Trp Ser Glu Ala Phe Ile
          85          90          95
Leu Leu Thr Lys Glu Glu Leu Ser His His Ser His Glu Tyr Ile Lys
          100         105         110
Lys Ile Arg
          115

```

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

413

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497

```

Met Leu Val Gly Pro Thr Gly Val Gly Lys Thr Thr Thr Leu Ala Lys
1      5      10      15
Leu Ala Ala Arg Tyr Ser Arg Met Leu Ala Lys Lys Tyr Lys Val Gly
20      25      30
Ile Ile Thr Leu Asp Asn Tyr Arg Ile Gly Ala Leu Glu Gln Leu Ser
35      40      45
Trp Tyr Ala Asn Lys Met Lys Met Ser Ile Glu Ala Val Ile Asp Ala
50      55      60
Lys Asp Phe Ala Lys Glu Ile Glu Ala Leu Glu Tyr Cys Asp Phe Ile
65      70      75      80
Leu Val Asp Thr Thr Gly His Ser Gln Tyr Asp Lys Glu Lys Ile Ala
85      90      95
Gly Leu Lys Glu Phe Ile Asp Gly Gly Tyr Asn Ile Asp Val Ser Leu
100      105      110
Val Leu Ser Val Thr Thr Lys Tyr Glu Asp Met Lys Asp Ile Tyr Asp
115      120      125
Ser Phe Gly Val Leu Gly Ile Asp Thr Leu Ile Phe Thr Lys Leu Asp
130      135      140
Glu Ser Arg Gly Leu Gly Asn Leu Phe Ser Leu Val His Glu Ser Gln
145      150      155      160
Lys Pro Ile Ser Tyr Leu Ser Val Gly Gln Glu Val Pro Met Asp Leu
165      170      175
Lys Val Ala Thr Asn Glu Tyr Leu Val Asp Cys Met Leu Asp Gly Phe
180      185      190
Ser Asn Pro Asn Lys Glu Gln Ala
195      200

```

(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498

```

Val Gly Gly Ala Ser Phe Ile Ser Gly Gly Asn Gly Thr Leu Tyr Gly
1      5      10      15
Leu Asn Val Gly Tyr Asp Arg Leu Val Lys Ser Val Ile Leu Gly Gly
20      25      30
Tyr Val Ala Tyr Gly Tyr Ser Gly Phe Asn Gly Asn Ile Met His Ser
35      40      45
Leu Ala Asn Asn Val Asp Val Gly Met Tyr Ala Arg Ala Phe Leu Lys
50      55      60
Arg Asn Glu Phe Thr Leu Ser Ala Asn Glu Thr Tyr Gly Gly Asn Ala
65      70      75      80

```

SUBSTITUTE SHEET (RULE 26)

414

Ser His Ile Asn Ser Ser Asn Ser Leu Leu Ser Val Leu Asn Gln Arg
 85 90 95
 Tyr Asn Tyr Asn Thr Trp Thr Thr Ser Val Asn Gly Asn Tyr Gly Tyr
 100 105 110
 Asp Phe Met Phe Lys Gln Lys Ser Val Val Leu Lys Pro Gln Val Gly
 115 120 125
 Leu Ser Tyr His Phe Ile Gly Leu Ser Gly Met Lys Gly Lys Met Gln
 130 135 140
 Asn Pro Ala Tyr Gln Gln Phe Val Met His Ser Asn Pro Ser Asn Glu
 145 150 155 160
 Ser Val Leu Thr Leu Asn Met Gly Leu Glu Ser Arg Lys Tyr Phe Gly
 165 170 175
 Lys Asn Ser Tyr Tyr Phe Val Thr Ala Arg Leu Gly Arg Asp Leu Leu
 180 185 190
 Ile Lys Ala Lys Gly Asp Asn Val Val Arg Phe Val Gly Glu Asn Thr
 195 200 205
 Leu Leu Tyr Arg Lys Gly Glu Ile Phe Asn Thr Phe Ala Ser Val Ile
 210 215 220
 Thr Gly Gly Glu Met His Leu Trp Arg Leu Met Tyr Val Asn Ala Gly
 225 230 235 240
 Val Gly Leu Lys Met Gly Leu Gln Tyr Gln Asp Leu Asn Ile Thr Gly
 245 250 255
 Asn Val Gly Met Arg Val Ala Phe
 260

(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499

Met Asp Gly Tyr Gly Phe Lys Met Gln Asp Leu Gly Gln Lys Thr Gln
 1 5 10 15
 Val Ile Gln His Ile Phe Ala Gly Asp Val Ser Ala Leu Glu Val
 20 25 30
 Lys Glu Asn Glu Cys Val Lys Ile Met Thr Gly Ala Met Val Pro Lys
 35 40 45
 Gly Ile Glu Thr Ile Val Pro Ile Glu Cys Met Leu Glu Ser His Lys
 50 55 60
 Asp Phe Ala Leu Ala Pro Lys Asp Phe Lys Ile His Ala Asn Ile Arg
 65 70 75 80
 Gln Lys Gly Glu Asn Ala Ser Leu Asn Ser Val Leu Val Pro Lys Asn
 85 90 95
 Thr Arg Leu Asn Tyr Gly His Ile Ala Leu Ile Ala Ser Gln Gly Phe
 100 105 110
 Lys Glu Ile Lys Ala Phe Arg Lys Leu Lys Ile Ala Leu Phe Ser Ser
 115 120 125
 Gly Asp Glu Leu Val Pro Leu Gly Gln Asn Ala Leu Glu Cys Gln Val
 130 135 140
 Tyr Asp Val Asn Ser Val Gly Val Phe Asn Met Leu Lys Asn Tyr Asn

SUBSTITUTE SHEET (RULE 26)

415

```

145          150          155          160
Thr His Phe Leu Gly Val Leu Lys Asp Asp Lys Asn Leu Gln Leu Lys
165          170          175
Ile Leu Glu Leu Gln Gly Tyr Asp Val Ile Leu Ser Ser Ala Gly Val
180          185          190
Ser Val Gly Asp Lys Asp Phe Phe Lys Asp Ala Leu Lys Glu Arg Asn
195          200          205
Ala Leu Phe Tyr Tyr Glu Lys Val Asn Leu Lys Pro Gly Lys Pro Val
210          215          220
Thr Leu Ala Gln Leu Asn Gln Ser Ile Ile Ile Gly Leu Pro Gly Asn
225          230          235          240
Pro Leu Ser Cys Leu Leu Val Leu Arg Val Leu Ile Leu Pro Leu Leu
245          250          255
Glu Arg Leu Ser Leu Asn Lys Asp Phe Lys Leu Lys Pro Phe Lys Ala
260          265          270
Gln Ile Asn Ala Pro Leu Lys Leu Asn Asn Lys Arg Thr His Leu Ile
275          280          285
Leu Gly Asn Tyr Ser Asn His Gln Phe Ile Pro Tyr Asn Asn Arg Tyr
290          295          300
Glu Ser Gly Ala Ile Gln Ala Leu Ala Gln Val Asp Ser Ile Thr Leu
305          310          315          320
Ile Asp Glu Gly Val Gly Leu Val Gln Gly Glu Ile Glu Ile Leu Arg
325          330          335
Phe Glu Asn

```

(2) INFORMATION FOR SEQ ID NO:500:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500

```

Met Pro Tyr Ala Leu Arg Lys Arg Phe Phe Lys Arg Leu Leu Leu Phe
1      5      10      15
Phe Leu Ile Val Cys Met Ile Asn Leu His Ala Lys Ser Tyr Leu Phe
20     25     30
Ser Pro Leu Pro Pro Ala His Gln Gln Ile Ile Lys Thr Glu Pro Cys
35     40     45
Ser Leu Glu Cys Leu Lys Asp Leu Met Leu Gln Asn Gln Ile Phe Ser
50     55     60
Phe Val Ser Gln Tyr Asp Asp Asn Asn Gln Asp Glu Ser Leu Lys Thr
65     70     75     80
Tyr Tyr Lys Asp Ile Leu Asn Lys Leu Asn Pro Val Phe Ile Ala Ser
85     90     95
Gln Thr Pro Ala Lys Glu Ser Tyr Glu Pro Lys Ile Glu Leu Ala Ile
100    105    110
Leu Leu Pro Lys Lys Val Val Gly Arg Tyr Ala Ile Leu Val Met Asn
115    120    125
Thr Leu Leu Ala Tyr Phe Glu His Gln Lys Gln Arg Phe Gln Tyr Pro
130    135    140

```

SUBSTITUTE SHEET (RULE 26)

416

Ser Leu
145

(2) INFORMATION FOR SEQ ID NO:501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501

```

Met Pro Ile Asn Pro Leu Tyr Leu Phe Pro Asn Leu Phe Thr Ala Ser
1           5           10           15
Ser Ile Phe Leu Gly Met Met Ser Ile Phe Tyr Ala Ser Ser Tyr Gln
          20           25           30
Phe Val Met Ala Cys Trp Leu Val Val Ala Ser Leu Ile Leu Asp Gly
          35           40           45
Leu Asp Gly Arg Val Ala Arg Leu Thr Lys His His
          50           55           60

```

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502

```

Met Ala Leu Arg Val Leu Leu Phe Phe Cys Phe Leu Phe Leu Gln Ala
1           5           10           15
Glu Asp Lys Ser Gln Glu Leu Ser Ser Ile Gln Lys Gln Met Ala Leu
          20           25           30
Val Asp Lys Lys Leu Ala Lys Asp Asp Asn Val Trp Leu Lys Lys Phe
          35           40           45
Glu Asn Tyr Lys Ile Tyr Asn Gln Ile Tyr Thr Glu Lys Glu Ser Val
          50           55           60
Arg Gln Glu Leu Arg Arg Leu Lys Asn Lys Lys Ser Lys Asp Leu Leu
          65           70           75           80
Lys Ile Ser Thr Leu Glu His Thr Leu Lys Ala Leu Glu Ser Gln Gln

```

SUBSTITUTE SHEET (RULE 26)

417

```

      85              90              95
Lys Met Phe Glu Ser Tyr Gly Val Asn Pro Phe Lys Asp Leu Ile Glu
      100              105              110
Arg Pro Asn Ile Pro Asn Ile Pro Asn Ile Ala Asn Pro Ile Ala Ile
      115              120              125
Ile Asp Gly Ile Ser Phe Ile Lys Ser Met Arg Leu Lys His Glu Asn
      130              135              140
Leu Lys Asn Asn Gln Thr Ser Leu Gly Glu Val Leu Lys Leu Leu Asp
      145              150              155              160
Gln Lys His Gln Leu Asn Gln Trp His Ala Leu Asp Lys Ser Ala
      165              170              175
Lys Leu Ser Asp Glu Ile Tyr Gln Thr Gln Ala Lys Arg Leu Glu Leu
      180              185              190
Gln Gly Ala Gln Asn Ile Leu Lys Thr Thr Ile Gly Ile Phe Gln Lys
      195              200              205
Asp Ser Asp Glu Ala Ile Ser Ile Val Lys Ser Gln Val Lys Asn Gln
      210              215              220
Leu Phe Lys Leu Val Tyr Val Phe Leu Ala Ala Leu Leu Ser Val Val
      225              230              235              240
Phe Ala Trp Ile Leu Lys Ile Ile Ser Ser Lys Tyr Ile Glu Asn Asn
      245              250              255
Glu Arg Val Tyr Thr Val Asn Lys Ala Ile Asn Phe Val Asn Val Ser
      260              265              270
Val Ile Unk Unk Ile Unk Leu Phe Ser Tyr Leu Glu Asn Val Thr Tyr
      275              280              285
Leu Val Thr Val Leu Gly Phe Ala Ser Ala Gly Leu Ala Ile Unk Met
      290              295              300
Lys Asp Leu Phe Met Ser Leu Leu Gly Trp Phe Ile Ile Leu Ile Gly
      305              310              315              320
Gly Ser Val His Val Gly Asp Arg Val Arg Ile Ala Lys Gly Thr Asp
      325              330              335
Ile Phe Ile Gly Asp Val Leu Asp Thr Ser Asn Val Val His
      340              345              350

```

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502

```

Met Ala Leu Arg Val Leu Leu Phe Phe Cys Phe Leu Phe Leu Gln Ala
1      5      10      15
Glu Asp Lys Ser Gln Glu Leu Ser Ser Ile Gln Lys Gln Met Ala Leu
20      25      30
Val Asp Lys Lys Leu Ala Lys Asp Asp Asn Val Trp Leu Lys Lys Phe
35      40      45
Glu Asn Tyr Lys Ile Tyr Asn Gln Ile Tyr Thr Glu Lys Glu Ser Val
50      55      60
Arg Gln Glu Leu Arg Arg Leu Lys Asn Lys Lys Ser Lys Asp Leu Leu
65      70      75      80

```

SUBSTITUTE SHEET (RULE 26)

418

Lys Ile Ser Thr Leu Glu His Thr Leu Lys Ala Leu Glu Ser Gln Gln
 85 90 95
 Lys Met Phe Glu Ser Tyr Gly Val Asn Pro Phe Lys Asp Leu Ile Glu
 100 105 110
 Arg Pro Asn Ile Pro Asn Ile Pro Asn Ile Ala Asn Pro Ile Ala Ile
 115 120 125
 Ile Asp Gly Ile Ser Phe Ile Lys Ser Met Arg Leu Lys His Glu Asn
 130 135 140
 Leu Lys Asn Asn Gln Thr Ser Leu Gly Glu Val Leu Lys Leu Leu Asp
 145 150 155 160
 Gln Lys His Gln Leu Leu Asn Gln Trp His Ala Leu Asp Lys Ser Ala
 165 170 175
 Lys Leu Ser Asp Glu Ile Tyr Gln Thr Gln Ala Lys Arg Leu Glu Leu
 180 185 190
 Gln Gly Ala Gln Asn Ile Leu Lys Thr Thr Ile Gly Ile Phe Gln Lys
 195 200 205
 Asp Ser Asp Glu Ala Ile Ser Ile Val Lys Ser Gln Val Lys Asn Gln
 210 215 220
 Leu Phe Lys Leu Val Tyr Val Phe Leu Ala Ala Leu Leu Ser Val Val
 225 230 235 240
 Phe Ala Trp Ile Leu Lys Ile Ile Ser Ser Lys Tyr Ile Glu Asn Asn
 245 250 255
 Glu Arg Val Tyr Thr Val Asn Lys Ala Ile Asn Phe Val Asn Val Ser
 260 265 270
 Val Ile Unk Unk Ile Unk Leu Phe Ser Tyr Leu Glu Asn Val Thr Tyr
 275 280 285
 Leu Val Thr Val Leu Gly Phe Ala Ser Ala Gly Leu Ala Ile Unk Met
 290 295 300
 Lys Asp Leu Phe Met Ser Leu Leu Gly Trp Phe Ile Ile Leu Ile Gly
 305 310 315 320
 Gly Ser Val His Val Gly Asp Arg Val Arg Ile Ala Lys Gly Thr Asp
 325 330 335
 Ile Phe Ile Gly Asp Val Leu Asp Thr Ser Asn Val Val His
 340 345 350

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503

Met Leu Ser Ala Leu Leu Ser Lys Met Gly Thr Tyr Ala Leu Leu Arg
 1 5 10 15
 Phe Leu Leu Pro Leu Phe Pro Glu Leu Ser Glu Ile Tyr Leu Thr Pro
 20 25 30
 Ile Ala Ile Val Ala Leu Cys Met Ile Ile Tyr Gly Gly Phe Leu Ala
 35 40 45
 Tyr Ala Gln Lys Asp Leu Lys Thr Leu Ile Ala Tyr Ser Ser Phe Ser
 50 55 60
 His Met Gly Val Val Val Leu Gly Val Phe Ser Phe Asn Val Glu Gly

SUBSTITUTE SHEET (RULE 26)

419

```

65          70          75          80
Val Ser Gly Ala Val Phe Met Met Phe Ala His Gly Val Ile Val Met
          85          90          95
Gly Leu Phe Leu Leu Ala Gly Ile Leu Glu Glu Arg Ala Ser Ser Leu
          100          105          110
Glu Ile Ala Arg Phe Gly Ser Ile Ala Lys Ser Ala Pro Val Phe Ala
          115          120          125
Ala Phe Phe Met Ile Val Leu Met Ala Asn Val Gly Met Pro Leu Ser
          130          135          140
Ile Gly Phe Val Gly Glu Phe Leu Asn Leu Leu Gly Phe Phe Ala Thr
145          150          155          160
Tyr Pro Leu Leu Ala Ile Ile Ala Gly Thr Ser Leu Ile Leu Ser Ala
          165          170          175
Val Tyr Ile Leu Thr.Ser Tyr Lys Asp Val Phe Phe Gly Asn Leu Lys
          180          185          190
Thr Gly Asn Asn Gln Ile Ser Val Phe Glu Asp Leu Asn Ala Arg Glu
          195          200          205
Val Gly Val Leu Ser Val Ile Leu Ala Phe Asp Leu Asn Phe Arg Asp
210          215          220
Leu Tyr Lys Ser Ala Phe Lys Thr Asp
225          230

```

(2) INFORMATION FOR SEQ ID NO:504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...32

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504

```

Val Glu Leu Ile Ser Asn Asn Pro Asn Ala Ser Gln Gln Ser Ile Val
1          5          10          15
Ile Pro Leu Glu Thr Phe Ala Leu Ala Arg Ala Leu Lys Gly Ile Phe
          20          25          30

```

(2) INFORMATION FOR SEQ ID NO:505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

420

(B) LOCATION 1...171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505

```

Met Lys Ile Phe Gly Thr Asp Gly Val Arg Gly Lys Ala Gly Val Lys
1      5      10      15
Leu Thr Pro Met Phe Val Met Arg Leu Gly Ile Ala Ala Gly Leu Tyr
      20      25      30
Phe Lys Lys His Ser Gln Thr Asn Lys Ile Leu Ile Gly Lys Asp Thr
      35      40      45
Arg Lys Ser Gly Tyr Met Val Glu Asn Ala Leu Val Ser Ala Leu Thr
      50      55      60
Ser Ile Gly Tyr Asn Val Ile Gln Ile Gly Pro Met Pro Thr Pro Ala
65      70      75      80
Ile Ala Phe Leu Thr Glu Asp Met Arg Cys Asp Ala Gly Ile Met Ile
      85      90      95
Ser Ala Ser His Asn Pro Phe Glu Asp Asn Gly Ile Lys Phe Phe Asn
      100     105     110
Ser Tyr Gly Tyr Lys Leu Lys Glu Glu Glu Glu Arg Ala Ile Glu Glu
      115     120     125
Ile Phe His Asp Glu Glu Leu Leu His Ser Ser Tyr Lys Val Gly Glu
130     135     140
Ser Val Gly Ser Ala Lys Arg Ile Asp Asp Val Ile Gly Pro Leu Tyr
145     150     155     160
Arg Ala Phe Glu Ala Leu Tyr Thr Gln Thr Phe
      165     170

```

(2) INFORMATION FOR SEQ ID NO:506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506

```

Val Arg Ala Val Phe Val Phe Gly Leu Lys Ala Ala Phe Cys Ile Gly
1      5      10      15
Ile Phe Phe Tyr Gly Ala Tyr Tyr Phe Leu Asp Glu Phe Leu Ile Lys
      20      25      30
Leu

```

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

421

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...99

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507

```

Met Lys Glu Gln Glu Trp Asp Leu Ser Ala Leu Phe Glu Asn Lys Glu
1           5           10           15
Ser Ala Glu Glu Phe Leu Lys Thr Leu Gln Thr Glu Val Gln Glu Phe
          20           25           30
Glu Asn Ala Tyr Gln Asn Asn Leu Lys Asn Leu Asp Ala Ala Lys Phe
          35           40           45
Ala Asn Thr Leu Lys His Tyr Glu Asn Leu Ser Glu Lys Ile Ser Arg
          50           55           60
Ala Met Ala Tyr Ala Asn Tyr Phe Leu Pro Arg Thr Leu Lys Lys Arg
65           70           75           80
Ser Phe Ile Arg Asn Ala Asn Gly Leu Cys Lys Tyr Pro Thr Thr Pro
          85           90           95
Phe Ile Leu

```

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...99

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507

```

Met Lys Glu Gln Glu Trp Asp Leu Ser Ala Leu Phe Glu Asn Lys Glu
1           5           10           15
Ser Ala Glu Glu Phe Leu Lys Thr Leu Gln Thr Glu Val Gln Glu Phe
          20           25           30
Glu Asn Ala Tyr Gln Asn Asn Leu Lys Asn Leu Asp Ala Ala Lys Phe
          35           40           45
Ala Asn Thr Leu Lys His Tyr Glu Asn Leu Ser Glu Lys Ile Ser Arg
          50           55           60
Ala Met Ala Tyr Ala Asn Tyr Phe Leu Pro Arg Thr Leu Lys Lys Arg
65           70           75           80
Ser Phe Ile Arg Asn Ala Asn Gly Leu Cys Lys Tyr Pro Thr Thr Pro
          85           90           95
Phe Ile Leu

```

(2) INFORMATION FOR SEQ ID NO:508:

SUBSTITUTE SHEET (RULE 26)

422

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...78

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508

```

Leu Arg Val Gly Met Tyr Glu Val Cys Asn His Lys Asp Gly Thr Ala
1      5      10      15
Tyr His Ser Thr Arg Gly Ser Lys Val Thr Leu Ala Cys Lys Thr Gly
      20      25      30
Thr Ala Gln Val Val Glu Ile Ala Gln Asn Ile Val Asn Arg Met Lys
      35      40      45
Glu Lys Asp Met Glu Tyr Phe His Unk Ser His Unk Trp Ile Thr Unk
      50      55      60
Tyr Leu Unk Pro Met Lys Asn Pro Asn Thr Leu Ser Leu Phe
65      70      75

```

(2) INFORMATION FOR SEQ ID NO:508:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...78

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508

```

Leu Arg Val Gly Met Tyr Glu Val Cys Asn His Lys Asp Gly Thr Ala
1      5      10      15
Tyr His Ser Thr Arg Gly Ser Lys Val Thr Leu Ala Cys Lys Thr Gly
      20      25      30
Thr Ala Gln Val Val Glu Ile Ala Gln Asn Ile Val Asn Arg Met Lys
      35      40      45
Glu Lys Asp Met Glu Tyr Phe His Unk Ser His Unk Trp Ile Thr Unk
      50      55      60
Tyr Leu Unk Pro Met Lys Asn Pro Asn Thr Leu Ser Leu Phe
65      70      75

```

(2) INFORMATION FOR SEQ ID NO:509:

- (i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

423

- (A) LENGTH: 70 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509

```

Val Arg Ser Gly Lys Arg Leu Gly Tyr Thr Asn Gln Val Ile Thr Asp
1      5      10      15
Ile Val Asn Ile Gly Ile Gly Gly Ser Asp Leu Gly Ala Leu Met Val
20     25     30
Cys Thr Ala Leu Lys Arg Tyr Gly His Pro Arg Leu Lys Met His Phe
35     40     45
Val Ser Asn Val Glu Trp His Ala Asp Phe Arg Arg Phe Gly Lys Asn
50     55     60
Gln Pro Gly Gln Arg Ala
65     70
  
```

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510

```

Met Asn Leu Val Phe Leu Trp Ala Ala Leu Gly Gly Ala Ile Gly Ser
1      5      10      15
Ser Leu Arg Tyr Phe Val Gly Lys Met Met Pro Ser Lys Phe Leu Met
20     25     30
Phe Glu Ser Phe Pro Leu Gly Thr Phe Ser Val Asn Leu Ile Gly Cys
35     40     45
Phe Ile Ile Gly Phe Met Gly His Leu Ala Ala Lys Lys Val Phe Gly
50     55     60
Asp Asp Phe Gly Ile Phe Phe Val Thr Gly Val Leu Gly Gly Phe Thr
65     70     75     80
Thr Phe Ser Ser Tyr Gly Leu Asp Thr Leu Lys Leu Leu Gln Lys Ser
85     90     95
Gln Tyr Leu Glu Ala Ile Ser Tyr Val Leu Gly Thr Asn Leu Leu Gly
100    105    110
Leu Ile Gly Val Ala Ile Gly Trp Phe Leu Ala Lys Asn Phe Val Gly
115    120    125
  
```

SUBSTITUTE SHEET (RULE 26)

424

Val Asn
130

(2) INFORMATION FOR SEQ ID NO:511:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...52

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511

Leu	Gly	Leu	Val	Unk	Gly	Ile	Ser	Leu	Leu	His	Leu	Ser	Leu	Glu	Gln
1				5				10						15	
Lys	Ile	Ser	Val	Phe	Leu	Gly	Unk	Asn	Leu	Met	Leu	Tyr	Pro	Val	Unk
			20				25						30		
Glu	Val	Leu	Phe	Ser	Ile	Leu	Arg	Arg	Lys	Ile	Lys	Arg	Gln	Lys	Ala
		35				40						45			
Thr	His	Ala	Gly												
			50												

(2) INFORMATION FOR SEQ ID NO:511:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...52

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511

Leu	Gly	Leu	Val	Unk	Gly	Ile	Ser	Leu	Leu	His	Leu	Ser	Leu	Glu	Gln
1				5				10						15	
Lys	Ile	Ser	Val	Phe	Leu	Gly	Unk	Asn	Leu	Met	Leu	Tyr	Pro	Val	Unk
			20				25						30		
Glu	Val	Leu	Phe	Ser	Ile	Leu	Arg	Arg	Lys	Ile	Lys	Arg	Gln	Lys	Ala
		35				40						45			
Thr	His	Ala	Gly												
			50												

(2) INFORMATION FOR SEQ ID NO:512:

SUBSTITUTE SHEET (RULE 26)

425

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 79 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...79

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512

```

Met Leu Glu Lys Leu Ile Glu Arg Val Leu Phe Ala Thr Arg Trp Leu
1           5           10           15
Leu Ala Pro Leu Cys Ile Ala Met Ser Leu Val Leu Val Val Leu Gly
          20           25           30
Tyr Val Phe Met Lys Glu Leu Trp His Met Leu Ser His Leu Asn Thr
          35           40           45
Ile Ser Glu Thr Asp Leu Val Leu Ser Ala Leu Gly Leu Val Asp Leu
          50           55           60
Leu Val His Gly Arg Ala Cys Phe Asp Gly Ala Ala Arg Gln Leu
65           70           75

```

(2) INFORMATION FOR SEQ ID NO:513:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513

```

Met His Tyr Gln Leu Thr Ser Phe Asn Ile Ile Gln Asp Leu Phe Ile
1           5           10           15
Thr Cys His Val Leu Arg Ile Lys Met Arg Val Phe Val Cys Phe Leu
          20           25           30
Gly Val Phe Val Ser Asn Gly Leu Ala Arg Phe Gly Tyr Val Val Leu
          35           40           45
Ile Pro Leu Leu Ile Leu Ser Gly Ser Leu Thr Pro His Gln Ser Phe
          50           55           60
Gln Leu Gly Ile Ala Val Leu Met Gly Tyr Val Phe Gly Ser Phe Leu
65           70           75           80
Ile Gln Phe Leu Ser Pro Leu Met Ser Leu Lys Ser Ile Ala Lys Ile
          85           90           95
Ser Phe Lys Leu Thr Leu
          100

```

SUBSTITUTE SHEET (RULE 26)

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514

Val	Asp	Met	Lys	Asp	Ala	Val	Gly	Thr	Tyr	Lys	Leu	Unk	Arg	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515

Leu	Ala	Gln	Pro	Val	Gln	Val	Arg	Thr	Val	Phe	Met	Ser	Met	Thr	Leu
1				5					10					15	
Asn	Ala	Met	Gly	Gln	Phe	Ala	Tyr	Asn	Phe	Pro	Ala	Asn	Ile	Ser	Lys
			20					25					30		
Asp	Lys	Gln	Lys	Leu	Thr	Met	Val	Tyr	Met	Asp	Lys	Asp	Tyr	Gly	Ala
		35				40					45				
Tyr	Gly	Asn	Ile	Val	Ala	Met	Gly	Gly	Glu	Tyr	Val	Lys	Ile	Glu	Leu
	50				55					60					
Gly	Thr	Asp	Thr	Gly	Leu	Asn	Pro	Phe	Ala	Trp	Ala	Ala	Cys	Val	Gln
65				70					75					80	
Lys	Thr	Asn	Ala	Thr	Met	Glu	Gln	Lys	Gln	Thr	Ala	Ile	Ser	Val	Val
			85				90						95		
Lys	Glu	Leu	Val	Lys	Asn	Leu	Ala	Thr	Lys	Ser	Asp	Glu	Lys	Asp	Glu
		100				105						110			
Asn	Gly	Asn	Ser	Ile	Ser	Phe	Ser	Leu	Ala	Asp	Ser	Asn	Thr	Leu	Ala
		115				120					125				
Ala	Ala	Val	Thr	Asn	Leu	Ile	Thr	Gly	Asp	Met	Asn	Leu	Asp	Tyr	Pro
130				135							140				
Ile	Thr	Gln	Leu	Ile	Asn	Ala	Phe	Gly	Lys	Asp	His	Asn	Asp	Pro	Asn

427

```

145          150          155          160
Gly Leu Val Ala Arg Leu Ala Pro Phe Cys Lys Ser Thr Asn Gly Glu
          165          170          175
Phe Gln Trp Leu Phe Asp Asn Lys Ala Thr Asp Arg Leu Asp Phe Ser
          180          185          190
Lys Thr Ile Ile Gly Val Asp Gly Ser Ser Phe Leu Asp Asn Asn Asp
          195          200          205
Val Ser Pro Phe Ile Cys Phe Tyr Leu Phe Ala Arg Ile Gln Glu Ala
          210          215          220
Met Asp Gly Arg Arg Phe Val Leu Asp Ile Asp Glu Ala Trp Lys Tyr
          225          230          235
Leu Gly Asp Pro Lys Val Ala Tyr Phe Val Arg Asp Met Leu Lys Thr
          245          250          255
Ala Arg Lys Arg Asn Ala Ile Val Arg Leu Ala Thr Gln Ser Ile Thr
          260          265          270
Asp Leu Leu Ala Cys Pro Ile Ala Asp Thr Ile Arg Glu Gln Cys Pro
          275          280          285
Thr Lys Ile Phe Leu Arg Asn Asp Gly Gly Asn Leu Ser Asp Tyr Gln
          290          295          300
Arg Leu Ala Asn Val Thr Glu Lys Glu Phe Glu Ile Ile Thr Lys Gly
          305          310          315
Leu Asp Arg Lys Ile Leu Tyr Lys Gln Asp Gly Ser Pro Ser Val Ile
          325          330          335
Ala Ser Phe Asn Leu Arg Gly Ile Pro Lys Glu Tyr Leu Lys Ile Leu
          340          345          350
Ser Thr Asp Thr Val Phe Val Lys Glu Ile Asp Lys Ile Ile Gln Asn
          355          360          365
His Ser Ile Ile Asp Lys Tyr Gln Pro
          370          375

```

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515

```

Leu Ala Gln Pro Val Gln Val Arg Thr Val Phe Met Ser Met Thr Leu
1          5          10          15
Asn Ala Met Gly Gln Phe Ala Tyr Asn Phe Pro Ala Asn Ile Ser Lys
          20          25          30
Asp Lys Gln Lys Leu Thr Met Val Tyr Met Asp Lys Asp Tyr Gly Ala
          35          40          45
Tyr Gly Asn Ile Val Ala Met Gly Gly Glu Tyr Val Lys Ile Glu Leu
          50          55          60
Gly Thr Asp Thr Gly Leu Asn Pro Phe Ala Trp Ala Ala Cys Val Gln
          65          70          75          80
Lys Thr Asn Ala Thr Met Glu Gln Lys Gln Thr Ala Ile Ser Val Val
          85          90          95
Lys Glu Leu Val Lys Asn Leu Ala Thr Lys Ser Asp Glu Lys Asp Glu
          100          105          110

```

SUBSTITUTE SHEET (RULE 26)

428

```

Asn Gly Asn Ser Ile Ser Phe Ser Leu Ala Asp Ser Asn Thr Leu Ala
  115      120      125
Ala Ala Val Thr Asn Leu Ile Thr Gly Asp Met Asn Leu Asp Tyr Pro
  130      135      140
Ile Thr Gln Leu Ile Asn Ala Phe Gly Lys Asp His Asn Asp Pro Asn
  145      150      155      160
Gly Leu Val Ala Arg Leu Ala Pro Phe Cys Lys Ser Thr Asn Gly Glu
  165      170      175
Phe Gln Trp Leu Phe Asp Asn Lys Ala Thr Asp Arg Leu Asp Phe Ser
  180      185      190
Lys Thr Ile Ile Gly Val Asp Gly Ser Ser Phe Leu Asp Asn Asn Asp
  195      200      205
Val Ser Pro Phe Ile Cys Phe Tyr Leu Phe Ala Arg Ile Gln Glu Ala
  210      215      220
Met Asp Gly Arg Arg Phe Val Leu Asp Ile Asp Glu Ala Trp Lys Tyr
  225      230      235      240
Leu Gly Asp Pro Lys Val Ala Tyr Phe Val Arg Asp Met Leu Lys Thr
  245      250      255
Ala Arg Lys Arg Asn Ala Ile Val Arg Leu Ala Thr Gln Ser Ile Thr
  260      265      270
Asp Leu Leu Ala Cys Pro Ile Ala Asp Thr Ile Arg Glu Gln Cys Pro
  275      280      285
Thr Lys Ile Phe Leu Arg Asn Asp Gly Gly Asn Leu Ser Asp Tyr Gln
  290      295      300
Arg Leu Ala Asn Val Thr Glu Lys Glu Phe Glu Ile Ile Thr Lys Gly
  305      310      315      320
Leu Asp Arg Lys Ile Leu Tyr Lys Gln Asp Gly Ser Pro Ser Val Ile
  325      330      335
Ala Ser Phe Asn Leu Arg Gly Ile Pro Lys Glu Tyr Leu Lys Ile Leu
  340      345      350
Ser Thr Asp Thr Val Phe Val Lys Glu Ile Asp Lys Ile Ile Gln Asn
  355      360      365
His Ser Ile Ile Asp Lys Tyr Gln Pro
  370      375

```

(2) INFORMATION FOR SEQ ID NO:516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1027 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516

```

Val Cys Leu Asp His Gln Val Gly Ala Gly Lys Thr Leu Cys Ala Ile
  1           5           10           15
Ala Ser Cys Met Glu Gln Lys Arg Met Gly Leu Val Asn Lys Thr Leu
  20           25           30
Ile Ala Val Pro Asn His Leu Thr Lys Gln Trp Gly Asp Glu Phe Tyr
  35           40           45
Lys Ala Tyr Pro Asn Ala Asn Val Leu Val Val Asp Ser Lys Asp Thr
  50           55           60
Thr Glu Lys Glu Arg Glu Leu Leu Phe Asn Gln Ile Ala Asn Asn Asn

```

SUBSTITUTE SHEET (RULE 26)

429

65		70		75		80									
Tyr	Asp	Ala	Val	Val	Ile	Ala	His	Thr	His	Leu	Glu	Leu	Leu	Ser	Asn
			85						90					95	
Pro	Arg	Gly	Ile	Ile	Glu	Glu	Leu	Lys	Glu	Glu	Glu	Leu	Val	Asn	Ala
		100						105					110		
Glu	Lys	Asn	Phe	Glu	Arg	Gln	Glu	Leu	Ala	Tyr	Lys	Asn	Asn	Pro	Arg
		115					120					125			
Glu	Thr	Lys	Lys	Pro	Asn	Glu	Arg	Ala	Phe	Lys	Asn	Lys	Leu	Asp	Lys
		130				135					140				
Ile	Arg	Ala	Lys	Tyr	Asp	Ala	Ile	Leu	Glu	Lys	Gln	Gly	Ser	His	Ile
145				150						155				160	
Asp	Ile	Ser	Gln	Met	Gly	Ile	Asp	Asn	Leu	Ile	Val	Asp	Glu	Ala	His
			165					170					175		
Leu	Phe	Lys	Asn	Leu	Ala	Phe	Glu	Thr	Ser	Met	Glu	Lys	Ile	Ala	Gly
		180					185						190		
Leu	Gly	Asn	Gln	Gln	Gly	Ser	Asn	Arg	Ala	Arg	Asp	Leu	Phe	Ile	Lys
		195					200					205			
Thr	Arg	Tyr	Leu	His	Gln	Asn	Asp	Lys	Lys	Ile	Met	Phe	Leu	Thr	Gly
		210				215					220				
Thr	Pro	Ile	Ala	Asn	Ser	Leu	Ser	Glu	Met	Tyr	His	Leu	Gln	Arg	Tyr
225				230						235				240	
Leu	Thr	Pro	Asp	Val	Leu	Lys	Glu	Arg	Gly	Leu	Glu	Phe	Phe	Asp	Asp
			245						250				255		
Trp	Ala	Lys	Thr	Tyr	Gly	Glu	Val	Val	Asn	Asp	Phe	Glu	Leu	Asp	Thr
		260					265						270		
Ser	Ala	Gln	Ser	Tyr	Lys	Met	Val	Asn	Arg	Phe	Ser	Lys	Phe	Ser	Asp
		275				280					285				
Val	Gln	Gly	Leu	Ser	Thr	Met	Tyr	Arg	Ala	Phe	Ala	Asp	Ile	Val	Ser
		290				295					300				
Asn	Asp	Asp	Ile	Leu	Lys	His	Asn	Pro	His	Phe	Val	Pro	Lys	Val	Tyr
305				310						315				320	
Gly	Asp	Lys	Pro	Ile	Asn	Val	Val	Val	Lys	Arg	Ser	Glu	Glu	Val	Ala
			325						330				335		
Gln	Phe	Ile	Gly	Val	Ala	Leu	Glu	Asn	Gly	Lys	Tyr	Asn	Glu	Gly	Ser
		340					345						350		
Ile	Ile	Asp	Arg	Met	Gln	Lys	Cys	Glu	Gly	Lys	Lys	Ser	Gln	Lys	Gly
		355				360						365			
Gln	Asp	Asn	Ile	Leu	Ser	Cys	Thr	Thr	Asp	Ala	Arg	Lys	Val	Ala	Leu
		370				375					380				
Asp	Tyr	Arg	Leu	Ile	Asp	Pro	Asn	Ala	Lys	Val	Glu	Lys	Glu	Phe	Ser
385				390						395				400	
Lys	Ser	Tyr	Ala	Met	Ala	Lys	Asn	Ile	Tyr	Glu	Asn	Tyr	Leu	Glu	Thr
			405						410				415		
His	Ala	Thr	Lys	Gly	Thr	Gln	Leu	Gly	Phe	Ile	Gly	Leu	Ser	Thr	Pro
			420				425						430		
Lys	Thr	His	Ser	Gln	Lys	Val	Ser	Leu	Glu	Ala	Leu	Asp	Asn	Ala	His
		435				440						445			
Glu	Thr	Glu	Asn	Lys	Asn	Pro	Leu	Asp	Lys	Ala	Gln	Glu	Leu	Leu	Glu
		450				455					460				
Ser	Leu	Ser	Ser	Tyr	Asp	Glu	Lys	Gly	Asn	Leu	Ile	Ala	Pro	Ser	Lys
465				470						475				480	
Lys	Glu	Leu	Glu	Asn	Glu	Leu	Lys	Glu	Lys	Glu	Ala	Lys	Ser	Val	Asn
			485						490					495	
Leu	Asp	Glu	Glu	Ile	Ala	Lys	Gly	Cys	Ser	Phe	Asp	Val	Tyr	Ser	Asp
		500					505						510		
Val	Leu	Arg	His	Leu	Val	Gln	Met	Gly	Ile	Pro	Gln	Asn	Glu	Ile	Ala
		515					520					525			
Phe	Ile	His	Asp	Ala	Lys	Thr	Glu	Glu	Gln	Lys	Gln	Asp	Leu	Phe	Lys
		530				535					540				
Lys	Leu	Asn	Arg	Gly	Gly	Val	Arg	Val	Leu	Leu	Gly	Ser	Pro	Ala	Lys
545				550						555				560	
Met	Gly	Val	Gly	Thr	Asn	Val	Gln	Glu	Arg	Leu	Val	Ala	Met	His	Glu
			565						570					575	
Leu	Asp	Cys	Pro	Trp	Arg	Pro	Asp	Glu	Leu	Leu	Gln	Met	Glu	Gly	Arg
			580					585						590	

SUBSTITUTE SHEET (RULE 26)

430

Gly Ile Arg Gln Gly Asn Ile Leu His Gln Asn Asp Pro Glu Asn Phe
 595 600 605
 Arg Met Lys Ile Tyr Arg Tyr Ala Thr Glu Lys Thr Tyr Asp Ser Arg
 610 615 620
 Met Trp Gln Ile Ile Glu Thr Lys Ser Lys Gly Ile Glu Gln Phe Arg
 625 630 635 640
 Asn Ala His Lys Leu Gly Leu Asn Glu Leu Glu Asp Phe Asn Met Gly
 645 650 655
 Ser Ser Asn Ala Ser Glu Met Lys Ala Glu Ala Thr Gly Asn Pro Leu
 660 665 670
 Ile Ile Glu Glu Val Lys Leu Arg Ala Glu Ile Lys Ser Glu Glu Ser
 675 680 685
 Lys Tyr Lys Ala Phe Asn Lys Glu His Tyr Phe Asn Glu Glu Ser Leu
 690 695 700
 Lys Asn Asn Ala Ser Lys Leu Asp Tyr Leu Lys Gln Glu Leu Lys Asp
 705 710 715 720
 Leu Glu Thr Leu Gln Arg Ser Val Ile Ile Pro Thr His Thr Glu Ile
 725 730 735
 Lys Leu Tyr Asp Leu Lys Asn Glu Glu Ser Lys Asp Tyr Glu Leu Ile
 740 745 750
 Lys Val Lys Glu Val Glu Pro Leu Lys Glu Asn Ala Ser Met Ser Glu
 755 760 765
 Glu Leu Thr His Lys Lys Leu Lys Glu Gln Asn Lys Gln Ile Ala Glu
 770 775 780
 Gln Asn Lys Glu Lys Leu Asp Ala Ile Lys Lys Gln Phe Ala Ser Asn
 785 790 795 800
 Leu Asn Thr Leu Phe Val Asn Glu Glu Glu Asp Tyr Lys Leu Leu Glu
 805 810 815
 Tyr Lys Gly Phe Val Val Asn Ala Tyr Lys Thr Lys Tyr Gln Val Glu
 820 825 830
 Phe Ser Leu Ser Pro Lys Asp Asn Pro Asn Ile Ala Tyr Ser Pro Ser
 835 840 845
 Asn Met Val Tyr Lys Asn Asp Thr Ile Asn Met Phe Ser Ser Tyr Asn
 850 855 860
 Phe Cys Ala Glu Ile Lys Phe Asp Gly Phe Leu Lys Arg Leu Asp Asn
 865 870 875 880
 Ala Ile Thr Lys Leu Pro Glu Lys Ile Lys Glu Leu Glu Asn Ser Ile
 885 890 895
 Glu Ile Thr Lys Lys Asn Ile Ala Lys Tyr Thr Arg Leu Val Glu Gln
 900 905 910
 Lys Pro Ser Tyr Pro Arg Leu Glu Tyr Leu Gln Ala Leu Lys Trp Asp
 915 920 925
 His Lys Thr Leu Ile Asp Asp Leu Ala Lys Met Ser Lys Asp Arg Asn
 930 935 940
 Tyr Lys Pro Ala Phe Asn Pro Lys Ser Lys Glu Val Leu Lys Asn Leu
 945 950 955 960
 Asn Ala Glu Lys Arg Ala Ser Leu Glu Asn Glu Arg Glu Glu Gln Gly
 965 970 975
 Val Lys Gly Asn Thr Lys Ser His Asp Glu Ile Glu Pro Ala Thr Glu
 980 985 990
 Gln Val Ile Glu Lys Glu Ile Glu Lys Gly Asp Glu Ile Ala Asn Asn
 995 1000 1005
 Val Asp Tyr Tyr Glu Asn Glu Gln Glu Val Glu Ile Thr Lys Ser Met
 1010 1015 1020
 Gly Arg Arg
 1025

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

431

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517

```

Met Lys Leu Val Ser Leu Ile Val Ala Leu Val Phe Cys Cys Phe Leu
1      5      10      15
Gly Ala Val Glu Leu Pro Gly Val Tyr Gln Thr Gln Glu Phe Leu Tyr
20      25      30
Met Lys Ser Ser Phe Val Glu Phe Phe Glu His Asn Gly Lys Phe Tyr
35      40      45
Ala Tyr Gly Ile Ser Asp Val Unk Unk Ser Lys Ala Lys Lys Asp Lys
50      55      60
Leu Asn Pro Asn Pro Lys Leu Arg Asn Arg Ser Asp Lys Gly Val Val
65      70      75      80
Phe Leu Ser Asp Leu Ile Lys Val Gly Glu Gln Ser Tyr Lys Gly Gly
85      90      95
Lys Ala Unk Asn Phe Unk Asp Gly Lys Thr Unk His Val Arg Val Thr
100     105     110
Gln Unk Ser Asn Gly Asp Leu Unk Phe Thr Ser Ser Tyr Unk Lys Trp
115     120     125
Gly Tyr Val Gly Lys Thr Phe Thr Trp Lys Arg Leu Ser Asp Glu Glu
130     135     140
Ile Lys Asn Leu Lys Leu Lys Arg Phe Asn
145     150

```

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517

```

Met Lys Leu Val Ser Leu Ile Val Ala Leu Val Phe Cys Cys Phe Leu
1      5      10      15
Gly Ala Val Glu Leu Pro Gly Val Tyr Gln Thr Gln Glu Phe Leu Tyr
20      25      30
Met Lys Ser Ser Phe Val Glu Phe Phe Glu His Asn Gly Lys Phe Tyr
35      40      45
Ala Tyr Gly Ile Ser Asp Val Unk Unk Ser Lys Ala Lys Lys Asp Lys
50      55      60
Leu Asn Pro Asn Pro Lys Leu Arg Asn Arg Ser Asp Lys Gly Val Val
65      70      75      80

```

SUBSTITUTE SHEET (RULE 26)

432

```

Phe Leu Ser Asp Leu Ile Lys Val Gly Glu Gln Ser Tyr Lys Gly Gly
      85          90          95
Lys Ala Unk Asn Phe Unk Asp Gly Lys Thr Unk His Val Arg Val Thr
      100        105        110
Gln Unk Ser Asn Gly Asp Leu Unk Phe Thr Ser Ser Tyr Unk Lys Trp
      115        120        125
Gly Tyr Val Gly Lys Thr Phe Thr Trp Lys Arg Leu Ser Asp Glu Glu
      130        135        140
Ile Lys Asn Leu Lys Leu Lys Arg Phe Asn
145          150

```

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...62

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518

```

Met Ala Glu Glu Glu Lys Thr Glu Leu Pro Ser Ala Lys Lys Ile Gln
1      5      10      15
Lys Ala Arg Glu Glu Gly Asn Val Pro Lys Ser Met Glu Val Val Gly
      20      25      30
Val Phe Arg Val Ile Gly Trp Ala Asn Glu Tyr Phe Cys Phe Phe Tyr
      35      40      45
Met Val Gly Gly Met Ala Leu Ala Arg Cys Ile Ala Met Cys
50          55          60

```

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519

```

Met Lys Thr Leu Val Lys Asn Thr Ile Tyr Ser Phe Leu Leu Leu Ser
1      5      10      15
Val Leu Met Ala Glu Asp Ile Thr Ser Gly Leu Lys Gln Leu Asp Asn

```

SUBSTITUTE SHEET (RULE 26)

433

```

      20      25      30
Thr Tyr Gln Glu Thr Asn Gln Gln Val Leu Lys Asn Leu Asp Glu Ile
      35      40      45
Phe Ser Thr Thr Ser Pro Ser Ala Asn Asn Lys Ile Gly Gln Glu Asp
      50      55      60
Ala Leu Asn Ile Lys Lys Ala Ala Ile Ala Leu Arg Gly Asp Leu Ala
      65      70      75      80
Leu Leu Lys Ala Asn Phe Glu Ala Asn Glu Leu Phe Phe Ile Ser Glu
      85      90      95
Asp Val Ile Phe Lys Thr Tyr Met Ser Ser Pro Glu Leu Leu Thr
      100      105      110
Tyr Met Lys Ile Asn Pro Leu Asp Gln Lys Thr Ala Glu Gln Gln Cys
      115      120      125
Gly Ile Ser Asp Lys Val Leu Val Leu Tyr Cys Glu Gly Lys Leu Lys
      130      135      140
Ile Glu Gln Glu Lys Gln Asn Ile Arg Glu Arg Leu Glu Thr Ser Leu
      145      150      155      160
Lys Ala Tyr Gln Ser Asn Ile Gly Gly Thr Ala Ser Leu Ile Thr Ala
      165      170      175
Ser Gln Thr Leu Val Glu Ser Leu Lys Asn Lys Asn Phe Ile Lys Gly
      180      185      190
Ile Lys Lys Leu Met Leu Ala His Asn Lys Val Phe Leu Asn Tyr Leu
      195      200      205
Glu Glu Leu Asp Ala Leu Glu Arg Ser Leu Glu Gln Ser Lys Arg Gln
      210      215      220
Tyr Leu Gln Glu Arg Gln Ser Ser Lys Ile Ile Val Lys
      225      230      235

```

(2) INFORMATION FOR SEQ ID NO:520:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 83 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520

```

Val Ser Glu Lys Asp Arg Ala Phe Leu Leu Ala Ser Leu Ser Cys Val
1      5      10      15
Asp Tyr Val Val Val Phe Gly Glu Asp Thr Pro Ile Lys Leu Ile Gln
      20      25      30
Ala Leu Lys Pro Asp Ile Leu Val Lys Gly Ala Asp Tyr Leu Asn Lys
      35      40      45
Glu Val Ile Gly Ser Glu Leu Ala Lys Glu Thr Arg Leu Ile Glu Phe
      50      55      60
Glu Glu Gly Tyr Ser Thr Ser Ala Ile Ile Glu Lys Ile Lys Arg Thr
      65      70      75      80
His Asn Asp

```

(2) INFORMATION FOR SEQ ID NO:521:

SUBSTITUTE SHEET (RULE 26)

434

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...7

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:521

Leu Glu Thr Leu Phe Leu Val
1 5

(2) INFORMATION FOR SEQ ID NO:521:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...7

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:521

Leu Glu Thr Leu Phe Leu Val
1 5

(2) INFORMATION FOR SEQ ID NO:522:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...64

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:522

SUBSTITUTE SHEET (RULE 26)

435

```

Val Tyr Asp Lys Ser Leu Cys Lys Thr Met Ala Leu Ala Leu Lys Ala
1      5      10      15
Leu Gly Val Lys Arg Ala Met Val Val Asn Gly Gly Gly Thr Gly Glu
      20      25      30
Ile Val Leu His Asp Ile Thr His Ala Cys Glu Leu Lys Asn Asn Glu
      35      40      45
Ile Leu Glu Tyr Asp Leu Ser Ala Lys Asp Phe Asp Leu Pro Pro Ser
      50      55      60

```

(2) INFORMATION FOR SEQ ID NO:523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523

```

Met Leu Val Glu Ile Glu Asn Leu Thr Lys Thr Tyr Gly Ser Leu Lys
1      5      10      15
Ala Leu Asp Asn Ile Ser Leu Lys Leu Pro Lys Gln Gln Phe Ile Gly
      20      25      30
Leu Leu Gly Pro Asn Gly Ala Gly Lys Thr Thr Leu Leu Lys Ile Leu
      35      40      45
Ala Gly Leu Asn Leu Asn Tyr Gln Gly Glu Val Lys Ile Leu Asn Gln
      50      55      60
Lys Ile Gly Ile Glu Thr Lys Lys Ser Val Ala Phe Leu Ser Asp Gly
      65      70      75      80
Asp Phe Leu Asp Pro Lys Leu Thr Pro Leu Lys Ala Ile Ala Phe Tyr
      85      90      95
Lys Asp Phe Phe Ser Asp Phe Asp Glu Ser Lys Ala Leu Asn Leu Leu
      100      105      110
Lys Arg Phe Ser Val Pro Leu Lys Arg Glu Phe Lys Ala Leu Ser Lys
      115      120      125
Gly Met Arg Glu Lys Leu Gln Leu Ile Leu Thr Leu Ser Arg Asn Ala
      130      135      140
Ser Leu Tyr Leu Phe Asp Glu Pro Val Ala Gly Ile Asp Pro Ile Ala
      145      150      155      160
Arg Glu Glu Ile Phe Glu Leu Ile Ala Lys Glu Phe Ser Gln Asn Ala
      165      170      175
Ser Leu Leu Val Ser Thr His Leu Val Val Asp Val Glu Lys Tyr Leu
      180      185      190
Asp Ser Ala Ile Phe Leu Lys Glu Ala Lys Val Val Ala Phe Gly Asp
      195      200      205
Val Gly Glu Leu Lys Lys Gly Tyr Ser Ser Leu Glu Ala Ala Tyr Lys
      210      215      220
Glu Arg Leu Lys
225

```

(2) INFORMATION FOR SEQ ID NO:524:

SUBSTITUTE SHEET (RULE 26)

436

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 273 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524

```

Met Asn Lys Leu Phe Leu Ala Phe Ile Val Gly Gly Met Leu Leu Ser
1      5      10      15
Ala Asp Ala Leu Asn Asp Lys Ile Glu Asn Leu Met Gly Glu Arg Ser
20     25     30
Tyr His Met Asn Lys Leu Phe Leu Glu Arg Leu Phe Lys Asn Arg Lys
35     40     45
Asp Phe Tyr Glu Met Gly Arg Leu Asp Ser Leu Lys Leu Leu Asn Thr
50     55     60
Leu Lys Glu Asn Gly Leu Leu Ser Phe Asn Phe Asp Lys Pro Ser Val
65     70     75     80
Leu Lys Ile Thr Phe Lys Ala Ser Ser Asn Pro Leu Ala Phe Ala Lys
85     90     95
Ser Ile Asn Asn Ser Leu Asn Met Met Gly Tyr Ser Tyr Val Leu Pro
100    105    110
Ile Arg Met Gln Ser Ser Ser Gly Glu Asn Val Phe Ser Tyr Glu Leu
115    120    125
Lys Thr Glu Tyr Val Leu Asp Pro Asn Ile Leu Ile Glu Thr Met Lys
130    135    140
Arg His Gly Phe Asp Phe Met Asp Ile Arg Arg Val Ser Leu Lys Glu
145    150    155    160
Trp Glu Tyr Asp Phe Ala Leu Gln Lys Ile Lys Leu Pro Asn Ala Arg
165    170    175
Ala Leu Val Leu Ser Ser Asp Pro Val Glu Phe Lys Glu Ala Ser Gly
180    185    190
Lys Tyr Trp Leu Ser Val Asn Gln Asn Ala Tyr Leu Lys Ile Ser Ser
195    200    205
Asn Asn Pro Leu Trp Gln Pro Lys Ile Ile Phe Tyr Asp Glu Asn Leu
210    215    220
Lys Ile Ile Gln Ile Ile Ala Lys Glu Asn Arg Gln Gln Glu Ile Ala
225    230    235    240
Leu Asn Leu Leu Asp Gly Val Arg Phe Ile His Ile Thr Asp Ala Lys
245    250    255
Asn Pro Ile Ile Leu Lys Asn Gly Ile Ser Val Val Phe Asp Ala Met
260    265    270
Pro

```

(2) INFORMATION FOR SEQ ID NO:525:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

437

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525

Val	Ser	Arg	Pro	Phe	Lys	Thr	Ile	Lys	Lys	Pro	Pro	Gln	Pro	Pro
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:526:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526

Met	Unk	Thr	His	Asp	Arg	Arg	Lys	Leu	Arg	Ile	Unk	Leu	Thr	Gln	Thr
1			5					10					15		
Thr	Thr	Leu	Val	Ala	Thr	Ile	Gly	Ser	Asn	Ala	Pro	Tyr	Ile	Gly	Leu
		20					25					30			
Leu	Gly	Thr	Val	Met	Gly	Ile	Met	Leu	Thr	Phe	Met	Asp	Leu	Gly	Ser
		35				40					45				
Ala	Ser	Gly	Ile	Asp	Thr	Lys	Ala	Ile	Met	Thr	Asn	Leu	Ala	Leu	Ala
	50				55					60					
Leu	Lys	Ala	Thr	Gly	Met	Gly	Leu	Leu	Val	Ala	Ile	Pro	Ala	Ile	Val
65				70				75						80	
Ile	Tyr	Asn	Leu	Leu	Val	Arg	Lys	Ser	Glu	Ile	Leu	Val	Thr	Lys	Trp
		85				90						95			
Asp	Ile	Phe	His	His	Pro	Val	Asp	Thr	Gln	Ser	His	Glu	Val	Tyr	Ser
		100				105						110			
Lys	Ala														

(2) INFORMATION FOR SEQ ID NO:526:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

SUBSTITUTE SHEET (RULE 26)

438

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526

```

Met Unk Thr His Asp Arg Arg Lys Leu Arg Ile Unk Leu Thr Gln Thr
1          5          10          15
Thr Thr Leu Val Ala Thr Ile Gly Ser Asn Ala Pro Tyr Ile Gly Leu
          20          25          30
Leu Gly Thr Val Met Gly Ile Met Leu Thr Phe Met Asp Leu Gly Ser
          35          40          45
Ala Ser Gly Ile Asp Thr Lys Ala Ile Met Thr Asn Leu Ala Leu Ala
          50          55          60
Leu Lys Ala Thr Gly Met Gly Leu Leu Val Ala Ile Pro Ala Ile Val
65          70          75          80
Ile Tyr Asn Leu Leu Val Arg Lys Ser Glu Ile Leu Val Thr Lys Trp
          85          90          95
Asp Ile Phe His His Pro Val Asp Thr Gln Ser His Glu Val Tyr Ser
          100          105          110
Lys Ala

```

(2) INFORMATION FOR SEQ ID NO:527:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...67

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527

```

Met Ile Ala Val Leu Pro Pro Leu Phe Ser Met Gly Ser Phe Asp Glu
1          5          10          15
Trp Ile Tyr Arg Gly Leu Val Ala Leu Met Val Ser Cys Pro Cys Ala
          20          25          30
Leu Val Ile Ser Val Pro Leu Gly Tyr Phe Gly Gly Val Gly Ala Ala
          35          40          45
Ser Arg Lys Gly Ile Leu Met Lys Gly Val His Val Leu Glu Gly Ala
          50          55          60
Tyr Pro Asn
65

```

(2) INFORMATION FOR SEQ ID NO:528:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 323 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

439

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...323

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528

```

Val Gln His Phe Asn Phe Leu Tyr Lys Asp Ser Leu Phe Ser Ile Ala
1          5          10          15
Leu Phe Thr Phe Ile Ile Ala Leu Val Ile Leu Leu Glu Gln Ala Arg
20          25          30
Ala Tyr Phe Thr Arg Lys Arg Asn Lys Lys Phe Leu Gln Lys Phe Ala
35          40          45
Gln Asn Gln Asn Ala Tyr Ala Ser Ser Glu Asn Leu Asp Glu Leu Leu
50          55          60
Lys His Ala Lys Ile Ser Ser Leu Met Phe Leu Ala Arg Ala Tyr Ser
65          70          75          80
Lys Ala Asp Val Glu Met Ser Ile Glu Ile Leu Lys Gly Leu Leu Asn
85          90          95
Arg Pro Leu Lys Asp Glu Glu Lys Ile Ala Val Leu Asp Leu Leu Ala
100          105          110
Lys Asn Tyr Phe Ser Val Gly Tyr Leu Gln Lys Thr Lys Asp Thr Val
115          120          125
Lys Glu Ile Leu Arg Phe Ser Pro Arg Asn Val Glu Ala Leu Leu Lys
130          135          140
Leu Leu His Ala Tyr Glu Leu Glu Lys Asp Tyr Ser Lys Ala Leu Glu
145          150          155          160
Thr Leu Glu Cys Leu Glu Glu Leu Glu Val Pro Lys Ile Glu Thr Ile
165          170          175
Lys Asn Tyr Leu Tyr Leu Met His Leu Ile Glu Asn Lys Glu Asp Ala
180          185          190
Ala Lys Ile Leu His Val Ser Lys Ala Ser Leu Asp Leu Lys Lys Ile
195          200          205
Ala Leu Asn His Leu Lys Ser His Asp Glu Asn Leu Phe Trp Gln Glu
210          215          220
Ile Asp Thr Thr Glu Arg Leu Glu Asn Val Ile Asp Leu Leu Trp Asp
225          230          235          240
Met Asn Ile Pro Ala Phe Ile Leu Glu Lys His Ala Leu Leu Gln Asp
245          250          255
Ile Ala Arg Ser Gln Gly Leu Leu Leu Asp His Lys Pro Cys Gln Ile
260          265          270
Phe Glu Leu Glu Val Leu Arg Ala Leu Leu His Ser Pro Ile Lys Ala
275          280          285
Ser Leu Thr Phe Glu Tyr Arg Cys Lys His Cys Lys Gln Ile Phe Pro
290          295          300
Phe Glu Ser His Arg Cys Pro Val Cys Tyr Gln Leu Ala Phe Met Asp
305          310          315          320
Met Val Ala

```

(2) INFORMATION FOR SEQ ID NO:529:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

440

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529

Met	Glu	His	Leu	Thr	Arg	Gly	Ile	Lys	His
1				5					10

(2) INFORMATION FOR SEQ ID NO:530:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530

Val	Val	Ile	Leu	Gly	Ser	His	Gly	Lys	Glu	Glu	Tyr
1				5							10

(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...79

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531

Met	Lys	Lys	Val	Ile	Val	Ala	Leu	Gly	Val	Leu	Ala	Phe	Ala	Asn	Val
1				5					10					15	
Leu	Met	Ala	Thr	Asp	Val	Lys	Ala	Leu	Val	Lys	Gly	Cys	Ala	Ala	Cys
			20					25						30	
His	Gly	Val	Lys	Phe	Glu	Lys	Lys	Ala	Leu	Gly	Lys	Ser	Lys	Ile	Val

SUBSTITUTE SHEET (RULE 26)

441

```

      35          40          45
Asn Met Met Ser Glu Lys Glu Ile Glu Glu Asp Leu Met Ala Phe Lys
 50          55          60
Ser Gly Ala Asn Lys Asn Pro Val Met Thr Arg Lys Leu Lys Asn
65          70          75

```

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532

```

Met Gly Ile Ala Thr Ser Leu Ile Ser Glu Val Ser Lys Phe Tyr Tyr
1          5          10          15
Ala Leu Lys Tyr His Ala Lys Phe Met Ser Leu Gly Glu Leu Gly Cys
 20          25          30
Tyr Ala Ser His Tyr Ser Leu Trp Gln Lys Cys Ile Glu Leu Asn Glu
 35          40          45
Ala Ile Cys Ile Leu Glu Asp Asp Ile Thr Leu Lys Glu Asp Phe Lys
 50          55          60
Glu Gly Leu Asp Phe Leu Glu Lys His Ile Gln Glu Leu Gly Tyr Ala
65          70          75          80
Arg Leu Met His Leu Leu Tyr Asp Ala Ser Val Lys Ser Glu Pro
      85          90          95

```

(2) INFORMATION FOR SEQ ID NO:533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533

```

Met His Leu Lys Ser Gly Ala Val Phe Ile Ser Asp Ala His Phe Leu
1          5          10          15
Pro Lys Ser Pro His Leu Ile His Thr Leu Lys Glu Leu Leu Ser Ala
 20          25          30

```

SUBSTITUTE SHEET (RULE 26)

442

```

Lys Pro Pro Gln Val Phe Phe Met Gly Asp Ile Phe His Val Leu Val
   35           40           45
Gly Tyr Leu Pro Leu Asp Lys Glu Gln Gln Lys Ile Ile Asp Leu Ile
   50           55           60
His Ala Leu Ser Glu Ile Ser Gln Val Phe Tyr Phe Glu Gly Asn His
   65           70           75           80
Asp Phe Ser Met Arg Phe Val Phe Asn Ser Lys Val Met Val Phe Glu
           85           90           95
Arg Gln Asn Gln Pro Ala Leu Phe Gln Tyr Asp Asn Lys Arg Phe Leu
           100          105          110
Leu Ala His Gly Asp Leu Phe Ile Thr Lys Ala Tyr Glu Phe Tyr Ile
           115          120          125
Thr Gln Leu Thr Ser Thr Trp Ala Arg Phe Phe Leu Thr Phe Leu Asn
           130          135          140
Leu Leu Ser Phe Lys Thr Leu Tyr Pro Phe
145           150

```

(2) INFORMATION FOR SEQ ID NO:534:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 67 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...67

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534

```

Met Gln Asp Leu Asp Asn Asn Met Ser Leu Asp Thr Ala His Asn Thr
1       5           10           15
Leu Ser Ser Asn Gly Lys Asn Ile Thr Ile Ala Gly Val Val Lys Ala
       20           25           30
Leu Gln Lys Ile Gly Val Ser Ala Lys Gly Met Val Ser Ile Leu Gln
       35           40           45
Ala Leu Lys Lys Ser Gly Ala Ile Ser Ala Lys Trp Arg Tyr Tyr Asp
       50           55           60
Lys Gln Gln
65

```

(2) INFORMATION FOR SEQ ID NO:534:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 67 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

SUBSTITUTE SHEET (RULE 26)

443

(A) NAME/KEY: misc_feature
(B) LOCATION 1...67

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534

```

Met Gln Asp Leu Asp Asn Asn Met Ser Leu Asp Thr Ala His Asn Thr
1      5      10      15
Leu Ser Ser Asn Gly Lys Asn Ile Thr Ile Ala Gly Val Val Lys Ala
20      25      30
Leu Gln Lys Ile Gly Val Ser Ala Lys Gly Met Val Ser Ile Leu Gln
35      40      45
Ala Leu Lys Lys Ser Gly Ala Ile Ser Ala Lys Trp Arg Tyr Tyr Asp
50      55      60
Lys Gln Gln
65

```

(2) INFORMATION FOR SEQ ID NO:535:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 313 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535

```

Val Gln Pro Met Lys Ser Lys Lys Leu Tyr Leu Ala Leu Ile Ile Gly
1      5      10      15
Val Leu Leu Ala Phe Leu Thr Leu Ser Ser Trp Leu Gly Asn Ser Gly
20      25      30
Leu Val Gly Arg Phe Gly Val Trp Phe Ala Ala Ile Asn Lys Lys Tyr
35      40      45
Phe Gly Tyr Leu Ser Leu Ile Asn Leu Pro Tyr Leu Ala Trp Val Leu
50      55      60
Phe Leu Leu Tyr Arg Ala Lys Asn Pro Phe Thr Glu Ile Val Leu Glu
65      70      75      80
Lys Thr Leu Gly His Leu Leu Gly Ile Leu Ser Leu Leu Phe Leu Gln
85      90      95
Ser Ser Leu Leu Asn Gln Gly Glu Ile Gly Asn Ser Ala Arg Leu Phe
100      105      110
Leu His Pro Phe Ile Gly Asp Phe Gly Leu Tyr Val Leu Ile Met Leu
115      120      125
Met Val Val Ile Ser Tyr Leu Ile Leu Phe Lys Leu Pro Pro Lys Ser
130      135      140
Val Phe Tyr Pro Tyr Met Asn Lys Thr Gln Ser Leu Leu Lys Glu Ile
145      150      155      160
Tyr Lys Gln Cys Leu Gln Ala Phe Ser Pro Asn Phe Ser Leu Lys Lys
165      170      175
Glu Gly Phe Glu Asn Thr Pro Ser Asp Ser Gln Lys Lys Glu Thr Asn
180      185      190
Asn Asp Lys Glu Lys Glu Asn Leu Lys Glu Asn Pro Ile Asp Glu Asn
195      200      205
His Asn Thr Pro Asn Glu Glu Ser Phe Leu Ala Ile Pro Thr Pro Tyr
210      215      220

```

SUBSTITUTE SHEET (RULE 26)

444

```

Asn Thr Thr Leu Asn Asn Ser Glu Pro Gln Glu Gly Leu Val Gln Ile
225                230                235                240
Ser Pro His Pro Pro Thr His Tyr Thr Ile Tyr Pro Lys Arg Asn Arg
                245                250                255
Phe Asp Asp Leu Thr Asn Pro Thr Leu Lys Glu Pro Lys Gln Glu Thr
                260                265                270
Lys Glu Arg Glu Pro Thr Leu Lys Lys Glu Thr Pro Thr Thr Leu Lys
                275                280                285
Pro Ile Met Pro Ile Ser Ala Ser Thr Gln Lys Ile Met Thr Lys Gln
                290                295                300
Lys Thr Thr Lys Pro Leu Thr Thr Pro
305                310

```

(2) INFORMATION FOR SEQ ID NO:536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536

```

Val Met Leu Ser Arg Asp Ile Val Gln Tyr Ser Lys Ile Arg Thr Glu
1                5                10                15
Leu Tyr Ala Tyr Leu Thr Tyr Leu Phe Ser His Asn Ile Arg Asn His
                20                25                30
Leu Pro Glu Ile Thr Leu Asp Tyr Leu Asn Arg Gln Ile Ser Lys Met
                35                40                45
Gln Ala Glu Ile Lys Met Ala Lys Ser Phe Phe Val Leu Asp Ala Lys
                50                55                60
Gly Met Leu Met Leu Lys Pro Ser Gln Phe Lys Glu Gln Gly His Lys
                65                70                75                80
Glu Gly Leu Leu Glu His Asp Leu Thr Glu Gly Ile Glu Leu Glu Ser
                85                90                95
His Val Ser Phe Ser Asp Lys Tyr Tyr Phe Tyr Gln Ala Val Asn Glu
                100               105               110
Lys Arg Cys Ile Leu Thr Asp Pro Tyr Pro Ser Lys Lys Gly Asn His
                115               120               125
Leu Val Val Ser Ala Ser Tyr Pro Val Tyr Asp Gln Asn Asn Asp Leu
                130               135               140
Ala Phe Val Val Cys Leu Gln Ile Pro Leu Arg Val Ala Ile Glu Ile
                145               150               155               160
Ser Ser Pro Ser Lys Tyr Phe Lys Thr Phe Ser Glu Gly Ser Met Val
                165               170               175
Met Tyr Phe Met Ile Ser Ile Met Leu Thr Leu Val Ser Leu Leu Leu
                180               185               190
Phe Val Lys Cys Ile Ser Ser Phe Trp Thr Ala Ile Val His Phe Ser
                195               200               205
Ser Phe Asp Ile Lys Glu Val Phe His Pro Ile Val Leu Leu Thr Leu
                210               215               220
Ala Leu Ala Thr Phe Asp Leu Val Lys Ala Ile Phe Glu Glu Glu Val
                225               230               235               240
Leu Gly Lys Asn Ser Gly Asp Asn His His Ala Ile His Arg Thr Met

```

SUBSTITUTE SHEET (RULE 26)